

SEQUENCE LISTING

<110> Dumas Milne Edwards, J.B.
Duclert A.
Giordano, J.Y.

<120> Expressed Sequence Tags and Encoded Human Proteins.

<130> GENSET.025CP1

<150> 09/057,719

<151> 1998-04-09

<150> 09/069,047

<151> 1998-04-28

<150> PCT/IB99/00712

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<160> 1622

<170> Patent.pm

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cgttcctgtt gagtacacgt tcctgttgat ttacaaaagg tgcaggtatg agcaggtctg      300
aagactaaca ttttgtgaag ttgtaaaaca gaaaacctgt tagaa atg tgg tgg ttt      357
                                     Met Trp Trp Phe
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cag caa ggc ctc agt ttc ctt cct tca gcc ctt gta att tgg aca tct      405
Gln Gln Gly Leu Ser Phe Leu Pro Ser Ala Leu Val Ile Trp Thr Ser
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 Asp Pro Ala Leu Pro Tyr Ile Ser Asp Thr Gly Thr Val Ala Pro Xaa
 20 25 30
 aaa tgc tta ttt ggg gca atg cta aat att gcg gca gtt tta tgt caa
 Lys Cys Leu Phe Gly Ala Met Leu Asn Ile Ala Ala Val Leu Cys Gln
 35 40 45
 aaa tagaaatcag gaarataatt caacttaaag aakttcattt catgaccaa
 Lys
 ctcttcaraa acatgtctttt acaagcatat ctcttgattt gctttctaca ctgttgaatt
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113

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Thr Ala Ile Leu Ala Val Ala Val Gly Phe Pro Val Ser Gln Asp Gln									
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gaa cga gaa aaa aga agt atc agt gac agc gat gaa tta gct tca ggr									209
Glu Arg Glu Lys Arg Ser Ile Ser Asp Ser Asp Glu Leu Ala Ser Gly									
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wtt ttt gtg ttc cct tac cca tat cca ttt cgc cca ctt cca cca att									257
Xaa Phe Val Phe Pro Tyr Pro Tyr Pro Phe Arg Pro Leu Pro Pro Ile									
			25					35	
cca ttt cca aga ttt cca tgg ttt aga cgt aan ttt cct att cca ata									305
Pro Phe Pro Arg Phe Pro Trp Phe Arg Arg Xaa Phe Pro Ile Pro Ile									
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cct gaa tct gcc cct aca act ccc ctt cct agc gaa aag taaacaaraa									354
Pro Glu Ser Ala Pro Thr Thr Pro Leu Pro Ser Glu Lys									
			60					65	
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caaaattcct gttaataaaaa raaaaacaaa tgtaattgaa atagcacaca gcattctcta									474
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Leu	Val	Thr	Ala	Ile	His	Ala	Glu	Leu	Cys	Gln	Pro	Gly	Ala	Glu	Asn	
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Ala	Phe	Lys	Val	Arg	Leu	Ser	Ile	Arg	Thr	Ala	Leu	Gly	Asp	Lys	Ala	
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tat	gcc	tgg	gat	acc	aat	gaa	gaa	tac	ctc	ttc	aaa	gcg	atg	gta	gct	196
Tyr	Ala	Trp	Asp	Thr	Asn	Glu	Glu	Tyr	Leu	Phe	Lys	Ala	Met	Val	Ala	
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Phe	Ser	Met	Arg	Lys	Val	Pro	Asn	Arg	Glu	Ala	Thr	Glu	Ile	Ser	His	
			45				50						55			
gtc	cta	ctt	tgc	aat	gta	acc	cag	agg	gta	tca	ttc	tgg	ttt	gtg	gtt	292
Val	Leu	Leu	Cys	Asn	Val	Thr	Gln	Arg	Val	Ser	Phe	Trp	Phe	Val	Val	
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Thr	Asp	Pro	Ser	Lys	Asn	His	Thr	Leu	Pro	Ala	Val	Glu	Val	Gln	Ser	
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gcc	ata	aga	atg	aac	aag	aac	cgg	atc	aac	aat	gcc	ttc	ttt	cta	aat	388
Ala	Ile	Arg	Met	Asn	Lys	Asn	Arg	Ile	Asn	Asn	Ala	Phe	Phe	Leu	Asn	
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gac	caa	act	ctg	gaa	ttt	tta	aaa	atc	cct	tcc	aca	ctt	gca	cca	ccc	436
Asp	Gln	Thr	Leu	Glu	Phe	Leu	Lys	Ile	Pro	Ser	Thr	Leu	Ala	Pro	Pro	
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Met	Asp	Pro	Ser	Val	Pro	Ile	Trp	Ile	Ile	Ile	Phe	Gly	Val	Ile	Phe	
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tgc	atc	atc	ata	gtt	gca	att	gca	cta	ctg	att	tta	tca	ggg	atc	tgg	532
Cys	Ile	Ile	Ile	Val	Ala	Ile	Ala	Leu	Leu	Ile	Leu	Ser	Gly	Ile	Trp	
	140					145					150					
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Pro	Leu	Asp	Met	Lys	Gly	Gly	His	Ile	Asn	Asp	Ala	Phe	Met	Thr	Glu	
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Asp	Glu	Arg	Leu	Thr	Pro	Leu										
			205													
attaaacatt	tgtttctgtg	tgactgctga	gcac	ctgaa	ataccaagag	cagatcatat										787
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<210> 7
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 Leu Leu Gly Leu Met Met Val Val Thr Gly Asp Glu Asp Glu Asn Ser
 -10 -5 1 5
 ccg tgt gcc cat gag gcc ctc ctg gac gag gac acc ctc ttt tgc cag 146
 Pro Cys Ala His Glu Ala Leu Leu Asp Glu Asp Thr Leu Phe Cys Gln
 10 15 20
 ggc ctt gaa gtt ttc tac cca gag ttg ggg aac att ggc tgc aag gtt 194
 Gly Leu Glu Val Phe Tyr Pro Glu Leu Gly Asn Ile Gly Cys Lys Val
 25 30 35
 gtt cct gat tgt aac aac tac aga cag aag atc acc tcc tgg atg gag 242
 Val Pro Asp Cys Asn Asn Tyr Arg Gln Lys Ile Thr Ser Trp Met Glu
 40 45 50
 ccg ata gtc aag ttc ccg ggg gcc gtg gac ggc gca acc tat atc ctg 290
 Pro Ile Val Lys Phe Pro Gly Ala Val Asp Gly Ala Thr Tyr Ile Leu
 55 60 65 70
 gtg atg gtg gat cca gat gcc cct agc aga gca gaa ccc aga cag aga 338
 Val Met Val Asp Pro Asp Ala Pro Ser Arg Ala Glu Pro Arg Gln Arg
 75 80 85
 ttc tgg aga cat tgg ctg gta aca gat atc aag ggc gcc gac ctg aag 386
 Phe Trp Arg His Trp Leu Val Thr Asp Ile Lys Gly Ala Asp Leu Lys
 90 95 100
 aaa ggg aag att cag ggc cag gag tta tca gcc tac cag gct ccc tcc 434
 Lys Gly Lys Ile Gln Gly Gln Leu Ser Ala Tyr Gln Ala Pro Ser
 105 110 115
 cca ccg gca cac agt ggc ttc cat cgc tac cag ttc ttt gtc tat ctt 482
 Pro Pro Ala His Ser Gly Phe His Arg Tyr Gln Phe Phe Val Tyr Leu
 120 125 130

cag gaa gga aag gtc atc tct ctc ctt ccc aag gaa aac aaa act cga	530
Gln Glu Gly Lys Val Ile Ser Leu Leu Pro Lys Glu Asn Lys Thr Arg	
135 140 145 150	
ggc tct tgg aaa atg gac aga ttt ctg aac cgt ttc cac ctg ggc gaa	578
Gly Ser Trp Lys Met Asp Arg Phe Leu Asn Arg Phe His Leu Gly Glu	
155 160 165	
cct gaa gca agc acc cag ttc atg acc cag aac tac cag gac tca cca	626
Pro Glu Ala Ser Thr Gln Phe Met Thr Gln Asn Tyr Gln Asp Ser Pro	
170 175 180	
acc ctc cag gct ccc aga gaa agg gcc agc gag ccc aag cac aaa aac	674
Thr Leu Gln Ala Pro Arg Glu Arg Ala Ser Glu Pro Lys His Lys Asn	
185 190 195	
cag gcg gag ata gct gcc tgc tagatagccg gctttgccat ccgggcatgt	725
Gln Ala Glu Ile Ala Ala Cys	
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15 20 25	
Phe Tyr Pro Glu Leu Gly Asn Ile Gly Cys Lys Val Val Pro Asp Cys	
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Asn Asn Tyr Arg Gln Lys Ile Thr Ser Trp Met Glu Pro Ile Val Lys	
45 50 55	
Phe Pro Gly Ala Val Asp Gly Ala Thr Tyr Ile Leu Val Met Val Asp	
60 65 70	
Pro Asp Ala Pro Ser Arg Ala Glu Pro Arg Gln Arg Phe Trp Arg His	
75 80 85 90	
Trp Leu Val Thr Asp Ile Lys Gly Ala Asp Leu Lys Lys Gly Lys Ile	
95 100 105	
Gln Gly Gln Glu Leu Ser Ala Tyr Gln Ala Pro Ser Pro Pro Ala His	
110 115 120	
Ser Gly Phe His Arg Tyr Gln Phe Phe Val Tyr Leu Gln Glu Gly Lys	
125 130 135	
Val Ile Ser Leu Leu Pro Lys Glu Asn Lys Thr Arg Gly Ser Trp Lys	
140 145 150	
Met Asp Arg Phe Leu Asn Arg Phe His Leu Gly Glu Pro Glu Ala Ser	
155 160 165 170	

Thr Gln Phe Met Thr Gln Asn Tyr Gln Asp Ser Pro Thr Leu Gln Ala
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 Ala Ala Cys
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 ctggacaagg attaagaatg tggatcaagc aggtttttaa atcaagattt aacattccaa 180
 cacataaaaa ttatttatcc aacagctcct cccagatcat atactcct atg aaa gga 237
 Met Lys Gly
 gga atc tcc aat gta tgg ttt gac aga ttt aaa ata acc aat gac tgc 285
 Gly Ile Ser Asn Val Trp Phe Asp Arg Phe Lys Ile Thr Asn Asp Cys
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 cca gaa cac ctt gaa tca att gat gtc atg tgt caa gtg ctt act gat 333
 Pro Glu His Leu Glu Ser Ile Asp Val Met Cys Gln Val Leu Thr Asp
 -65 -60 -55
 ttg att gat gaa gaa gta aaa agt ggc atc aag aag aac agg ata tta 381
 Leu Ile Asp Glu Val Lys Ser Gly Ile Lys Lys Asn Arg Ile Leu
 -50 -45 -40
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 Ile Gly Gly Phe Ser Met Gly Gly Cys Met Ala Met His Leu Ala Tyr
 -35 -30 -25
 aga aat cat caa gat gtg gca gga gta ttt gct ctt tct agt ttt ctg 477
 Arg Asn His Gln Asp Val Ala Gly Val Phe Ala Leu Ser Ser Phe Leu
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 aat aaa gca tct gct gtt tac cag gct ctt cag aag agt aat ggt gta 525
 Asn Lys Ala Ser Ala Val Tyr Gln Ala Leu Gln Lys Ser Asn Gly Val
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 ctt cct gaa tta ttt cag tgt cat ggt act gca gat gag tta gtt ctt 573
 Leu Pro Glu Leu Phe Gln Cys His Gly Thr Ala Asp Glu Leu Val Leu
 15 20 25
 cat tct tgg gca gaa gag aca aac tca atg tta aaa tct cta gga gtg 621
 His Ser Trp Ala Glu Glu Thr Asn Ser Met Leu Lys Ser Leu Gly Val
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 Thr Thr Lys Phe His Ser Phe Pro Asn Val Tyr His Glu Leu Ser Lys
 45 50 55

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gaa atg gaa aaa caa aaa tgaatgaatc aagagtgatt tgttaatgta      765
Glu Met Glu Lys Gln Lys
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Leu Thr Asp Leu Ile Asp Glu Glu Val Lys Ser Gly Ile Lys Lys Asn
      -55          -50          -45
Arg Ile Leu Ile Gly Gly Phe Ser Met Gly Gly Cys Met Ala Met His
      -40          -35          -30          -25
Leu Ala Tyr Arg Asn His Gln Asp Val Ala Gly Val Phe Ala Leu Ser
      -20          -15          -10
Ser Phe Leu Asn Lys Ala Ser Ala Val Tyr Gln Ala Leu Gln Lys Ser
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Asn Gly Val Leu Pro Glu Leu Phe Gln Cys His Gly Thr Ala Asp Glu
      10          15          20
Leu Val Leu His Ser Trp Ala Glu Glu Thr Asn Ser Met Leu Lys Ser
      25          30          35          40
Leu Gly Val Thr Thr Lys Phe His Ser Phe Pro Asn Val Tyr His Glu
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<222> 24..170

<223> score 5.6

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							-45					-40				
ctg	ccc	tgg	gag	gac	ggc	agg	tcc	ggg	ttg	ctc	tcc	ggc	ggc	ctc	cct	101
Leu	Pro	Trp	Glu	Asp	Gly	Arg	Ser	Gly	Leu	Leu	Ser	Gly	Gly	Leu	Pro	
			-35					-30						-25		
cgg	aag	tgt	tcc	gtc	ttc	cac	ctg	ttc	gtg	gcc	tgc	ctc	tcg	ctg	ggc	149
Arg	Lys	Cys	Ser	Val	Phe	His	Leu	Phe	Val	Ala	Cys	Leu	Ser	Leu	Gly	
			-20					-15						-10		
ttc	ttc	tcc	cta	ctc	tgg	ctg	cag	ctc	agc	tgc	tct	ggg	gac	gtg	gcc	197
Phe	Phe	Ser	Leu	Leu	Trp	Leu	Gln	Leu	Ser	Cys	Ser	Gly	Asp	Val	Ala	
			-5				1				5					
cgg	gca	gtc	agg	gga	caa	ggg	cag	gag	acc	tcg	ggc	cct	ccc	cgt	gcc	245
Arg	Ala	Val	Arg	Gly	Gln	Gly	Gln	Glu	Thr	Ser	Gly	Pro	Pro	Arg	Ala	
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Cys	Pro	Pro	Glu	Pro	Pro	Pro	Glu	His	Trp	Glu	Glu	Asp	Ala	Ser	Trp	
				30				35						40		
ggc	ccc	cac	cgc	ctg	gca	gtg	ctg	gtg	ccc	ttc	cgc	gaa	cgc	ttc	gag	341
Gly	Pro	His	Arg	Leu	Ala	Val	Leu	Val	Pro	Phe	Arg	Glu	Arg	Phe	Glu	
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gag	ctc	ctg	gtc	ttc	gtg	ccc	cac	atg	cgc	cgc	ttc	ctg	agc	agg	aag	389
Glu	Leu	Leu	Val	Phe	Val	Pro	His	Met	Arg	Arg	Phe	Leu	Ser	Arg	Lys	
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aag	atc	cgg	cac	cac	atc	tac	gtg	ctc	aac	cag	gtg	gac	cac	ttc	agg	437
Lys	Ile	Arg	His	His	Ile	Tyr	Val	Leu	Asn	Gln	Val	Asp	His	Phe	Arg	
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ttc	aac	cgg	gca	gcg	ctc	atc	aac	gtg	ggc	ttc	ctg	gag	agc	agc	aac	485
Phe	Asn	Arg	Ala	Ala	Leu	Ile	Asn	Val	Gly	Phe	Leu	Glu	Ser	Ser	Asn	
90					95				100						105	
agc	acg	gac	tac	att	gcc	atg	cac	gac	gtt	gac	ctg	ctc	cct	ctc	aac	533
Ser	Thr	Asp	Tyr	Ile	Ala	Met	His	Asp	Val	Asp	Leu	Leu	Pro	Leu	Asn	
				110				115						120		
gag	gag	ctg	gac	tat	ggc	ttt	cct	gag	gct	ggg	ccc	ttc	cac	gtg	gcc	581
Glu	Glu	Leu	Asp	Tyr	Gly	Phe	Pro	Glu	Ala	Gly	Pro	Phe	His	Val	Ala	
			125					130					135			
tcc	ccg	gag	ctc	cac	cct	ctc	tac	cac	tac	aag	acc	tat	gtc	ggc	ggc	629
Ser	Pro	Glu	Leu	His	Pro	Leu	Tyr	His	Tyr	Lys	Thr	Tyr	Val	Gly	Gly	
			140				145					150				
atc	ctg	ctg	ctc	tcc	aag	cag	cac	tac	cgg	ctg	tgc	aat	ggg	atg	tcc	677
Ile	Leu	Leu	Leu	Ser	Lys	Gln	His	Tyr	Arg	Leu	Cys	Asn	Gly	Met	Ser	
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aac	cgc	ttc	tgg	ggc	tgg	ggc	cgc	gag	gac	gac	gag	ttc	tac	cgg	cgc	725
Asn	Arg	Phe	Trp	Gly	Trp	Gly	Arg	Glu	Asp	Asp	Glu	Phe	Tyr	Arg	Arg	
170					175				180						185	
att	aag	gga	gct	ggg	ctc	cag	ctt	ttc	cgc	ccc	tcg	gga	atc	aca	act	773
Ile	Lys	Gly	Ala	Gly	Leu	Gln	Leu	Phe	Arg	Pro	Ser	Gly	Ile	Thr	Thr	
				190				195					200			
ggg	tac	aag	aca	ttt	cgc	cac	ctg	cat	gac	cca	gcc	tgg	cgg	aag	agg	821

Gly	Tyr	Lys	Thr	Phe	Arg	His	Leu	His	Asp	Pro	Ala	Trp	Arg	Lys	Arg		
			205					210					215				
gac	cag	aag	cg	atc	gca	gct	caa	aaa	cag	gag	cag	ttc	aag	gtg	gac		869
Asp	Gln	Lys	Arg	Ile	Ala	Ala	Gln	Lys	Gln	Glu	Gln	Phe	Lys	Val	Asp		
		220					225					230					
agg	gag	gga	ggc	ctg	aac	act	gtg	aag	tac	cat	gtg	gct	tcc	cg	act		917
Arg	Glu	Gly	Gly	Leu	Asn	Thr	Val	Lys	Tyr	His	Val	Ala	Ser	Arg	Thr		
		235				240					245						
gcc	ctg	tct	gtg	ggc	ggg	gcc	ccc	tgc	act	gtc	ctc	aac	atc	atg	ttg		965
Ala	Leu	Ser	Val	Gly	Gly	Ala	Pro	Cys	Thr	Val	Leu	Asn	Ile	Met	Leu		
250				255				260			265						
gac	tgt	gac	aag	acc	gcc	aca	ccc	tgg	tgc	aca	ttc	agc	tgagctggat				1014
Asp	Cys	Asp	Lys	Thr	Ala	Thr	Pro	Trp	Cys	Thr	Phe	Ser					
			270					275									
ggacagt	gag	gaagc	ctgta	cctac	aggcc	atatt	gctca	ggctc	aggac	aaggc	cctcag						1074
gtcgt	ggg	ccc	ctgac	aggat	gtgga	gtggc	cagga	ccaag	acagc	aagct	acgca						1134
attgc	agcca	ccggc	cgcc	aaggc	aggct	tgggt	gggc	caggac	acgt	gggtg	cctg						1194
ggacg	ctgct	tgccat	gcac	agtga	tcaga	gagag	gctgg	ggtgt	gtcct	gtccg	ggacc						1254
ccccct	gcct	tctgt	ctcac	cctact	ctga	cctcct	tcac	gtgcc	caggc	ctgtg	ggtag						1314
tgggg	agggc	tgaac	caggac	aacct	ctcat	caccccc	act	tttgt	tcctt	cctgt	ggggc						1374
tgccct	gctgc	agagac	acag	tgtag	ggggc	atgcag	ctgg	cgtag	ggtgg	agttg	ggcct						1434
ggtgag	gggtt	aggact	tcag	aaacc	agagc	acaag	cccca	cagag	gggga	acagc	cagca						1494
ccgct	ctagc	tggtt	gttgc	catgc	cgga	tgtgg	gccta	gtgtt	gccag	atctt	ctgat						1554
ttttc	gaaag	aaacta	gaat	gctg	gattct	caaaaaa	aaaaa	aaaaa	aaaaa								1602

<210> 12
 <211> 327
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -49..-1
 <223> score 5.6
 seq ACLSLGFFSLLWL/QL

<400> 12
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 -45 -40 -35
 Arg Ser Gly Leu Leu Ser Gly Gly Leu Pro Arg Lys Cys Ser Val Phe
 -30 -25 -20
 His Leu Phe Val Ala Cys Leu Ser Leu Gly Phe Phe Ser Leu Leu Trp
 -15 -10 -5
 Leu Gln Leu Ser Cys Ser Gly Asp Val Ala Arg Ala Val Arg Gly Gln
 1 5 10 15
 Gly Gln Glu Thr Ser Gly Pro Pro Arg Ala Cys Pro Pro Glu Pro Pro
 20 25 30
 Pro Glu His Trp Glu Glu Asp Ala Ser Trp Gly Pro His Arg Leu Ala
 35 40 45
 Val Leu Val Pro Phe Arg Glu Arg Phe Glu Glu Leu Leu Val Phe Val
 50 55 60
 Pro His Met Arg Arg Phe Leu Ser Arg Lys Lys Ile Arg His His Ile
 65 70 75
 Tyr Val Leu Asn Gln Val Asp His Phe Arg Phe Asn Arg Ala Ala Leu

80		85		90		95
Ile Asn Val Gly	Phe Leu Glu Ser Ser	Asn Ser Thr Asp Tyr	Ile Ala			
	100	105	110			
Met His Asp Val Asp	Leu Leu Pro Leu	Asn Glu Glu Leu Asp	Tyr Gly			
	115	120	125			
Phe Pro Glu Ala Gly	Pro Phe His Val Ala	Ser Pro Glu Leu His	Pro			
	130	135	140			
Leu Tyr His Tyr Lys	Thr Tyr Val Gly Gly	Ile Leu Leu Leu Ser	Lys			
	145	150	155			
Gln His Tyr Arg Leu	Cys Asn Gly Met Ser	Asn Arg Phe Trp Gly	Trp			
	160	165	170			
Gly Arg Glu Asp Asp	Glu Phe Tyr Arg Arg	Ile Lys Gly Ala Gly	Leu			
	180	185	190			
Gln Leu Phe Arg Pro	Ser Gly Ile Thr Thr	Gly Tyr Lys Thr Phe	Arg			
	195	200	205			
His Leu His Asp Pro	Ala Trp Arg Lys Arg	Asp Gln Lys Arg Ile	Ala			
	210	215	220			
Ala Gln Lys Gln Glu	Gln Phe Lys Val Asp	Arg Glu Gly Gly Leu	Asn			
	225	230	235			
Thr Val Lys Tyr His	Val Ala Ser Arg Thr	Ala Leu Ser Val Gly	Gly			
	240	245	250			
Ala Pro Cys Thr Val	Leu Asn Ile Met Leu	Asp Cys Asp Lys Thr	Ala			
	260	265	270			
Thr Pro Trp Cys Thr	Phe Ser					
	275					

<210> 13
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 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 75..1259

<221> sig_peptide
 <222> 75..1004
 <223> score 4.4
 seq VLILLFSLALIIL/PS

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agaaaagggtg tagtggtttgg ggcgggtcaac gggctatgct ggcttgacag ggctgggctc	60
ttcagaacag aagc atg gat ctc gga atc cct gac ctg ctg gac gcg tgg	110
Met Asp Leu Gly Ile Pro Asp Leu Leu Asp Ala Trp	
-310 -305 -300	
ctg gag ccc cca gag gat atc ttc tcg aca gga tcc gtc ctg gag ctg	158
Leu Glu Pro Pro Glu Asp Ile Phe Ser Thr Gly Ser Val Leu Glu Leu	
-295 -290 -285	
gga ctc cac tgc ccc cct cca gag gtt ccg gta act agg cta cag gaa	206
Gly Leu His Cys Pro Pro Pro Glu Val Pro Val Thr Arg Leu Gln Glu	
-280 -275 -270	
cag gga ctg caa ggc tgg aag tcc ggt ggg gac cgt ggc tgt ggc ctt	254
Gln Gly Leu Gln Gly Trp Lys Ser Gly Gly Asp Arg Gly Cys Gly Leu	
-265 -260 -255	

caa gag agt gag cct gaa gat ttc ttg aag ctt ttc att gat ccc aat	302
Gln Glu Ser Glu Pro Glu Asp Phe Leu Lys Leu Phe Ile Asp Pro Asn	
-250 -245 -240 -235	
gag gtg tac tgc tca gaa gca tct cct ggc agt gac agt ggc atc tct	350
Glu Val Tyr Cys Ser Glu Ala Ser Pro Gly Ser Asp Ser Gly Ile Ser	
-230 -225 -220	
gag gac tcc tgc cat cca gac agt ccc cct gcc ccc agg gca acc agt	398
Glu Asp Ser Cys His Pro Asp Ser Pro Pro Ala Pro Arg Ala Thr Ser	
-215 -210 -205	
tct cct atg ctc tat gag gtt gtc tat gag gca ggg gcc ctg gag agg	446
Ser Pro Met Leu Tyr Glu Val Val Tyr Glu Ala Gly Ala Leu Glu Arg	
-200 -195 -190	
atg cag ggg gaa act ggg cca aat gta ggc ctt atc tcc atc cag cta	494
Met Gln Gly Glu Thr Gly Pro Asn Val Gly Leu Ile Ser Ile Gln Leu	
-185 -180 -175	
gat cag tgg agc cca gca ttt atg gtg cct gat tcc tgc atg gtc agt	542
Asp Gln Trp Ser Pro Ala Phe Met Val Pro Asp Ser Cys Met Val Ser	
-170 -165 -160 -155	
gag ctg ccc ttt gat gct cat gcc cac atc ctg ccc aga gca ggc acc	590
Glu Leu Pro Phe Asp Ala His Ala His Ile Leu Pro Arg Ala Gly Thr	
-150 -145 -140	
gta gcc cca gtg ccc tgt aca acc ctg ctg ccc tgt caa acc ctg ttc	638
Val Ala Pro Val Pro Cys Thr Thr Leu Leu Pro Cys Gln Thr Leu Phe	
-135 -130 -125	
ctg acc gat gag gag aag cgt ctg ctg ggg cag gaa ggg gtt tcc ctg	686
Leu Thr Asp Glu Glu Lys Arg Leu Leu Gly Gln Glu Gly Val Ser Leu	
-120 -115 -110	
ccc tct cac ctg ccc ctc acc aag gca gag gag agg gtc ctc aag aag	734
Pro Ser His Leu Pro Leu Thr Lys Ala Glu Glu Arg Val Leu Lys Lys	
-105 -100 -95	
gtc agg agg aaa atc cgt aac aag cag tca gct cag gac agt cgg cgg	782
Val Arg Arg Lys Ile Arg Asn Lys Gln Ser Ala Gln Asp Ser Arg Arg	
-90 -85 -80 -75	
cgg aag aag gag tac att gat ggg ctg gag agc agg gtg gca gcc tgt	830
Arg Lys Lys Glu Tyr Ile Asp Gly Leu Glu Ser Arg Val Ala Ala Cys	
-70 -65 -60	
tct gca cag aac caa gaa tta cag aaa aaa gtc cag gag ctg gag agg	878
Ser Ala Gln Asn Gln Glu Leu Gln Lys Lys Val Gln Glu Leu Glu Arg	
-55 -50 -45	
cac aac atc tcc ttg gta gct cag ctc cgc cag ctg cag acg cta att	926
His Asn Ile Ser Leu Val Ala Gln Leu Arg Gln Leu Gln Thr Leu Ile	
-40 -35 -30	
gct caa act tcc aac aaa gct gcc cag acc agc act tgt gtt ttg att	974
Ala Gln Thr Ser Asn Lys Ala Ala Gln Thr Ser Thr Cys Val Leu Ile	
-25 -20 -15	
ctt ctt ttt tcc ctg gct ctc atc atc ctg ccc agc ttc agt cca ttc	1022
Leu Leu Phe Ser Leu Ala Leu Ile Ile Leu Pro Ser Phe Ser Pro Phe	
-10 -5 1 5	
cag agt cga cca gaa gct ggg tct gag gat tac cag cct cac gga gtg	1070
Gln Ser Arg Pro Glu Ala Gly Ser Glu Asp Tyr Gln Pro His Gly Val	
10 15 20	
act tcc aga aat atc ctg acc cac aag gac gta aca gaa aat ctg gag	1118
Thr Ser Arg Asn Ile Leu Thr His Lys Asp Val Thr Glu Asn Leu Glu	
25 30 35	

acc	caa	gtg	gta	gag	tcc	aga	ctg	agg	gag	cca	cct	gga	gcc	aag	gat	1166
Thr	Gln	Val	Val	Glu	Ser	Arg	Leu	Arg	Glu	Pro	Pro	Gly	Ala	Lys	Asp	
40						45				50						
gca	aat	ggc	tca	aca	agg	aca	ctg	ctt	gag	aag	atg	gga	ggg	aag	cca	1214
Ala	Asn	Gly	Ser	Thr	Arg	Thr	Leu	Leu	Glu	Lys	Met	Gly	Gly	Lys	Pro	
55					60				65					70		
aga	ccc	agt	ggg	cgc	atc	cgg	tcc	gtg	ctg	cat	gca	gat	gag	atg	1259	
Arg	Pro	Ser	Gly	Arg	Ile	Arg	Ser	Val	Leu	His	Ala	Asp	Glu	Met		
			75					80					85			
tgagctggaa	cagaccttcc	tggcccactt	cctgatcaca	aggaatcctg	ggcttcctta	1319										
tggcttttctt	cccactggga	ttcctactta	ggtgtctgccc	ctcagggggtc	caaatacactt	1379										
caggacacccc	caagagatgt	ccttttagtct	ctgcctgagg	cctagtctgc	atttgtttgc	1439										
atatatgaga	gggtacctca	aatacttctg	ttatgtatct	gtgattttat	ttcttctttg	1499										
ggtatagggt	tgaggggaaa	taagttttga	gtgagaaata	aacgttttag	ctgaaaaaaa	1559										
aaaaaaaa						1568										

<210> 14
 <211> 395
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -310..-1
 <223> score 4.4
 seq VLILLFSLALIIL/PS

<400> 14
 Met Asp Leu Gly Ile Pro Asp Leu Leu Asp Ala Trp Leu Glu Pro Pro
 -310 -305 -300 -295
 Glu Asp Ile Phe Ser Thr Gly Ser Val Leu Glu Leu Gly Leu His Cys
 -290 -285 -280
 Pro Pro Pro Glu Val Pro Val Thr Arg Leu Gln Glu Gln Gly Leu Gln
 -275 -270 -265
 Gly Trp Lys Ser Gly Gly Asp Arg Gly Cys Gly Leu Gln Glu Ser Glu
 -260 -255 -250
 Pro Glu Asp Phe Leu Lys Leu Phe Ile Asp Pro Asn Glu Val Tyr Cys
 -245 -240 -235
 Ser Glu Ala Ser Pro Gly Ser Asp Ser Gly Ile Ser Glu Asp Ser Cys
 -230 -225 -220 -215
 His Pro Asp Ser Pro Pro Ala Pro Arg Ala Thr Ser Ser Pro Met Leu
 -210 -205 -200
 Tyr Glu Val Val Tyr Glu Ala Gly Ala Leu Glu Arg Met Gln Gly Glu
 -195 -190 -185
 Thr Gly Pro Asn Val Gly Leu Ile Ser Ile Gln Leu Asp Gln Trp Ser
 -180 -175 -170
 Pro Ala Phe Met Val Pro Asp Ser Cys Met Val Ser Glu Leu Pro Phe
 -165 -160 -155
 Asp Ala His Ala His Ile Leu Pro Arg Ala Gly Thr Val Ala Pro Val
 -150 -145 -140 -135
 Pro Cys Thr Thr Leu Leu Pro Cys Gln Thr Leu Phe Leu Thr Asp Glu
 -130 -125 -120
 Glu Lys Arg Leu Leu Gly Gln Glu Gly Val Ser Leu Pro Ser His Leu
 -115 -110 -105

Pro Leu Thr Lys Ala Glu Glu Arg Val Leu Lys Lys Val Arg Arg Lys
 -100 -95 -90
 Ile Arg Asn Lys Gln Ser Ala Gln Asp Ser Arg Arg Arg Lys Lys Glu
 -85 -80 -75
 Tyr Ile Asp Gly Leu Glu Ser Arg Val Ala Ala Cys Ser Ala Gln Asn
 -70 -65 -60 -55
 Gln Glu Leu Gln Lys Lys Val Gln Glu Leu Glu Arg His Asn Ile Ser
 -50 -45 -40
 Leu Val Ala Gln Leu Arg Gln Leu Gln Thr Leu Ile Ala Gln Thr Ser
 -35 -30 -25
 Asn Lys Ala Ala Gln Thr Ser Thr Cys Val Leu Ile Leu Leu Phe Ser
 -20 -15 -10
 Leu Ala Leu Ile Ile Leu Pro Ser Phe Ser Pro Phe Gln Ser Arg Pro
 -5 1 5 10
 Glu Ala Gly Ser Glu Asp Tyr Gln Pro His Gly Val Thr Ser Arg Asn
 15 20 25
 Ile Leu Thr His Lys Asp Val Thr Glu Asn Leu Glu Thr Gln Val Val
 30 35 40
 Glu Ser Arg Leu Arg Glu Pro Pro Gly Ala Lys Asp Ala Asn Gly Ser
 45 50 55
 Thr Arg Thr Leu Leu Glu Lys Met Gly Gly Lys Pro Arg Pro Ser Gly
 60 65 70
 Arg Ile Arg Ser Val Leu His Ala Asp Glu Met
 75 80 85

<210> 15
 <211> 25
 <212> DNA
 <213> Artificial Sequence
 <400> 15
 gggaagatgg agatagtatt gcctg

25

<210> 16
 <211> 26
 <212> DNA
 <213> Artificial Sequence
 <400> 16
 ctgccatgta catgatagag agattc

26

<210> 17
 <211> 546
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> promoter
 <222> 1..517

<221> transcription start site
 <222> 518

<221> protein_bind
 <222> 17..25
 <223> matinspector prediction

name CMYB_01
score 0.983
sequence tgtcagttg

<221> protein_bind
<222> complement(18..27)
<223> matinspector prediction
name MYOD_Q6
score 0.961
sequence cccaactgac

<221> protein_bind
<222> complement(75..85)
<223> matinspector prediction
name S8_01
score 0.960
sequence aatagaattag

<221> protein_bind
<222> 94..104
<223> matinspector prediction
name S8_01
score 0.966
sequence aactaaattag

<221> protein_bind
<222> complement(129..139)
<223> matinspector prediction
name DELTAEF1_01
score 0.960
sequence gcacacctcag

<221> protein_bind
<222> complement(155..165)
<223> matinspector prediction
name GATA_C
score 0.964
sequence agataaatcca

<221> protein_bind
<222> 170..178
<223> matinspector prediction
name CMYB_01
score 0.958
sequence cttcagttg

<221> protein_bind
<222> 176..189
<223> matinspector prediction
name GATA1_02
score 0.959
sequence ttgtagataggaca

<221> protein_bind

<222> 180..190
 <223> matinspector prediction
 name GATA_C
 score 0.953
 sequence agataggacat

<221> protein_bind
 <222> 284..299
 <223> matinspector prediction
 name TAL1ALPHA47_01
 score 0.973
 sequence cataacagatggtaag

<221> protein_bind
 <222> 284..299
 <223> matinspector prediction
 name TAL1BETA47_01
 score 0.983
 sequence cataacagatggtaag

<221> protein_bind
 <222> 284..299
 <223> matinspector prediction
 name TAL1BETAITF2_01
 score 0.978
 sequence cataacagatggtaag

<221> protein_bind
 <222> complement(287..296)
 <223> matinspector prediction
 name MYOD_Q6
 score 0.954
 sequence accatctgtt

<221> protein_bind
 <222> complement(302..314)
 <223> matinspector prediction
 name GATA1_04
 score 0.953
 sequence tcaagataaagta

<221> protein_bind
 <222> 393..405
 <223> matinspector prediction
 name IK1_01
 score 0.963
 sequence agttgggaattcc

<221> protein_bind
 <222> 393..404
 <223> matinspector prediction
 name IK2_01
 score 0.985
 sequence agttgggaattc

<221> protein_bind
 <222> 396..405
 <223> matinspector prediction
 name CREL_01
 score 0.962
 sequence tgggaattcc

<221> protein_bind
 <222> 423..436
 <223> matinspector prediction
 name GATA1_02
 score 0.950
 sequence tcagtgatatggca

<221> protein_bind
 <222> complement(478..489)
 <223> matinspector prediction
 name SRY_02
 score 0.951
 sequence taaaacaaaaca

<221> protein_bind
 <222> 486..493
 <223> matinspector prediction
 name E2F_02
 score 0.957
 sequence tttagcgc

<221> protein_bind
 <222> complement(514..521)
 <223> matinspector prediction
 name MZF1_01
 score 0.975
 sequence tgagggga

<400> 17
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 gttattgact gaggtgtgct aatctcccat tatgtggatt tatctatttc ttcagttgta 180
 gataggacat tgatagatac ataagtacca ggacaaaagc agggagatct tttttccaaa 240
 atcaggagaa aaaaatgaca tctggaaaac ctatagggaa aggcataaca gatggtaagg 300
 atactttatc ttgagtagga ggccttcct gtggcaacgt ggagaaggga agaggtcgtg 360
 gaattgagga gtcagctcag ttagaagcag ggagttggga attccgttca tgtgatttag 420
 catcagtgat atggcaaatg tgggactaag ggtagtgatc agagggttaa aattgtgtgt 480
 tttgttttag cgctgctggg gcatcgcctt ggtccctc aaacagattc ccatgaatct 540
 cttcat 546

<210> 18
 <211> 23
 <212> DNA
 <213> Artificial Sequence
 <400> 18
 gtaccaggga ctgtgaccat tgc

23

<210> 19
<211> 24
<212> DNA
<213> Artificial Sequence
<400> 19
ctgtgaccat tgctcccaag agag

24

<210> 20
<211> 861
<212> DNA
<213> Homo Sapiens

<220>
<221> promoter
<222> 1..806

<221> transcription start site
<222> 807

<221> protein_bind
<222> complement(60..70)
<223> matinspector prediction
name NFY_Q6
score 0.956
sequence ggaccaatcat

<221> protein_bind
<222> 70..77
<223> matinspector prediction
name MZF1_01
score 0.962
sequence cctgggga

<221> protein_bind
<222> 124..132
<223> matinspector prediction
name CMYB_01
score 0.994
sequence tgaccgttg

<221> protein_bind
<222> complement(126..134)
<223> matinspector prediction
name VMYB_02
score 0.985
sequence tccaacggt

<221> protein_bind
<222> 135..143
<223> matinspector prediction
name STAT_01
score 0.968
sequence ttcctggaa

<221> protein_bind
<222> complement(135..143)
<223> matinspector prediction
name STAT_01
score 0.951
sequence ttccaggaa

<221> protein_bind
<222> complement(252..259)
<223> matinspector prediction
name MZF1_01
score 0.956
sequence ttggggga

<221> protein_bind
<222> 357..368
<223> matinspector prediction
name IK2_01
score 0.965
sequence gaatgggatttc

<221> protein_bind
<222> 384..391
<223> matinspector prediction
name MZF1_01
score 0.986
sequence agagggga

<221> protein_bind
<222> complement(410..421)
<223> matinspector prediction
name SRY_02
score 0.955
sequence gaaaacaaaaca

<221> protein_bind
<222> 592..599
<223> matinspector prediction
name MZF1_01
score 0.960
sequence gaagggga

<221> protein_bind
<222> 618..627
<223> matinspector prediction
name MYOD_Q6
score 0.981
sequence agcatctgcc

<221> protein_bind
<222> 632..642
<223> matinspector prediction
name DELTAEF1_01

score 0.958
sequence tcccaccttcc

<221> protein_bind
<222> complement(813..823)
<223> matinspector prediction
name S8_01
score 0.992
sequence gaggcaattat

<221> protein_bind
<222> complement(824..831)
<223> matinspector prediction
name MZF1_01
score 0.986
sequence agagggga

<221> misc_feature
<222> 335,376
<223> n=a, g, c or t
Oligonucleotide

<400> 20
tactataggg cacgcgtggt cgacggccgg gctgttctgg agcagagggc atgtcagtaa 60
tgatttgtcc ctggggaagg tctggctggc tccagcacag tgaggcattt aggtatctct 120
cggtgaccgt tggattcctg gaagcagtag ctgttctggt tggatctggt agggacaggg 180
ctcagagggc taggcacgag ggaaggtcag aggagaaggs aggsarggcc cagtgagarg 240
ggagcatgcc ttcccccaac cctggcttsc ycttggyam agggcgkty tgggmacttr 300
aaytcagggc ccaascagaa scacaggccc aktcntggct smaagcacia tagcctgaat 360
gggatttcag gttagncagg gtgagagggg aggcctctctg gcttagtttt gttttgtttt 420
ccaaatcaag gtaacttgct cccttctgct acgggccttg gtcttggett gtcctcacc 480
agtcggaact ccctaccact ttcaggagag tggtttttag cccgtggggc tgttctgttc 540
caagcagtggt gagaacatgg ctggttagagg ctctagctgt gtgcggggcc tgaaggggag 600
tgggttctcg cccaaagagc atctgccccat ttcccacett cccttctccc accagaagct 660
tgcctgagct gtttgacaa aaatccaaac cccacttggc tactctggcc tggcttcagc 720
ttggaaccca atacctaggc ttacaggcca tcctgagcca ggggcctctg gaaattctct 780
tcctgatggt ccttttaggt tgggcacaaa atataattgc ctctcccctc tcccattttc 840
tctcttgga gcaatgtca c 861

<210> 21
<211> 20
<212> DNA
<213> Artificial Sequence
<400> 21
ctgggatgga aggcacggta 20

<210> 22
<211> 20
<212> DNA
<213> Artificial Sequence
<400> 22
gagaccacac agctagacaa 20

<210> 23

<211> 555
<212> DNA
<213> Homo Sapiens

<220>
<221> promoter
<222> 1..500

<221> transcription start site
<222> 501

<221> protein_bind
<222> 191..206
<223> matinspector prediction
name ARNT_01
score 0.964
sequence ggactcacgtgctgct

<221> protein_bind
<222> 193..204
<223> matinspector prediction
name NMYC_01
score 0.965
sequence actcacgtgctg

<221> protein_bind
<222> 193..204
<223> matinspector prediction
name USF_01
score 0.985
sequence actcacgtgctg

<221> protein_bind
<222> complement(193..204)
<223> matinspector prediction
name USF_01
score 0.985
sequence cagcacgtgagt

<221> protein_bind
<222> complement(193..204)
<223> matinspector prediction
name NMYC_01
score 0.956
sequence cagcacgtgagt

<221> protein_bind
<222> complement(193..204)
<223> matinspector prediction
name MYCMAX_02
score 0.972
sequence cagcacgtgagt

<221> protein_bind

<222> 195..202
<223> matinspector prediction
name USF_C
score 0.997
sequence tcacgtgc

<221> protein_bind
<222> complement(195..202)
<223> matinspector prediction
name USF_C
score 0.991
sequence gcacgtga

<221> protein_bind
<222> complement(210..217)
<223> matinspector prediction
name MZF1_01
score 0.968
sequence catgggga

<221> protein_bind
<222> 397..410
<223> matinspector prediction
name ELK1_02
score 0.963
sequence ctctccggaagcct

<221> protein_bind
<222> 400..409
<223> matinspector prediction
name CETS1P54_01
score 0.974
sequence tccggaagcc

<221> protein_bind
<222> complement(460..470)
<223> matinspector prediction
name AP1_Q4
score 0.963
sequence agtgactgaac

<221> protein_bind
<222> complement(460..470)
<223> matinspector prediction
name AP1FJ_Q2
score 0.961
sequence agtgactgaac

<221> protein_bind
<222> 547..555
<223> matinspector prediction
name PADS_C
score 1.000
sequence tgttgtctc

```

<400> 23
ctatagggca cgcktggctg acggcccggg ctggtctggt ctgtkgtgga gtcggggttga      60
aggacagcat ttgtkacatc tggctctactg caccttccct ctgccgtgca cttggcccttt      120
kawaagctca gcaccgggtgc ccatcacagg gccggcagca cacacatccc attactcaga      180
aggaactgac ggactcacgt gctgctccgt ccccatgagc tcagtggacc tgtctatgta      240
gagcagtcag acagtgcctg ggatagagtg agagttcagc cagtaaatacc aagtgattgt      300
cattcctgtc tgcattagta actcccaacc tagatgtgaa aacttagttc tttctcatag      360
gttgctctgc ccatgggtccc actgcagacc caggcactct ccggaagcct ggaaatcacc      420
cgtgtcttct gcctgtctccc gctcacatcc cacacttggtg ttcagtcact gagttacaga      480
ttttgcctcc tcaattttctc ttgtcttagt cccatcctct gttcccctgg ccagtttgtc      540
tagctgtgtg gtctc

```

```

<210> 24
<211> 536
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> 266..535
<221> sig_peptide
<222> 266..307
<223> Von Heijne matrix
      score 15
      seq LLPLLLLLPMCWA/VE

```

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<400> 24
acttttgggg tcacgtgctc attccgtttc cctacctccc ccaaccttat cccgccctg      60
ggggttcgcg ggcatttttc aggaactttc tttccggcctt gagaagccgc cactcccaag      120
atgsagcagg aaccgcggct gctggacaag aggggtgcgg tggatactga cctttgctcc      180
ggcctcgctg tgaagacaca gcgcactctcc ccgctgtagg cttcctccca cagaaccctg      240
ttcgggcctc agagcgtctg gtgag atg ctg ttg ccg ctg ctg ctg ctg cta      292
                               Met Leu Leu Pro Leu Leu Leu Leu
                               -10
ccc atg tgc tgg gcc gtg gag gtc aag agg ccc cgg ggc gtc tcc ctc      340
Pro Met Cys Trp Ala Val Glu Val Lys Arg Pro Arg Gly Val Ser Leu
-5                               1                               5                               10
acc aat cat cac ttc tac gat gag tcc aag cct ttc acc tgc ctg gac      388
Thr Asn His His Phe Tyr Asp Glu Ser Lys Pro Phe Thr Cys Leu Asp
                               15                               20                               25
ggg tgc gcc acc atc cca ttt gat cag gtc aac gat gac tat tgc gac      436
Gly Ser Ala Thr Ile Pro Phe Asp Gln Val Asn Asp Asp Tyr Cys Asp
                               30                               35                               40
tgc aaa gat ggc tct gac gag cca ggc acg gct gcc tgt cct aat ggc      484
Cys Lys Asp Gly Ser Asp Glu Pro Gly Thr Ala Ala Cys Pro Asn Gly
                               45                               50                               55
agc ttc cac tgc acc aac act ggc tat aag ccc ctg tat atc ccc tcc      532
Ser Phe His Cys Thr Asn Thr Gly Tyr Lys Pro Leu Tyr Ile Pro Ser
60                               65                               70                               75
aac c
Asn

```

<210> 25
 <211> 274
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 35..274

<221> sig_peptide
 <222> 35..82
 <223> Von Heijne matrix
 score 14.8000001907349
 seq SLPLLLLLLGAWA/IP

<400> 25
 acagactaca cttgctgaac tggctcctgg ggcc atg agg ctg tca ctg cca ctg 55
 Met Arg Leu Ser Leu Pro Leu
 -15 -10
 ctg ctg ctg ctg ctg gga gcc tgg gcc atc cca ggg ggc ctc ggg gac 103
 Leu Leu Leu Leu Leu Gly Ala Trp Ala Ile Pro Gly Gly Leu Gly Asp
 -5 1 5
 agg gcg cca ctc aca gcc aca gcc cca caa ctg gat gat gag gag atg 151
 Arg Ala Pro Leu Thr Ala Thr Ala Pro Gln Leu Asp Asp Glu Glu Met
 10 15 20
 tac tca gcc cac atg ccc gct cac ctg cgc tgt gat gcc tgc aga gct 199
 Tyr Ser Ala His Met Pro Ala His Leu Arg Cys Asp Ala Cys Arg Ala
 25 30 35
 gtg gct tac cag gtg agt cct tca cca ctg tca cct gcc ctg ctc aca 247
 Val Ala Tyr Gln Val Ser Pro Ser Pro Leu Ser Pro Ala Leu Leu Thr
 40 45 50 55
 ccc ctt ctc aag cca gcc ccc acc ggg 274
 Pro Leu Leu Lys Pro Ala Pro Thr Gly
 60

<210> 26
 <211> 230
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 29..229

<221> sig_peptide
 <222> 29..94
 <223> Von Heijne matrix
 score 13.8000001907349
 seq LGLLLLWLRGARC/GV

<400> 26
 aaggagtcag tctcagtcag gacacagc atg gac atg agg gtc ccc gct cag 52
 Met Asp Met Arg Val Pro Ala Gln
 -20 -15

ctc	ctg	ggg	ctc	ctg	cta	ctc	tgg	ctc	cga	ggt	gcc	aga	tgt	ggc	gtc	100
Leu	Leu	Gly	Leu	Leu	Leu	Leu	Trp	Leu	Arg	Gly	Ala	Arg	Cys	Gly	Val	
			-10						-5					1		
cag	atg	acc	cag	ttt	cca	ctg	tcc	ctg	tct	gca	tcg	gta	gga	gac	aga	148
Gln	Met	Thr	Gln	Phe	Pro	Leu	Ser	Leu	Ser	Ala	Ser	Val	Gly	Asp	Arg	
		5					10					15				
gtc	acc	atc	act	tgc	cgg	aca	agc	cat	ata	att	aac	atc	ttt	tta	aat	196
Val	Thr	Ile	Thr	Cys	Arg	Thr	Ser	His	Ile	Ile	Asn	Ile	Phe	Leu	Asn	
	20					25					30					
tgg	tat	cag	cag	aaa	cca	ggc	aaa	gcc	cct	tgg	g					230
Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Trp						
35					40					45						

<210> 27
 <211> 195
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 44..193

<221> sig_peptide
 <222> 44..112
 <223> Von Heijne matrix
 score 13.8000001907349
 seq VLLLLLLSGDVQS/SE

<400> 27																
agaggggcttc	cggggctgcc	ggtctgagtg	cagagctgct	gtc	atg	gcg	gcc	gct								55
					Met	Ala	Ala	Ala								
									-20							
ctg	tgg	ggc	ttc	ttt	ccc	gtc	ctg	ctg	ctg	ctg	cta	tcg	ggg	gat		103
Leu	Trp	Gly	Phe	Phe	Pro	Val	Leu	Leu	Leu	Leu	Leu	Ser	Gly	Asp		
			-15						-10				-5			
gtc	cag	agc	tcg	gag	gtg	ccc	ggg	gct	gct	gct	gag	gga	tcg	gga	ggg	151
Val	Gln	Ser	Ser	Glu	Val	Pro	Gly	Ala	Ala	Ala	Glu	Gly	Ser	Gly	Gly	
			1				5					10				
agt	ggg	gtc	ggc	ata	gga	gac	cgc	ttc	aag	att	gag	gga	ctg	gg		195
Ser	Gly	Val	Gly	Ile	Gly	Xaa	Arg	Phe	Lys	Ile	Glu	Gly	Leu			
	15					20					25					

<210> 28
 <211> 276
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 25..276

<221> sig_peptide
 <222> 25..90
 <223> Von Heijne matrix

score 13.5
seq LGLLLLWLXGARC/DI

```
<400> 28
agtcagtctc agacaggaca cagc atg gac atg agg gtc ccc gct cag ctc      51
                               Met Asp Met Arg Val Pro Ala Gln Leu
                               -20                               -15

ctg ggg ctc ctg cta ctc tgg ctc yka ggt gcc aga tgt gac atc cag      99
Leu Gly Leu Leu Leu Leu Trp Leu Xaa Gly Ala Arg Cys Asp Ile Gln
                               -10                               -5                               1

atg aca cag tct cca gtc ctg cct gca tct gta gga gac aga gtc acc      147
Met Thr Gln Ser Pro Val Leu Pro Ala Ser Val Gly Asp Arg Val Thr
                               5                               10                               15

atc act tgc cgg gca agt cag agc att ggc agc tat tta aac tgg tat      195
Ile Thr Cys Arg Ala Ser Gln Ser Ile Gly Ser Tyr Leu Asn Trp Tyr
20                               25                               30                               35

cag cat aaa cca ggg cat gcc cct cgc ctc ctg atc tat gct gca act      243
Gln His Lys Pro Gly His Ala Pro Arg Leu Leu Ile Tyr Ala Ala Thr
                               40                               45                               50

act ttg tcg agg ggc ggs ccg gcc aga ttc agt      276
Thr Leu Ser Arg Gly Gly Pro Ala Arg Phe Ser
                               55                               60
```

<210> 29
<211> 240
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 25..240

<221> sig_peptide
<222> 25..120
<223> Von Heijne matrix
score 13.5
seq LLLLLLLPPPGSC/AG

```
<400> 29
agggcgctgc gcggcgagc gaaa atg gcg gct tcc agg tgg gcg cgc aag      51
                               Met Ala Ala Ser Arg Trp Ala Arg Lys
                               -30                               -25

gcc gtg gtc ctg ctt tgt gcc tct gac ctg ctg ctg ctg ctg cta ctg      99
Ala Val Val Leu Leu Cys Ala Ser Asp Leu Leu Leu Leu Leu Leu Leu
                               -20                               -15                               -10

cta cca ccg cct ggg tcc tgc gcc ggc cga agg tcg ccy dgg acg ccc      147
Leu Pro Pro Pro Gly Ser Cys Ala Gly Arg Arg Ser Pro Xaa Thr Pro
                               -5                               1                               5

gac gag tct acc cca cct ccc cgg aag aag aag aag gat att cgc gat      195
Asp Glu Ser Thr Pro Pro Pro Arg Lys Lys Lys Lys Asp Ile Arg Asp
10                               15                               20                               25

tac aat gat gca gac atg gcg cgt ctt ctg gag caa ggg gag ggg      240
Tyr Asn Asp Ala Asp Met Ala Arg Leu Leu Glu Gln Gly Glu Gly
                               30                               35                               40
```

<210> 30
 <211> 461
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 80..460

<221> sig_peptide
 <222> 80..136
 <223> Von Heijne matrix
 score 13.5
 seq WVLLLALLEGVQC/DV

<221> misc_feature
 <222> 280..281,311..313
 <223> n=a, g, c or t
 Oligonucleotide

<400> 30
 agctctcaga gaggtgcctt agccctggat tccaaggcat ttccacttgg tgatcagcac 60
 tgaacacaga ggactcacc atg gag ttg ggg ctg tgc tgg gtt ctc ctt tta 112
 Met Glu Leu Gly Leu Cys Trp Val Leu Leu Leu
 -15 -10
 gct ctt tta gaa ggt gtc caa tgt gac gtg gaa tta gtg gag tct ggg 160
 Ala Leu Leu Glu Gly Val Gln Cys Asp Val Glu Leu Val Glu Ser Gly
 -5 1 5
 ggc ggc ttg gtg cag cct gga ggg tct ctg aga ctt tcc tgt gca gcc 208
 Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala
 10 15 20
 tct gga ttc aat ttt agc act tat gag atg cat tgg atc cgc cag gct 256
 Ser Gly Phe Asn Phe Ser Thr Tyr Glu Met His Trp Ile Arg Gln Ala
 25 30 35 40
 cca ggg aag ggg ccg gag tgg gtn nca tat gtc agt ggt gga ggt gga 304
 Pro Gly Lys Gly Pro Glu Trp Val Xaa Tyr Val Ser Gly Gly Gly Gly
 45 50 55
 acc agh nnn aac gcv sac tct gtg aag ggc cga ttc acc atc tcc aga 352
 Thr Xaa Xaa Asn Ala Xaa Ser Val Lys Gly Arg Phe Thr Ile Ser Arg
 60 65 70
 gac aat gcc aac agt ttt gtg tat cta caa atg gac agt ctg cga gtc 400
 Asp Asn Ala Asn Ser Phe Val Tyr Leu Gln Met Asp Ser Leu Arg Val
 75 80 85
 gag gac acc gct ctc tat tac tgt gcg aga rgg gat tac gac ttc tgg 448
 Glu Asp Thr Ala Leu Tyr Tyr Cys Ala Arg Xaa Asp Tyr Asp Phe Trp
 90 95 100
 agt ggt tat tat a 461
 Ser Gly Tyr Tyr
 105

<210> 31
 <211> 112
 <212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 28..111

<221> sig_peptide

<222> 28..84

<223> Von Heijne matrix

score 13.3999996185303

seq LLLLLSHCTGSLS/QP

<400> 31

aactgtgcat gtcaggctgt gtccacc atg gcc tgg act cct ctt ctt ctc ttg 54
Met Ala Trp Thr Pro Leu Leu Leu Leu

-15

ctc ctc tct cac tgc aca ggt tcc ctc tcc cag cct gtg ctg act cag 102

Leu Leu Ser His Cys Thr Gly Ser Leu Ser Gln Pro Val Leu Thr Gln

-10 -5 1 5

cca cgc ggg g 112

Pro Arg Gly

<210> 32

<211> 445

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 80..445

<221> sig_peptide

<222> 80..136

<223> Von Heijne matrix

score 12.8000001907349

seq WVFLVALLRGVQC/QV

<221> misc_feature

<222> 2,7

<223> n=a, g, c or t

Oligonucleotide

<400> 32

anctctngga gaggagccca gcactagaag tcggcgggtgt ttccattcgg tgatcagcac 60

tgaacacaga ggactcacc atg gag ttt ggg ctg aat tgg gtt ttc ctc gtt 112

Met Glu Phe Gly Leu Asn Trp Val Phe Leu Val

-15

-10

gct ctt tta aga ggt gtc cag tgt cag gtt cag ttg gtg gag tct ggg 160

Ala Leu Leu Arg Gly Val Gln Cys Gln Val Gln Leu Val Glu Ser Gly

-5

1

5

gga ggc gtg gtc cag cct ggg acg tcc ctg aca ctt tcc tgt gca ggc 208

Gly Gly Val Val Gln Pro Gly Thr Ser Leu Thr Leu Ser Cys Ala Gly

10

15

20

tcg gga ttc agt ttc agt gat tat ggc atc cac tgg gtc cgc cag gct 256

Ser	Gly	Phe	Ser	Phe	Ser	Asp	Tyr	Gly	Ile	His	Trp	Val	Arg	Gln	Ala	
25					30					35					40	
cca	ggc	aag	ggg	ctg	gaa	tgg	gtg	gcg	gtt	att	tca	cac	gat	gga	aat	304
Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val	Ala	Val	Ile	Ser	His	Asp	Gly	Asn	
				45				50						55		
aac	aaa	tat	tat	gga	ggc	tcc	atg	aag	ggc	cga	gtc	acc	atc	tcc	aga	352
Asn	Lys	Tyr	Tyr	Gly	Gly	Ser	Met	Lys	Gly	Arg	Val	Thr	Ile	Ser	Arg	
			60					65					70			
gac	aac	tcc	agg	cat	acc	gtg	tct	ttg	caa	atg	agc	agc	ttg	gga	cct	400
Asp	Asn	Ser	Arg	His	Thr	Val	Ser	Leu	Gln	Met	Ser	Ser	Leu	Gly	Pro	
			75				80					85				
gag	gac	acg	gca	gtg	tat	tac	tgt	gcg	aaa	gat	cga	acc	ggg	ggg		445
Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala	Lys	Asp	Arg	Thr	Gly	Gly		
	90					95					100					

<210> 33
 <211> 321
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 41..319

<221> sig_peptide
 <222> 41..97
 <223> Von Heijne matrix
 score 12.6000003814697
 seq FLLLLAAPRWLS/QV

<400> 33																
aaatacttts	kgcagagtcc	tggacctcct	gtgcaagaac	atg	aaa	ctt	ctg	tgg								55
				Met	Lys	Leu	Leu	Trp								
								-15								
ttc	ttc	ctt	ctc	ctg	ctg	gca	gct	ccc	aga	tgg	gtc	ctg	tcc	cag	gtg	103
Phe	Phe	Leu	Leu	Leu	Leu	Ala	Ala	Pro	Arg	Trp	Val	Leu	Ser	Gln	Val	
				-10				-5						1		
cag	ctg	gtg	smg	tcg	ggc	cca	gga	ctg	gtg	aag	cct	tcg	ggg	acc	ctg	151
Gln	Leu	Val	Xaa	Ser	Gly	Pro	Gly	Leu	Val	Lys	Pro	Ser	Gly	Thr	Leu	
		5				10					15					
tcc	cta	acg	tgc	act	gts	ksb	ggk	grs	ksc	ata	act	aat	tac	tac	tgg	199
Ser	Leu	Thr	Cys	Thr	Val	Xaa	Gly	Xaa	Xaa	Ile	Thr	Asn	Tyr	Tyr	Trp	
		20				25				30						
agt	bgg	atc	cgg	cag	tcc	cca	ggg	aag	gga	ctg	gag	tgg	att	ggg	act	247
Ser	Xaa	Ile	Arg	Gln	Ser	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Ile	Gly	Thr	
					40					45					50	
atc	tac	tac	agt	ggg	agc	gcc	gac	cac	aac	ccc	tcc	ctc	agg	agt	mga	295
Ile	Tyr	Tyr	Ser	Gly	Ser	Ala	Asp	His	Asn	Pro	Ser	Leu	Arg	Ser	Arg	
				55					60					65		
gcc	act	att	tca	tta	gac	acg	cgc	gg								321
Ala	Thr	Ile	Ser	Leu	Asp	Thr	Arg									
				70												

<210> 34

<211> 193
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 49..192

<221> sig_peptide
 <222> 49..108
 <223> Von Heijne matrix
 score 12.5
 seq LLXLLLTALPPLWS/SS

<400> 34
 agagctcagg gtgckgagcg tgtgaccagc agtgagcaga ggccggcc atg gcc agc 57
 Met Ala Ser
 -20
 ctg ggg ctg ctg ctc ctg ckc tta ctg aca gca ctg cca ccg ctg tgg 105
 Leu Gly Leu Leu Leu Leu Xaa Leu Leu Thr Ala Leu Pro Pro Leu Trp
 -15 -10 -5
 tcc tcc tca ctg cct ggg ctg gac ack gct gaa agt aaa gcc acc akt 153
 Ser Ser Ser Leu Pro Gly Leu Asp Thr Ala Glu Ser Lys Ala Thr Xaa
 1 5 10 15
 gca gac ctg atc ctg tct gcg ctg gag aga gcc acc ggg g 193
 Ala Asp Leu Ile Leu Ser Ala Leu Glu Arg Ala Thr Gly
 20 25

<210> 35
 <211> 438
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 151..438

<221> sig_peptide
 <222> 151..234
 <223> Von Heijne matrix
 score 12.5
 seq LLLLLLLPLRGQA/NT

<400> 35
 acgagaaggg gagggggccc agccctgctt tgggcaatcc ttgctctgac cactcagaca 60
 ccgtgtcctc ttgcctggga gaggggaagc agatctgagg acatctctgt gccaggccag 120
 aaaccgcca cctgcagttc cttctccggg atg gac gtg ggg ccc agc tcc ctg 174
 Met Asp Val Gly Pro Ser Ser Leu
 -25
 ccc cac ctt ggg ctg aag ctg ctg ctg ctc ctg ctg ctg ctg ccc ctc 222
 Pro His Leu Gly Leu Lys Leu Leu Leu Leu Leu Leu Leu Pro Leu
 -20 -15 -10 -5
 agg ggc caa gcc aac aca ggc tgc tac ggg atc cca ggg atg ccc ggc 270
 Arg Gly Gln Ala Asn Thr Gly Cys Tyr Gly Ile Pro Gly Met Pro Gly

	1	5	10	
ctg ccc ggg gca cca ggg aag gat ggg tac gac gga ctg ccg ggg ccc				318
Leu Pro Gly Ala Pro Gly Lys Asp Gly Tyr Asp Gly Leu Pro Gly Pro				
15	20	25		
aag ggg gag cca gga atc cca gcc att ccc ggg atc cga gga ccc aaa				366
Lys Gly Glu Pro Gly Ile Pro Ala Ile Pro Gly Ile Arg Gly Pro Lys				
30	35	40		
ggg cag aag gga gaa ccc ggc tta ccc ggc cat cct ggg aaa aat ggc				414
Gly Gln Lys Gly Glu Pro Gly Leu Pro Gly His Pro Gly Lys Asn Gly				
45	50	55	60	
ccc atg gga ccc cct ggg atg cca				438
Pro Met Gly Pro Pro Gly Met Pro				
65				

<210> 36
 <211> 488
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 59..487

<221> sig_peptide
 <222> 59..115
 <223> Von Heijne matrix
 score 12.3999996185303
 seq ILLLVAAATGTHA/QV

<221> misc_feature
 <222> 26..28
 <223> n=a, g, c or t
 Oligonucleotide

<400> 36	
atcacacaac agmcacatcs swmvsnnnmc agaagccccc agagtgcagc acctcacc	58
atg gac tgc acc tgg agg atc ctc ctc ttg gtg gca gca gct aca ggc	106
Met Asp Cys Thr Trp Arg Ile Leu Leu Leu Val Ala Ala Ala Thr Gly	
-15	-10
acc cac gcc cag gtc cag ttg gta cag tct ggg cct gag gtg aaa aag	154
Thr His Ala Gln Val Gln Leu Val Gln Ser Gly Pro Glu Val Lys Lys	
1	5
cct ggg gcc tca gtg aag gtc tcc tgc cag gtt tcc gga tac aac gtc	202
Pro Gly Ala Ser Val Lys Val Ser Cys Gln Val Ser Gly Tyr Asn Val	
15	20
gtg gaa tta tcc atc cac tgg gtg cgt cag tcg cct gga aaa ggg ctt	250
Val Glu Leu Ser Ile His Trp Val Arg Gln Ser Pro Gly Lys Gly Leu	
30	35
gag tgg atg gga ggt ttt gac ctt gaa agt ggt gaa aca atc tac gca	298
Glu Trp Met Gly Gly Phe Asp Leu Glu Ser Gly Glu Thr Ile Tyr Ala	
50	55
cag agg ttc cag ggc aga atc acc atg acc gag gac tca tct tca gac	346
Gln Arg Phe Gln Gly Arg Ile Thr Met Thr Glu Asp Ser Ser Ser Asp	
65	70
	75

aca gcc ttc atg gag ctg atc agc ctg aga cct gaa gat gcg gcc gtc	394
Thr Ala Phe Met Glu Leu Ile Ser Leu Arg Pro Glu Asp Ala Ala Val	
80 85 90	
tac tac tgt gca acg atc cgg ctg cca gta gtg ctt ttt ttc gcg gct	442
Tyr Tyr Cys Ala Thr Ile Arg Leu Pro Val Val Leu Phe Phe Ala Ala	
95 100 105	
tct ggg gcc agg gaa ccc tgg tcg ccg tct cct cag cmt cca cgg g	488
Ser Gly Ala Arg Glu Pro Trp Ser Pro Ser Pro Gln Xaa Pro Arg	
110 115 120	

<210> 37
 <211> 138
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 26..136

<221> sig_peptide
 <222> 26..79
 <223> Von Heijne matrix
 score 12.1000003814697
 seq VLLLA VLLLA VLC/KV

<400> 37	
ttttaccgga cccgacgccg gcgtg atg tgg ctt ccg ctg gtg ctg ctc ctg	52
Met Trp Leu Pro Leu Val Leu Leu Leu	
-15 -10	
gct gtg ctg ctg ctg gcc gtc ctc tgc aaa gtt tac ttg gga cta ttc	100
Ala Val Leu Leu Leu Ala Val Leu Cys Lys Val Tyr Leu Gly Leu Phe	
-5 1 5	
tct ggc agc tcc ccg aat cct ttc tcc gaa gaa agg gg	138
Ser Gly Ser Ser Pro Asn Pro Phe Ser Glu Glu Arg	
10 15	

<210> 38
 <211> 163
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 9..161

<221> sig_peptide
 <222> 9..83
 <223> Von Heijne matrix
 score 11.8999996185303
 seq WLLLLPLLLGLNA/GA

<400> 38	
aacttgct atg gag ctg gca ctg cgg cgc tct ccc gtc ccg cgg tgg ttg	50
Met Glu Leu Ala Leu Arg Arg Ser Pro Val Pro Arg Trp Leu	

	-25		-20		-15		
ctg	ctg	ctg	ccg	ctg	ctg	ctg	ggc
Leu	Leu	Leu	Pro	Leu	Leu	Leu	Gly
	-10				-5		
tgg	ccc	aca	gag	gag	ggc	aag	gaa
Trp	Pro	Thr	Glu	Glu	Gly	Lys	Glu
			10			15	
aag	gat	gcc	tac	atg	gg		
Lys	Asp	Ala	Tyr	Met			
			25				

98

146

163

<210> 39
 <211> 427
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 35..427
 <221> sig_peptide
 <222> 35..91
 <223> Von Heijne matrix
 score 11.8999996185303
 seq FLFLLTCCPGSNS/QA

<221> misc_feature
 <222> 138..139
 <223> n=a, g, c or t
 Oligonucleotide

<400> 39	
tctggcacca ggggtccctt ccaatatcag cacc atg gcc tgg act cct ctc ttt	55
Met Ala Trp Thr Pro Leu Phe	

	-15	
ctg ttc ctc ctc act tgc tgc cca ggg tcc aat tcc cag gct gtg gkg		103
Leu Phe Leu Leu Thr Cys Cys Pro Gly Ser Asn Ser Gln Ala Val Xaa		
	-10	
act cag gag ccc ctc act gac tgt gtc ccc cgg ann aca gtc act ctc		151
Thr Gln Glu Pro Leu Thr Asp Cys Val Pro Arg Xaa Thr Val Thr Leu		
5	10	15
acc tgt ggc tcc agt att gga gct gtc acc aat ggt cat ttt ccc tac		199
Thr Cys Gly Ser Ser Ile Gly Ala Val Thr Asn Gly His Phe Pro Tyr		
	25	30
tgg ttc caa cag aag cct ggc caa gcc ccc agg aca ctg att tct gat		247
Trp Phe Gln Gln Lys Pro Gly Gln Ala Pro Arg Thr Leu Ile Ser Asp		
	40	45
acg ttc aac aga cag tcc tcg aca cct gcc cgc ttc tct ggc tcc ctc		295
Thr Phe Asn Arg Gln Ser Ser Thr Pro Ala Arg Phe Ser Gly Ser Leu		
	55	60
ctg ggg ggc aaa gct gtc ctg act ctt tcg gat gcg caa cct gac gat		343
Leu Gly Gly Lys Ala Val Leu Thr Leu Ser Asp Ala Gln Pro Asp Asp		
	70	75
gag gct gaa tat tat tgt gtc ctc tcc tat agt ggt ggt cgg ccg gtg		391

Glu	Ala	Glu	Tyr	Tyr	Cys	Val	Leu	Ser	Tyr	Ser	Gly	Gly	Arg	Pro	Val	
85					90					95					100	
ttc	ggc	gga	ggg	acc	aag	ctg	acc	gtc	cta	agt	cag					427
Phe	Gly	Gly	Gly	Thr	Lys	Leu	Thr	Val	Leu	Ser	Gln					
				105					110							

<210> 40
 <211> 97
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 22..96

<221> sig_peptide
 <222> 22..84
 <223> Von Heijne matrix
 score 11.8999996185303
 seq LALCLLLGPLAGA/KP

<400> 40																
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			Met	Gln	Ala	Cys	Met	Val	Pro	Gly	Leu	Ala				
			-20						-15							
ctc	tgc	ctc	cta	ctg	ggg	cct	ctt	gca	ggg	gcc	aag	cct	gtg	cag	g	97
Leu	Cys	Leu	Leu	Leu	Gly	Pro	Leu	Ala	Gly	Ala	Lys	Pro	Val	Gln		
-10					-5						1					

<210> 41
 <211> 251
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 13..249

<221> sig_peptide
 <222> 13..81
 <223> Von Heijne matrix
 score 11.8000001907349
 seq CLFVCLFLSQSFA/FV

<400> 41																
aaaagtattg	gg	atg	cct	agt	tac	aar	gtg	tgt	ggg	ggt	ttt	tgt	ttg	ttt		51
			Met	Pro	Ser	Tyr	Lys	Val	Cys	Gly	Val	Phe	Cys	Leu	Phe	
			-20						-15							
ggt	tgt	ttg	ttt	ttg	agc	cag	agt	ttt	gct	ttt	gtc	ctc	cag	gct	gga	99
Val	Cys	Leu	Phe	Leu	Ser	Gln	Ser	Phe	Ala	Phe	Val	Leu	Gln	Ala	Gly	
-10				-5				1					5			
gtg	cag	tgg	cgc	gat	ctc	tgc	tca	ctg	caa	cct	cag	ctt	ccc	agg	ttc	147
Val	Gln	Trp	Arg	Asp	Leu	Cys	Ser	Leu	Gln	Pro	Gln	Leu	Pro	Arg	Phe	
			10				15						20			

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ggg cca tcc tcc tgc ctc agc ctc cca agt ggc tgg gac tgc agg cgc      195
Gly Pro Ser Ser Cys Leu Ser Leu Pro Ser Gly Trp Asp Cys Arg Arg
      25                      30                      35
cca cca cca cgc ctg gct aat tct tgt gtt ttc ggt gga gac ggg gtt      243
Pro Pro Pro Arg Leu Ala Asn Ser Cys Val Phe Gly Gly Asp Gly Val
      40                      45                      50
tca ccg gg                                                                251
Ser Pro
55

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<210> 42
<211> 319
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> 143..319
<221> sig_peptide
<222> 143..205
<223> Von Heijne matrix
      score 11.6000003814697
      seq LLLCLALSGAAET/KP

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<221> misc_feature
<222> 139
<223> n=a, g, c or t
      Oligonucleotide

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<400> 42
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cccttcttcc gccgggcctc gcaagcagcg taggactgtg gagaagggcg gtgggcaagg      120
agggaactcg agagcarchy cc atg ggc aca cag gag ggc tgg wgc ctg ctg      172
                      Met Gly Thr Gln Glu Gly Trp Xaa Leu Leu
                      -20                      -15
ctc tgc ctg gct cta tct gga gca gca gaa acc aag ccc cac cca gca      220
Leu Cys Leu Ala Leu Ser Gly Ala Ala Glu Thr Lys Pro His Pro Ala
      -10                      -5                      1                      5
gag ggg cag tgg cgg gca gtg gdc gtg gtc cta gac ygt ttc ctg gtg      268
Glu Gly Gln Trp Arg Ala Val Xaa Val Val Leu Asp Xaa Phe Leu Val
      10                      15                      20
aag gac svt gcg cac cgt gga gct ctc gcc agc agt gag gac agg gca      316
Lys Asp Xaa Ala His Arg Gly Ala Leu Ala Ser Ser Glu Asp Arg Ala
      25                      30                      35
agg                                                                319
Arg

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<210> 43
<211> 412
<212> DNA
<213> Homo sapiens

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<220>

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<221> CDS
 <222> 35..412

<221> sig_peptide
 <222> 35..82
 <223> Von Heijne matrix
 score 11.1999998092651
 seq LVVFLLLWGVTWG/PV

<221> misc_feature
 <222> 148
 <223> n=a, g, c or t
 Oligonucleotide

<400> 43
 agacactcac tgcaccggag tgagcgcgac catc atg tcc atg ctc gtg gtc ttt 55
 Met Ser Met Leu Val Val Phe
 -15 -10
 ctc ttg ctg tgg ggt gtc acc tgg ggc cca gtg aca gaa gca gcc ata 103
 Leu Leu Leu Trp Gly Val Thr Trp Gly Pro Val Thr Glu Ala Ala Ile
 -5 1 5
 ttt tat gag acg cag scc agc ctg tgg gca gag tcc gaa cac tgn ctg 151
 Phe Tyr Glu Thr Gln Xaa Ser Leu Trp Ala Glu Ser Glu His Xaa Leu
 10 15 20
 aaa acc ctt ggc caa tgt gac gct gac gtg cca ggc ccg cct gga gac 199
 Lys Thr Leu Gly Gln Cys Asp Ala Asp Val Pro Gly Pro Pro Gly Asp
 25 30 35
 tcc aga ctt cca gct gtt caa gaa tgg ggg gcc cag gag cct gtg cac 247
 Ser Arg Leu Pro Ala Val Gln Glu Trp Gly Ala Gln Glu Pro Val His
 40 45 50 55
 ctt gac tca cct gcc atc aag cac cag ttc ctg ctg acg ggt gac acc 295
 Leu Asp Ser Pro Ala Ile Lys His Gln Phe Leu Leu Thr Gly Asp Thr
 60 65 70
 cag ggc cgc tac cgc tgc cgc tcg ggc ttg tcc aca gga tgg mcc cag 343
 Gln Gly Arg Tyr Arg Cys Arg Ser Gly Leu Ser Thr Gly Trp Xaa Gln
 75 80 85
 ctg agc aag ctc ctg gag ctg aca ggg cca aaa gtc ctt gcc tgc tcc 391
 Leu Ser Lys Leu Leu Glu Leu Thr Gly Pro Lys Val Leu Ala Cys Ser
 90 95 100
 ctg gct ctc gat ggc gcc agt 412
 Leu Ala Leu Asp Gly Ala Ser
 105 110

<210> 44
 <211> 331
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 32..331

<221> sig_peptide
 <222> 32..88

<223> Von Heijne matrix
 score 11.1999998092651
 seq IGFLLLWVPASRG/EI

<400> 44

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atgagcaaaa ctgacaagtc aaggcaggaa g atg ttg cca tca caa ctc att      52
                               Met Leu Pro Ser Gln Leu Ile
                               -15
ggg ttt ctg ctg ctc tgg gtt cca gcc tcc agg ggt gaa att gtg ctg      100
Gly Phe Leu Leu Leu Trp Val Pro Ala Ser Arg Gly Glu Ile Val Leu
      -10                               -5                               1
act cag tct cca gac ttt ctg tct gtg act cca aag gag aaa gtc acc      148
Thr Gln Ser Pro Asp Phe Leu Ser Val Thr Pro Lys Glu Lys Val Thr
      5                               10                               15                               20
atc acc tgc cgg gcc agt sag agc att ggt agt agt tta tac tgg tac      196
Ile Thr Cys Arg Ala Ser Xaa Ser Ile Gly Ser Ser Leu Tyr Trp Tyr
      25                               30                               35
cag cag aaa cca cat cag tct cca aag ctc gtc atc aag tat gct tcc      244
Gln Gln Lys Pro His Gln Ser Pro Lys Leu Val Ile Lys Tyr Ala Ser
      40                               45                               50
cag tcc ttc tca ggg gtc tcc tcg agg ttc agt ggc agt gga tct ggg      292
Gln Ser Phe Ser Gly Val Ser Ser Arg Phe Ser Gly Ser Gly Ser Gly
      55                               60                               65
aca gat ttc acc ctc aca atc aat agc ctg gaa cct ggg      331
Thr Asp Phe Thr Leu Thr Ile Asn Ser Leu Glu Pro Gly
      70                               75                               80

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<210> 45
 <211> 520
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 176..520

<221> sig_peptide
 <222> 176..235
 <223> Von Heijne matrix
 score 11.1999998092651
 seq AFLLLVALSYTLA/RD

<400> 45

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gaagataatc acttggggaa aggaagggttc gtttctgagt tagcaacaag taaatgcagc      60
actagtgggt gggattgagg tatgccctgg tgcataaata gagactcagc tgtgctggca      120
cactcagaag cttggaccgc atcctagccg ccgactcaca caaggcagag ttgcc atg      178
                               Met
                               -20
gag aaa att cca gtg tca gca ttc ttg ctc ctt gtg gcc ctc tcc tac      226
Glu Lys Ile Pro Val Ser Ala Phe Leu Leu Leu Val Ala Leu Ser Tyr
      -15                               -10                               -5
act ctg gcc aga gat acc aca gtc aaa cct gga gcc aaa aag gac aca      274
Thr Leu Ala Arg Asp Thr Thr Val Lys Pro Gly Ala Lys Lys Asp Thr
      1                               5                               10

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aag gac tct cga ccc aaa ctg ccc cag acc ctc tcc aga ggt tgg ggt	322
Lys Asp Ser Arg Pro Lys Leu Pro Gln Thr Leu Ser Arg Gly Trp Gly	
15 20 25	
gac caa ctc atc tgg act cag aca tat gaa gaa gct cta tat aaa tcc	370
Asp Gln Leu Ile Trp Thr Gln Thr Tyr Glu Glu Ala Leu Tyr Lys Ser	
30 35 40 45	
aag aca agc aac aaa ccc ttg atg att att cat cac ttg gat gag tgc	418
Lys Thr Ser Asn Lys Pro Leu Met Ile Ile His His Leu Asp Glu Cys	
50 55 60	
cca cac agt caa gct tta aag aaa gtg ttt gct gaa aat aaa gaa atc	466
Pro His Ser Gln Ala Leu Lys Lys Val Phe Ala Glu Asn Lys Glu Ile	
65 70 75	
cag aaa ttg gca gag cag ttt gtc ctc ctc aat ctg gtt tat gaa aca	514
Gln Lys Leu Ala Glu Gln Phe Val Leu Leu Asn Leu Val Tyr Glu Thr	
80 85 90	
act gac	520
Thr Asp	
95	

<210> 46
 <211> 383
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 25..381

<221> sig_peptide
 <222> 25..84
 <223> Von Heijne matrix
 score 11.1000003814697
 seq LLALLFFLGQAAG/DL

<400> 46	
agcggctcca gctaagagga caag atg agg ccc ggc ctc tca ttt ctc cta	51
Met Arg Pro Gly Leu Ser Phe Leu Leu	
-20 -15	
gcc ctt ctg ttc ttc ctt ggc caa gct gca ggg gat ttg ggg gat gtg	99
Ala Leu Leu Phe Phe Leu Gly Gln Ala Ala Gly Asp Leu Gly Asp Val	
-10 -5 1 5	
gga cct cca att ccc agc ccc ggc ttc agc tct ttc cca ggt gtt gac	147
Gly Pro Pro Ile Pro Ser Pro Gly Phe Ser Ser Phe Pro Gly Val Asp	
10 15 20	
tcc agc tcc agc ttc agc tcc agc tcc agg tcg ggc tcc agc tcc agc	195
Ser Ser Ser Ser Phe Ser Ser Ser Ser Arg Ser Gly Ser Ser Ser Ser	
25 30 35	
cgc agc tta ggc agc gga ggt tct gtg tcc cag ttg ttt tcc aat ttc	243
Arg Ser Leu Gly Ser Gly Gly Ser Val Ser Gln Leu Phe Ser Asn Phe	
40 45 50	
acc ggc tcc gtg gat gac cgt ggg acc tgc cag tgc tct gtt tcc ctg	291
Thr Gly Ser Val Asp Asp Arg Gly Thr Cys Gln Cys Ser Val Ser Leu	
55 60 65	
cca gac acc acc ttt ccc gtg gac aga gtg gaa cgc ttg gaa ttc aca	339

Pro	Asp	Thr	Thr	Phe	Pro	Val	Asp	Arg	Val	Glu	Arg	Leu	Glu	Phe	Thr	
70					75					80					85	
gct	cat	gtt	ctt	tct	cag	aag	ttt	gag	aaa	gaa	ctt	tct	aaa	gc		383
Ala	His	Val	Leu	Ser	Gln	Lys	Phe	Glu	Lys	Glu	Leu	Ser	Lys			
				90					95							

<210> 47
 <211> 459
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 17..457

<221> sig_peptide
 <222> 17..94
 <223> Von Heijne matrix
 score 11.1000003814697
 seq FLLLVAAPRWVRS/QV

<221> misc_feature
 <222> 399
 <223> n=a, g, c or t
 Oligonucleotide

<400> 47																
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		Met	Asp	Leu	Leu	His	Lys	Asn	Met	Lys	His	Leu	Trp			
			-25				-20					-15				
ttc	ttc	ctc	ctc	ctg	gtg	gca	gct	ccc	aga	tgg	gtc	cgg	tct	car	gtg	100
Phe	Phe	Leu	Leu	Leu	Val	Ala	Ala	Pro	Arg	Trp	Val	Arg	Ser	Gln	Val	
			-10					-5					1			
cag	ctg	cak	gag	tcg	ggc	cca	gga	ctg	gtg	aag	cct	tcg	ggg	acc	ctg	148
Gln	Leu	Xaa	Glu	Ser	Gly	Pro	Gly	Leu	Val	Lys	Pro	Ser	Gly	Thr	Leu	
	5				10			15								
tcc	ctc	atc	tgc	ggg	gtc	tct	ggg	gat	tcc	gtc	acc	att	agt	ggg	tgg	196
Ser	Leu	Ile	Cys	Gly	Val	Ser	Gly	Asp	Ser	Val	Thr	Ile	Ser	Gly	Trp	
	20				25			30								
tgg	agt	tgg	gtc	cgc	cag	ccc	cca	ggg	aag	gga	ctg	gag	tgg	att	tcg	244
Trp	Ser	Trp	Val	Arg	Gln	Pro	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Ile	Ser	
	35			40				45						50		
gaa	atc	gat	cat	ggg	gga	aac	acc	aac	tac	aac	ccg	tcc	ctc	aag	agt	292
Glu	Ile	Asp	His	Gly	Gly	Asn	Thr	Asn	Tyr	Asn	Pro	Ser	Leu	Lys	Ser	
			55			60								65		
cga	gtc	kcc	att	tct	tta	gac	aag	tcc	aag	aac	aag	ttc	tcc	ctg	agg	340
Arg	Val	Xaa	Ile	Ser	Leu	Asp	Lys	Ser	Lys	Asn	Lys	Phe	Ser	Leu	Arg	
		70				75						80				
ctg	acc	tct	gtg	acc	gcc	gcg	gac	acc	gcc	atg	tat	kac	tgt	gcg	aga	388
Leu	Thr	Ser	Val	Thr	Ala	Ala	Asp	Thr	Ala	Met	Tyr	Xaa	Cys	Ala	Arg	
		85				90						95				
ggc	ggg	gcg	bnc	agc	tcg	tcc	gct	ttt	gat	gtc	tgg	ggc	cta	rgg	aca	436
Gly	Gly	Ala	Xaa	Ser	Ser	Ser	Ala	Phe	Asp	Val	Trp	Gly	Leu	Xaa	Thr	
	100					105					110					

atg gtc atc atc tct tca gcc tc
 Met Val Ile Ile Ser Ser Ala
 115 120

459

<210> 48
 <211> 437
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 20..436

<221> sig_peptide
 <222> 20..76
 <223> Von Heijne matrix
 score 11
 seq TLLLLTVPSWVLS/QV

<400> 48
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 Met Asp Ile Leu Cys Ser Thr Leu Leu Leu Leu
 -15 -10
 ack gtc ccg tcc tgg gtc tta tcc car gtc acc ttg arg gaa tct ggt 100
 Thr Val Pro Ser Trp Val Leu Ser Gln Val Thr Leu Xaa Glu Ser Gly
 -5 1 5
 cct gcg ctg gtg aaa gcc aca cag acc ctc aga ctg acc tgc acc ttc 148
 Pro Ala Leu Val Lys Ala Thr Gln Thr Leu Arg Leu Thr Cys Thr Phe
 10 15 20
 tct ggg ttc tca ctc agc act aat aga atg cgt gtg agt tgg atc cgt 196
 Ser Gly Phe Ser Leu Ser Thr Asn Arg Met Arg Val Ser Trp Ile Arg
 25 30 35 40
 cag ccc cca ggg aag gcc ctg gag tgg ctt gca cgg att gat tgg gat 244
 Gln Pro Pro Gly Lys Ala Leu Glu Trp Leu Ala Arg Ile Asp Trp Asp
 45 50 55
 gat tat aag agg tac agc aca tct ctg aag acc agg gtc acc atc tcc 292
 Asp Tyr Lys Arg Tyr Ser Thr Ser Leu Lys Thr Arg Val Thr Ile Ser
 60 65 70
 aag gac acg tcc aaa aac cag gtg atc ctg aca atg acc aac gtg gac 340
 Lys Asp Thr Ser Lys Asn Gln Val Ile Leu Thr Met Thr Asn Val Asp
 75 80 85
 cct gcg gac aca gcc acc tat tac tgt gca cgc ctt tca acg gca gct 388
 Pro Ala Asp Thr Ala Thr Tyr Tyr Cys Ala Arg Leu Ser Thr Ala Ala
 90 95 100
 acc cca cag ttt ttt gac ttc tgg ggc cag gga gtc ctg gtc tcc gtc t 437
 Thr Pro Gln Phe Phe Asp Phe Trp Gly Gln Gly Val Leu Val Ser Val
 105 110 115 120

<210> 49
 <211> 456
 <212> DNA
 <213> Homo sapiens

<220>

<221> CDS
 <222> 40..456

<221> sig_peptide
 <222> 40..96
 <223> Von Heijne matrix
 score 10.8999996185303
 seq FLLLVAAPRWLS/QV

<400> 49
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 Met Xaa His Leu Trp
 -15
 ttc ttc ctt ctc ctg gtg gca gct ccc aga tgg gtc ctg tcc cag gtg 102
 Phe Phe Leu Leu Val Ala Ala Pro Arg Trp Val Leu Ser Gln Val
 -10 -5 1
 cag ctg cag gag tcg ggc cca gga ctg gtg aag cct tcg kwg acc ctg 150
 Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Xaa Thr Leu
 5 10 15
 tcc ctc acc tgc act gtc tct ggt gac tcc atc agt agt tac tac tgg 198
 Ser Leu Thr Cys Thr Val Ser Gly Asp Ser Ile Ser Ser Tyr Tyr Trp
 20 25 30
 agc tgg atc cgg cag ccc cca ggg aag gga ctg gag tgg att ggc tat 246
 Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile Gly Tyr
 35 40 45 50
 atc tat tac agt ggg agc acc aac tac aac ccc tcc ctc aag agt cga 294
 Ile Tyr Tyr Ser Gly Ser Thr Asn Tyr Asn Pro Ser Leu Lys Ser Arg
 55 60 65
 gtc acc ata tca gtg gac acg tcc aag aac caa ttc tcc ctg aag ctg 342
 Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu Lys Leu
 70 75 80
 agc tct gtg acc gca gcg gac acg gcc gtg tat tac tgt gcg aga sgg 390
 Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Arg Xaa
 85 90 95
 ctg cma tac tat gat agg agt ggt tat ttc aga tat ttt gac tac tgg 438
 Leu Xaa Tyr Tyr Asp Arg Ser Gly Tyr Phe Arg Tyr Phe Asp Tyr Trp
 100 105 110
 ggc cag gga acc tgg tca 456
 Gly Gln Gly Thr Trp Ser
 115 120

<210> 50
 <211> 447
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 38..445
 <221> sig_peptide
 <222> 38..94
 <223> Von Heijne matrix
 score 10.8999996185303

seq FLLLVAAPRWLS/QV

<221> misc_feature

<222> 16

<223> n=a, g, c or t
Oligonucleotide

<400> 50

atacttttctg agagtntctgg acctcctgtg caagaac atg aaa cat ctg tgg ttc 55
Met Lys His Leu Trp Phe

-15

ttc ctc ctc ctg gtg gca gct ccc aga tgg gtc ctg tcc cag gtg cag 103
Phe Leu Leu Leu Val Ala Ala Pro Arg Trp Val Leu Ser Gln Val Gln

-10

-5

1

ctg cag gag tcg ggc cca gga ctg gtg aag cct tca cag acc ctg tcc 151
Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln Thr Leu Ser

5

10

15

ctc acc tgc aca gtc tct ggt ggc tcc atc gac agt ggt aat tac tac 199
Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Asp Ser Gly Asn Tyr Tyr

20

25

30

35

tgg agc tgg atc cgg cag ccc gcc ggg aag gga ctg gag tgg att ggg 247
Trp Ser Trp Ile Arg Gln Pro Ala Gly Lys Gly Leu Glu Trp Ile Gly

40

45

50

cgc atc tat agt act ggg agc acc aat tac aac ccc tcc ctc agc agt 295
Arg Ile Tyr Ser Thr Gly Ser Thr Asn Tyr Asn Pro Ser Leu Ser Ser

55

60

65

cga gtc cag ata tcg tta gac acg tcc aag aac ctg ctc tcc ttg aac 343
Arg Val Gln Ile Ser Leu Asp Thr Ser Lys Asn Leu Leu Ser Leu Asn

70

75

80

ctg acc tct gtg acc gcc gca gac acg gcc gtc tat ttt tgt gcg cga 391
Leu Thr Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Phe Cys Ala Arg

85

90

95

acc ttc ccc ttc tac tgg tac ctc gat ctc tgg ggc cgt ggc atc ctg 439
Thr Phe Pro Phe Tyr Trp Tyr Leu Asp Leu Trp Gly Arg Gly Ile Leu

100

105

110

115

gtc act gt 447
Val Thr

<210> 51

<211> 466

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 38..466

<221> sig_peptide

<222> 38..94

<223> Von Heijne matrix
score 10.8999996185303
seq FLLLVAAPRWLS/QV

<221> misc_feature

<222> 423

<223> n=a, g, c or t
Oligonucleotide

<400> 51

atacttttctg agagtcctgg acctcctgtg caagaac atg aaa cac ctg tgg ttc 55
Met Lys His Leu Trp Phe

-15

ttc ctc ctg ctg gtg gca gct ccc aga tgg gtc ctg tcc cag gtg cag 103
Phe Leu Leu Leu Val Ala Ala Pro Arg Trp Val Leu Ser Gln Val Gln

-10

-5

1

ctg cag gag tgc ggc cca aga ctg gtg aag cct tca cag acc ctg tcc 151
Leu Gln Glu Ser Gly Pro Arg Leu Val Lys Pro Ser Gln Thr Leu Ser

5

10

15

ctc acc tgc act gtc tct ggt ggc tcc atc agc agt ggt ggt tac ttc 199
Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Gly Gly Tyr Phe

20

25

30

35

tgg agt tgg atc cgc cag cac cca ggg cgg ggc ctg gag tgg att ggc 247
Trp Ser Trp Ile Arg Gln His Pro Gly Arg Gly Leu Glu Trp Ile Gly

40

45

50

tac atc tat tac aat tgg agc acc tac tac aat ccg tcc ctc agg agt 295
Tyr Ile Tyr Tyr Asn Trp Ser Thr Tyr Tyr Asn Pro Ser Leu Arg Ser

55

60

65

cga gtt acc atg tca atg gac acg tct aag aac cag ttc tcc ctg aac 343
Arg Val Thr Met Ser Met Asp Thr Ser Lys Asn Gln Phe Ser Leu Asn

70

75

80

ctg aac tct gta act gcc gcg gac acg gsc atg tat tac tgt gcs aga 391
Leu Asn Ser Val Thr Ala Ala Asp Thr Xaa Met Tyr Tyr Cys Ala Arg

85

90

95

ggt cgc gga cgc ctt ggc tgg ttc ash mct tng ggg mca ggg rac cca 439
Gly Arg Gly Arg Leu Gly Trp Phe Xaa Xaa Xaa Gly Xaa Gly Xaa Pro

100

105

110

115

ggt cac cgt ctc atc agc cgt cca ggg 466
Gly His Arg Leu Ile Ser Arg Pro Gly

120

<210> 52

<211> 392

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 59..391

<221> sig_peptide

<222> 59..115

<223> Von Heijne matrix
score 10.8999996185303
seq FLLLVAAPRWVLS/QV

<221> misc_feature

<222> 342

<223> n=a, g, c or t

Oligonucleotide

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<400> 52
agggtcctgc tcacatggga aatacttttct gagagtcctg gacctcctgt gcaagaac      58
atg aaa cac ctg tgg ttc ttc ctc ctg ctg gtg gca gct ccc aga tgg      106
Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
          -15          -10          -5

gtc ctg tcc cag gtg cag ctg cag gag tcg ggc cca gga ctg gtg aag      154
Val Leu Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys
          1          5          10

cct tca gag acc ctg tcc ctc acc tgc act gtc tct ggt ggc tcc atc      202
Pro Ser Glu Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile
          15          20          25

agg act ggt tct tac tac tgg act tgg gtt cgc cag ccc ccc ggg aag      250
Arg Thr Gly Ser Tyr Tyr Trp Thr Trp Val Arg Gln Pro Pro Gly Lys
          30          35          40          45

ggc ctg gag tgg att ggc tac att tat tat act ggg gac acc tac tac      298
Gly Leu Glu Trp Ile Gly Tyr Ile Tyr Tyr Thr Gly Asp Thr Tyr Tyr
          50          55          60

aac ccg tcc ctc aag agt cga att acc atg tcr cta gac acg tny wag      346
Asn Pro Ser Leu Lys Ser Arg Ile Thr Met Ser Leu Asp Thr Xaa Xaa
          65          70          75

aac cag ttc kcc ctg agc ctg acc tct gtg act gtc gca gac acg g      392
Asn Gln Phe Xaa Leu Ser Leu Thr Ser Val Thr Val Ala Asp Thr
          80          85          90

<210> 53
<211> 172
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 14..172

<221> sig_peptide
<222> 14..58
<223> Von Heijne matrix
      score 10.8999996185303
      seq LSVCLLLVTLALC/CY

<400> 53
aaaacaagcc acc atg aag ctg tcg gtg tgt ctc ctg ctg gtc acg ctg      49
          Met Lys Leu Ser Val Cys Leu Leu Leu Val Thr Leu
          -15          -10          -5

gcc ctc tgc tgc tac cag gcc aat gcc gag ttc tgc cca gct ctt gtt      97
Ala Leu Cys Cys Tyr Gln Ala Asn Ala Glu Phe Cys Pro Ala Leu Val
          1          5          10

tct gag ctg tta gac ttc ttc ttc att agt gaa cct ctg ttc aag tta      145
Ser Glu Leu Leu Asp Phe Phe Phe Ile Ser Glu Pro Leu Phe Lys Leu
          15          20          25

agt ctt gcc aaa ttt gat gcc cct cga      172
Ser Leu Ala Lys Phe Asp Ala Pro Arg
          30          35

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<210> 54
 <211> 259
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 190..258

<221> sig_peptide
 <222> 190..237
 <223> Von Heijne matrix
 score 10.8999996185303
 seq VLLVLSLSQCLLS/DP

<400> 54
 tacctgaaa gaacagaaat ttgttaattt acaggtctga aggtgagaaa tctgaaatta 60
 gtcttacaaa actaaaatga agttgttga agccttggt cttctggag gttccagggg 120
 aaaaaagtat gtttccttga cttccagcc kstacaggcc cacagcattc ctgcttgcag 180
 ccctatgtc atg tca cct gtc ctc ttg gtg ctg tca ttg tca caa tgc ctt 231
 Met Ser Pro Val Leu Leu Val Leu Ser Leu Ser Gln Cys Leu
 -15 -10 -5
 ctt tct gac cct gtc att cct ggc ctc c 259
 Leu Ser Asp Pro Val Ile Pro Gly Leu
 1 5

<210> 55
 <211> 320
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 40..318

<221> sig_peptide
 <222> 40..96
 <223> Von Heijne matrix
 score 10.8999996185303
 seq FLLLVAAPRWVLS/QV

<400> 55
 aaacacsyyt tgagagtcct ggacctcctg tgcaggacc atg aaa cat ctg tgg 54
 Met Lys His Leu Trp
 -15
 ttc ttc ctt ctc ctg gtg gca gct ccc aga tgg gtc ctg tcc cag gtg 102
 Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp Val Leu Ser Gln Val
 -10 -5 1
 cgg ctg cag gag tgc ggc cca cgg ctg gtg aag cct tgc gag amc ctg 150
 Arg Leu Gln Glu Ser Gly Pro Arg Leu Val Lys Pro Ser Glu Xaa Leu
 5 10 15
 tcc ctc acc tgt agt gtc tct ggt gtc tcc gtc act aat ttc ttc tgg 198
 Ser Leu Thr Cys Ser Val Ser Gly Val Ser Val Thr Asn Phe Phe Trp

20	25	30	
aac tgg atc cgg aag ccc cca ggc aag ggc ctg gag tgg ctt ggc tac			246
Asn Trp Ile Arg Lys Pro Pro Gly Lys Gly Leu Glu Trp Leu Gly Tyr			
35	40	45	50
atg tct tat ggc gtg agc aca aac tat cac ccc gcc tac cag agt cgg			294
Met Ser Tyr Gly Val Ser Thr Asn Tyr His Pro Ala Tyr Gln Ser Arg			
	55	60	65
gtc agt ata tcg att gac acg tgg gg			320
Val Ser Ile Ser Ile Asp Thr Trp			
70			

<210> 56
 <211> 457
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 39..455

<221> sig_peptide
 <222> 39..95
 <223> Von Heijne matrix
 score 10.8999996185303
 seq FLLLVAAPRWVLS/QV

<400> 56	
aatacttttct gagagtcctg gacctcctgt gcaagaac atg aaa cat ctg tgg ttc	56
Met Lys His Leu Trp Phe	
-15	
ttc ctt ctc ctg gtg gca gct ccc aga tgg gtc ctg tcc cag gtg cag	104
Phe Leu Leu Leu Val Ala Ala Pro Arg Trp Val Leu Ser Gln Val Gln	
-10	-5
ctg cag gag gcg ggc cca cga ctg gtg aag cct tcg gag gcc ctg tcc	152
Leu Gln Glu Ala Gly Pro Arg Leu Val Lys Pro Ser Glu Ala Leu Ser	
5	10
ctc acc tgc act gtc tct ggt gtc tcc agc agc aat tac gac tgg agt	200
Leu Thr Cys Thr Val Ser Gly Val Ser Ser Ser Asn Tyr Asp Trp Ser	
20	25
tgg att cgg cag gcc cca ggg aag gga ctg gaa tgg att ggg tat ata	248
Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Ile Gly Tyr Ile	
40	45
gac gat agt aag aat aga ggg agt acg acc tac aac ccc tcc ctc aag	296
Asp Asp Ser Lys Asn Arg Gly Ser Thr Thr Tyr Asn Pro Ser Leu Lys	
55	60
agt cga gtc acc ata tcg stg gac acg tcc aag ast cag ttg tcc ctg	344
Ser Arg Val Thr Ile Ser Xaa Asp Thr Ser Lys Xaa Gln Leu Ser Leu	
70	75
agg ctg acc tct gtg acc kcs gca gac acg gcc gtc tat tat tgt gcg	392
Arg Leu Thr Ser Val Thr Xaa Ala Asp Thr Ala Val Tyr Tyr Cys Ala	
85	90
aga aag tca tct atg cat agt agt ggc tgg cat aac cgg agt ctc tac	440
Arg Lys Ser Ser Met His Ser Ser Gly Trp His Asn Arg Ser Leu Tyr	
100	105
	110
	115

tgg tac ttc gat cct gg
 Trp Tyr Phe Asp Pro
 120

457

<210> 57
 <211> 420
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 17..418

<221> sig_peptide
 <222> 17..94
 <223> Von Heijne matrix
 score 10.8999996185303
 seq FLLLVAAPRWLS/QV

<400> 57
 atactttctg agactc atg gac ctc ctg cac aag aac atg aaa gac ctg tgg 52
 Met Asp Leu Leu His Lys Asn Met Lys Asp Leu Trp
 -25 -20 -15
 ttc ttc ctc ctc ctg gtg gca gct ccc aga tgg gtc ctg tct cag gtg 100
 Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp Val Leu Ser Gln Val
 -10 -5 1
 ctg cag gag tcg ggc cca gga ctg gtg aag cct tcg ggg acc ctg tcc 148
 Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gly Thr Leu Ser
 5 10 15
 ctc acc tgc gct gtc tct ggt ggc tcc atc ata agt agt aat tgg tgg 196
 Leu Thr Cys Ala Val Ser Gly Gly Ser Ile Ile Ser Ser Asn Trp Trp
 20 25 30
 agt tgg gtc cgc cag acc cca ggg aag ggg ctg gag tgg att ggg gaa 244
 Ser Trp Val Arg Gln Thr Pro Gly Lys Gly Leu Glu Trp Ile Gly Glu
 35 40 45 50
 atc tat gaa gat ggg atc acc aac tac aac ccg tcc ctc aag agt cga 292
 Ile Tyr Glu Asp Gly Ile Thr Asn Tyr Asn Pro Ser Leu Lys Ser Arg
 55 60 65
 gtc atc att tca gtg gac aag gcc aag aac cag ttc tcc ctg aag atg 340
 Val Ile Ile Ser Val Asp Lys Ala Lys Asn Gln Phe Ser Leu Lys Met
 70 75 80
 agg tct gtg acc gcc tcg gac acg gcc gtc tat tac tgt gcg aga ggt 388
 Arg Ser Val Thr Ala Ser Asp Thr Ala Val Tyr Tyr Cys Ala Arg Gly
 85 90 95
 agc agc tcg gtt cgg aca gac tac tgg ggc ca 420
 Ser Ser Ser Val Arg Thr Asp Tyr Trp Gly
 100 105

<210> 58
 <211> 469
 <212> DNA
 <213> Homo sapiens

<220>

<221> CDS
 <222> 38..469

<221> sig_peptide
 <222> 38..94
 <223> Von Heijne matrix
 score 10.8999996185303
 seq FLLLVAAPRWLS/QV

<400> 58
 atactttctg agagtcctgg acctcctgtg caagaac atg aaa cac ctg tgg ttc 55
 Met Lys His Leu Trp Phe
 -15
 ttc ctc ctg ctg gtg gca gct ccc aga tgg gtc ctg tcc cag gtg cag 103
 Phe Leu Leu Leu Val Ala Ala Pro Arg Trp Val Leu Ser Gln Val Gln
 -10 -5 1
 ctg cag gag tcc ggt tca gga ccg gtg gat sct tsa cag acc ctg tsc 151
 Leu Gln Glu Ser Gly Ser Gly Pro Val Asp Xaa Xaa Gln Thr Leu Xaa
 5 10 15
 ctc acc tgc act gks tct ggt gtc tcc atc agc agt agt gat aat tgt 199
 Leu Thr Cys Thr Xaa Ser Gly Val Ser Ile Ser Ser Ser Asp Asn Cys
 20 25 30 35
 tgg agc tgg atc cgg cag cca cca ggg aag ggc ctg gag tgg att gga 247
 Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile Gly
 40 45 50
 tac atc tat cay agt ggg ggg acc tac tac aac ccg acc ctc aag agc 295
 Tyr Ile Tyr His Ser Gly Gly Thr Tyr Tyr Asn Pro Thr Leu Lys Ser
 55 60 65
 cga gtc acc atc tcg gba gac agg atc agg aac caa ttc tcc ctg aag 343
 Arg Val Thr Ile Ser Xaa Asp Arg Ile Arg Asn Gln Phe Ser Leu Lys
 70 75 80
 ctg agc tct gtg acg gcc gyg gac acg gcc gtg tat kac tgt ggc aga 391
 Leu Ser Ser Val Thr Ala Xaa Asp Thr Ala Val Tyr Xaa Cys Gly Arg
 85 90 95
 gca cag ggt aga atg ggg atc ggg acg acg att ttt gat ctc tgg ggc 439
 Ala Gln Gly Arg Met Gly Ile Gly Thr Thr Ile Phe Asp Leu Trp Gly
 100 105 110 115
 ggg gga caa tgg tca ccg tct ctg cag cct 469
 Gly Gly Gln Trp Ser Pro Ser Leu Gln Pro
 120 125

<210> 59
 <211> 471
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 52..471
 <221> sig_peptide
 <222> 52..108
 <223> Von Heijne matrix
 score 10.8000001907349

seq ILFLVAAATGAHS/QV

<221> misc_feature

<222> 210

<223> n=a, g, c or t
Oligonucleotide

<400> 59

acccaacaac cacatccctc ctcagmagcc cccagagcac aackcctyac c atg gac	57
	Met Asp
tgg acc tgg agg atc ctc ttt ttg gtg gca gca gcc aca ggt gcc cac	105
Trp Thr Trp Arg Ile Leu Phe Leu Val Ala Ala Ala Thr Gly Ala His	
-15 -10 -5	
tcc cag gtc cag ctt gtg cag tct ggg gct gag gtg aag aag cct ggg	153
Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly	
1 5 10 15	
gcc tca gtg aag gtt tcc tgc aag gct tct gga tac ayc ttc act ary	201
Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Xaa Phe Thr Xaa	
20 25 30	
tmt gct atn cat tgg gtg cgc cag gcc ccc gga car agr ctt gag tgg	249
Xaa Ala Xaa His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp	
35 40 45	
atg ggr tgg atc aac gct gcc amt ggt wam aca awa tat tca cag aas	297
Met Gly Trp Ile Asn Ala Ala Xaa Gly Xaa Thr Xaa Tyr Ser Gln Xaa	
50 55 60	
ttc cag grc aga gtc acc wtt acc agg gac aca tcc gcg agc aca gtc	345
Phe Gln Xaa Arg Val Thr Xaa Thr Arg Asp Thr Ser Ala Ser Thr Val	
65 70 75	
tcc atg gag ctg agc agc ctg aga tct gaa gac acg gct gtg tat ttc	393
Ser Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Phe	
80 85 90 95	
tgt gcg aga gat tgg gaa att gca gta gta cca act gct ata aac tct	441
Cys Ala Arg Asp Trp Glu Ile Ala Val Val Pro Thr Ala Ile Asn Ser	
100 105 110	
tac ggg ttc gac cct ggg gcc agg gaa cct	471
Tyr Gly Phe Asp Pro Gly Ala Arg Glu Pro	
115 120	

<210> 60

<211> 348

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 193..348

<221> sig_peptide

<222> 193..270

<223> Von Heijne matrix
score 10.8000001907349
seq VLFLCVFLGMSWA/GA

<400> 60

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agagcaaaga ggcaatctga agagaaaagc ataggaaagg aaacagtggg aataggaatt      60
ggggtaaaat gaggatcctt cccacaaaac attgctatta ttcagctcat ttcaaaggat      120
tccgstgcwg ccatttgtga gagccgctgg aggctgagtg aaagtcattt tgaaagactg      180
atccaaagaa ga atg gag gcc aga gtg gag cgt gct gtg cag aaa agg caa      231
          Met Glu Ala Arg Val Glu Arg Ala Val Gln Lys Arg Gln
          -25          -20          -15

gtc tta ttt ctt tgt gta ttt ctg gga atg tct tgg gct ggc gcc gaa      279
Val Leu Phe Leu Cys Val Phe Leu Gly Met Ser Trp Ala Gly Ala Glu
          -10          -5          1

ccg ctt cgg tat ttt gtg gcg gag gaa acc gag aga ggc acc tdk ctt      327
Pro Leu Arg Tyr Phe Val Ala Glu Glu Thr Glu Arg Gly Thr Xaa Leu
          5          10          15

acc aac ttg gca aaa gac cta      348
Thr Asn Leu Ala Lys Asp Leu
20          25

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<210> 61
<211> 457
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 55..456

<221> sig_peptide
<222> 55..111
<223> Von Heijne matrix
      score 10.8000001907349
      seq ILFLVAAATGAHS/QV

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<400> 61
acccaaaaaac cacacccctc cttgggagaa tcccctagat cacagctcct cacc atg      57
                                     Met
gac tgg acc tgg agc atc ctt ttc ttg gtg gca gca gcg aca ggt gcc      105
Asp Trp Thr Trp Ser Ile Leu Phe Leu Val Ala Ala Ala Thr Gly Ala
          -15          -10          -5

cac tcc cag gtt cag ctg gtg cag tct gga ggt gag gtg aag aag cct      153
His Ser Gln Val Gln Leu Val Gln Ser Gly Gly Glu Val Lys Lys Pro
          1          5          10

ggg gcc tcc gtc aag gtc tcc tgc aag gct tct ggt tac acc ttt acc      201
Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr
          15          20          25          30

aga tat gat atc aac tgg gtg cga cag gcc cct gga caa ggg ctt gag      249
Arg Tyr Asp Ile Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu
          35          40          45

tgg atg gga tgg atc agc gct dcc aat ggt aac aca aat tat gca cag      297
Trp Met Gly Trp Ile Ser Ala Xaa Asn Gly Asn Thr Asn Tyr Ala Gln
          50          55          60

daa gtc cag ggc aga gtc acc atg acc aca gac aca tcc acg aga aca      345
Xaa Val Gln Gly Arg Val Thr Met Thr Thr Asp Thr Ser Thr Arg Thr
          65          70          75

gcc tac atg gaa ctg agg agc ctg cga tct gac gac acg gcc att tat      393
Ala Tyr Met Glu Leu Arg Ser Leu Arg Ser Asp Asp Thr Ala Ile Tyr

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80	85	90	
tac tgt gcg cga gag atm bta gtg gba sta tgt gat gga cag ttg ggg			441
Tyr Cys Ala Arg Glu Ile Xaa Val Xaa Xaa Cys Asp Gly Gln Leu Gly			
95	100	105	110
cca ggg aac ctg gtc a			457
Pro Gly Asn Leu Val			
115			

<210> 62
 <211> 439
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 18..437

<221> sig_peptide
 <222> 18..95
 <223> Von Heijne matrix
 score 10.8000001907349
 seq FLLLVAAPRWVLS/QE

<400> 62	
agtgcttyct gasagtc atg gac gtc ctg cac aaa cac atg aaa cac ctg	50
Met Asp Val Leu His Lys His Met Lys His Leu	
-25	-20
tgg ttc ttc ctc ctc ctg gtg gca gct ccc aga tgg gtc ctg tcc cag	98
Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp Val Leu Ser Gln	
-15	-10
gag cag tta cgg cag tgg ggc gca sga ctg ttg aag cct tcg gag acc	146
Glu Gln Leu Arg Gln Trp Gly Ala Xaa Leu Leu Lys Pro Ser Glu Thr	
5	10
ctg tcc ctc acc tgt agt gtc tat ggt ggg tcc ttc aat ggt tac tac	194
Leu Ser Leu Thr Cys Ser Val Tyr Gly Gly Ser Phe Asn Gly Tyr Tyr	
20	25
tgg agc tgg atc cgc cag tcc cca ggg aag ggg ctg gag tgg att ggg	242
Trp Ser Trp Ile Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Ile Gly	
35	40
gga atc aat cac agc gga agc acc ctc tcc aac ccg tcc ctc aag agt	290
Gly Ile Asn His Ser Gly Ser Thr Leu Ser Asn Pro Ser Leu Lys Ser	
50	55
cgc gtc gac ctc tca gtt gat gcg tcc aag gac cag gtg tcc ctg agg	338
Arg Val Asp Leu Ser Val Asp Ala Ser Lys Asp Gln Val Ser Leu Arg	
70	75
ctg aaa ctt gtg acc gcc gcg gac acg gct gtg tac ttc tgc gcg aga	386
Leu Lys Leu Val Thr Ala Ala Asp Thr Ala Val Tyr Phe Cys Ala Arg	
85	90
ccc cat tac gat atg tcg act gat tct tcg ttt gac ggt ttt gat ctc	434
Pro His Tyr Asp Met Ser Thr Asp Ser Ser Phe Asp Gly Phe Asp Leu	
100	105
tgg gg	439
Trp	

<210> 63
 <211> 214
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 82..213

<221> sig_peptide
 <222> 82..126
 <223> Von Heijne matrix
 score 10.6999998092651
 seq LLALFFLLRIALA/SQ

<400> 63
 accattggtg tgtctgtttt tatgccagta ctgtgatgtt ttggttatat agctttgtaa 60
 tatattttga agccagatag t atg atg ctt cta gct ttg ttc ttt ttg ctt 111
 Met Met Leu Leu Ala Leu Phe Phe Leu Leu
 -15 -10
 agg att gct ttg gct agt caa ggt ctt ttg tgg ttc cat aca aat ttt 159
 Arg Ile Ala Leu Ala Ser Gln Gly Leu Leu Trp Phe His Thr Asn Phe
 -5 1 5 10
 aag gtt ttt gtt gtt tcy att tgt gtg aag act atc att ggg att tcg 207
 Lys Val Phe Val Val Ser Ile Cys Val Lys Thr Ile Ile Gly Ile Ser
 15 20 25
 ggg ggc a 214
 Gly Gly

<210> 64
 <211> 297
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 63..296

<221> sig_peptide
 <222> 63..119
 <223> Von Heijne matrix
 score 10.6999998092651
 seq ILFLVAAATGALS/QV

<400> 64
 gtgcatcacc cagcaaccac atctgtcctc tagagaatcc cctgagadht ccgttcctca 60
 cc atg gac tgg acc tgg agg atc ctc ttc ttg gtg gca gcr gcc aca 107
 Met Asp Trp Thr Trp Arg Ile Leu Phe Leu Val Ala Ala Ala Thr
 -15 -10 -5
 gga gcc ctc tcc cag gtg cag ctg gtr cag tct gga ggt gar gtg aag 155
 Gly Ala Leu Ser Gln Val Gln Leu Val Gln Ser Gly Gly Glu Val Lys
 1 5 10
 aag cct ggg gcc tca gtg agg gtc tcc tgc aag gcc tct gga tac agc 203
 Lys Pro Gly Ala Ser Val Arg Val Ser Cys Lys Ala Ser Gly Tyr Ser

15	20	25	
ttc atc ggc tat tat gta cac tgg ata cga cag act cct ggg cga sgc			251
Phe Ile Gly Tyr Tyr Val His Trp Ile Arg Gln Thr Pro Gly Arg Xaa			
30	35	40	
ctt gag tgg atg ggg tgg gtc aac cct crs act ggc gac aac ggg g			297
Leu Glu Trp Met Gly Trp Val Asn Pro Xaa Thr Gly Asp Asn Gly			
45	50	55	

<210> 65
 <211> 370
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 237..368

<221> sig_peptide
 <222> 237..347
 <223> Von Heijne matrix
 score 10.6000003814697
 seq YLLLVLSSLCS/CS

<400> 65	
aaaggtacac aattgaaaaa aattgtatcc ttcacaacag atgtgggcag tcaactttta	60
gacctgtgtg ctttagtttg acctgtcctt cagtgagtgt atataaaatt ctaagctaaa	120
acatattttc tgaaattgtg aaggattatgc atgtctatct tcttgcctac tctaaatata	180
tcaatcgttt tcttgggaag ttagtctttc tttcacactt gtctgtagat ctttac atg	239
	Met
ttc ttt cag ttt tgg aag tcc tct gca tat tta ata ttt gtt agt att	287
Phe Phe Gln Phe Trp Lys Ser Ser Ala Tyr Leu Ile Phe Val Ser Ile	
-35 -30 -25	
tgt aaa ggt ttt ctt cct gtc tac ctc ctt ctt gtt ctc tct ctc tct	335
Cys Lys Gly Phe Leu Pro Val Tyr Leu Leu Val Leu Ser Leu Ser	
-20 -15 -10 -5	
ctc tct ctc tgt tgc tct ctc ttg ctc tct ctc ca	370
Leu Ser Leu Cys Cys Ser Leu Leu Leu Ser Leu	
1 5	

<210> 66
 <211> 428
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 45..428

<221> sig_peptide
 <222> 45..101
 <223> Von Heijne matrix
 score 10.6000003814697
 seq ILFLVAAATGVHS/QV

<221> misc_feature
 <222> 342..343
 <223> n=a, g, c or t
 Oligonucleotide

<400> 66
 aaccacmycc ctcctcagaa gccccagag cacaacgcct cacc atg gac tgg acc 56
 Met Asp Trp Thr
 tgg agg atc ctc ttt ttg gtg gca gca gcc aca ggt gtc cac tcc cag 104
 Trp Arg Ile Leu Phe Leu Val Ala Ala Ala Thr Gly Val His Ser Gln
 -15 -10 -5 1
 gtc cac ctt gtt cag tct ggg gct gar gtg aag aag cct ggg act ccg 152
 Val His Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Thr Pro
 5 10 15
 gtg aac att tcc tgt aag gct ttt ggc tac acc ttc cct gcc ttt gct 200
 Val Asn Ile Ser Cys Lys Ala Phe Gly Tyr Thr Phe Pro Ala Phe Ala
 20 25 30
 ata cat tgg gtt cgc cag gcc ccc gga caa agt ctt gag tgg atg gga 248
 Ile His Trp Val Arg Gln Ala Pro Gly Gln Ser Leu Glu Trp Met Gly
 35 40 45
 tgg gtc aac att ggc cat ggc aac aca aag tat tca cag aag ttt cag 296
 Trp Val Asn Ile Gly His Gly Asn Thr Lys Tyr Ser Gln Lys Phe Gln
 50 55 60 65
 ggc aga ctc gcc atc tcc aga gac acg tcc gcg aac ata gtc tac nng 344
 Gly Arg Leu Ala Ile Ser Arg Asp Thr Ser Ala Asn Ile Val Tyr Xaa
 70 75 80
 gaa ctg agc ggc ctg aga tct gaa gac acg gct gtc tat tac tgt gcg 392
 Glu Leu Ser Gly Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala
 85 90 95
 agg gat aat ctt ttc ttt ggc agt atg ggc ttt gac 428
 Arg Asp Asn Leu Phe Phe Gly Ser Met Gly Phe Asp
 100 105

<210> 67
 <211> 493
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 38..493

<221> sig_peptide
 <222> 38..85
 <223> Von Heijne matrix
 score 10.6000003814697
 seq TVLLLGLLSHCTG/SV

<400> 67
 ctgggcctaa ggaagcagca ctggtggtgc ctcagcc atg gcc tgg acc gtt ctc 55
 Met Ala Trp Thr Val Leu
 -15
 ctc ctc ggc ctc ctc tct cac tgc aca ggc tct gtg acc tcc tat gtg 103
 Leu Leu Gly Leu Leu Ser His Cys Thr Gly Ser Val Thr Ser Tyr Val

-10		-5		1		5	
ctg act cag cct ccc tcg gtg tca gtg gcc cca gga aag acg gcc agc	151						
Leu Thr Gln Pro Pro Ser Val Ser Val Ala Pro Gly Lys Thr Ala Ser							
10 15 20							
att acc tgt ggg gga gac aac att gaa agt caa gtt gta cac tgg cac	199						
Ile Thr Cys Gly Gly Asp Asn Ile Glu Ser Gln Val Val His Trp His							
25 30 35							
cag cag aag cca ggg cag gcc cct ata ttg gtc atc tat gat gat acc	247						
Gln Gln Lys Pro Gly Gln Ala Pro Ile Leu Val Ile Tyr Asp Asp Thr							
40 45 50							
gac cgg ccc tca ggg atc cct gac cga ttc tct ggc tcc aac tct ggg	295						
Asp Arg Pro Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser Asn Ser Gly							
55 60 65 70							
cac acg gcc acc ctg acc atc agc agg gtc gaa gcc ggg gat gag gcc	343						
His Thr Ala Thr Leu Thr Ile Ser Arg Val Glu Ala Gly Asp Glu Ala							
75 80 85							
gac tat tat tgt cag gtg tgg gat aga agt agt ggt cag gga ata ttc	391						
Asp Tyr Tyr Cys Gln Val Trp Asp Arg Ser Ser Gly Gln Gly Ile Phe							
90 95 100							
ggc gga ggg acc aag ctg acc gtc cta cgt cag ccc aag gct gcc ccc	439						
Gly Gly Gly Thr Lys Leu Thr Val Leu Arg Gln Pro Lys Ala Ala Pro							
105 110 115							
tcg gtc act ctg ttc ccg ccc tcc tct gag gag ctt caa gcc aac aag	487						
Ser Val Thr Leu Phe Pro Pro Ser Ser Glu Glu Leu Gln Ala Asn Lys							
120 125 130							
gcc aca	493						
Ala Thr							
135							

<210> 68
 <211> 180
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 36..179

<221> sig_peptide
 <222> 36..80
 <223> Von Heijne matrix
 score 10.6000003814697
 seq LLFLLLFVCF SRQ/GL

<400> 68	
tggcagttac tccagctccc aaatatagat attcc atg agg ttg ttg ttt ttg	53
Met Arg Leu Leu Phe Leu	
-15 -10	
ttg ttg ttt gtt tgt ttt tcg aga cag ggt ctc gct ttg tct ctc agg	101
Leu Leu Phe Val Cys Phe Ser Arg Gln Gly Leu Ala Leu Ser Leu Arg	
-5 1 5	
ctg gaa tgc agt ggt atg atc atg gct tac tgc agc atc agc ctc cca	149
Leu Glu Cys Ser Gly Met Ile Met Ala Tyr Cys Ser Ile Ser Leu Pro	
10 15 20	

ggc tca agc agt cct ctc acc tca gcc tcc a 180
 Gly Ser Ser Ser Pro Leu Thr Ser Ala Ser
 25 30

<210> 69
 <211> 259
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 38..259

<221> sig_peptide
 <222> 38..94
 <223> Von Heijne matrix
 score 10.6000003814697
 seq FLLLV SAPRWLS/QV

<400> 69
 atacttyctg agagtcctgg acctcctgca caagaac atg aaa cac ctg tgg ttc 55
 Met Lys His Leu Trp Phe
 -15

ttc ctc ctc ctg gtg tca gct ccc aga tgg gtc ctg tct cag gtg cag 103
 Phe Leu Leu Leu Val Ser Ala Pro Arg Trp Val Leu Ser Gln Val Gln
 -10 -5 1

cta cag gag tcg ggc cca gga ctg gtg aag cct tcg ggg agg ctg tcc 151
 Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gly Arg Leu Ser
 5 10 15

ctc gcc tgc gat gtg gtg gaa ttg agt ccg ccg gcc ccc agg ggc ggc 199
 Leu Ala Cys Asp Val Val Glu Leu Ser Pro Pro Ala Pro Arg Gly Gly
 20 25 30 35

tct gca gtg cat ctc aga aat ctt tca tca tgg gag ccc cac cta caa 247
 Ser Ala Val His Leu Arg Asn Leu Ser Ser Trp Glu Pro His Leu Gln
 40 45 50

ccc gtc tcg ggg 259
 Pro Val Ser Gly
 55

<210> 70
 <211> 178
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 7..177

<221> sig_peptide
 <222> 7..102
 <223> Von Heijne matrix
 score 10.6000003814697
 seq VVFLLLLVSTLSS/VV

<400> 70
 cgtata atg act tac ttt cct ctg ggt aga tac cca gta atg gga ttg 48
 Met Thr Tyr Phe Pro Leu Gly Arg Tyr Pro Val Met Gly Leu
 -30 -25 -20
 ctg gat caa atg gta gtt gtg ttt tta ctt ctt tta gtc tcc aca ctt 96
 Leu Asp Gln Met Val Val Val Phe Leu Leu Leu Leu Val Ser Thr Leu
 -15 -10 -5
 tct tcc gta gtg gtt tta cta gtt tgc att ccc acc agc agt gta aaa 144
 Ser Ser Val Val Val Leu Leu Val Cys Ile Pro Thr Ser Ser Val Lys
 1 5 10
 ttg ttc cct ttt cac cat atc cac acc aac tgg g 178
 Leu Phe Pro Phe His His Ile His Thr Asn Trp
 15 20 25

<210> 71
 <211> 131
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 40..129
 <221> sig_peptide
 <222> 40..96
 <223> Von Heijne matrix
 score 10.5
 seq WVLLVAMLRGLQC/QV

<400> 71
 agctctggga gacgagccca gctctgcagt ggactcacc atg gag ttt ggg ctg 54
 Met Glu Phe Gly Leu
 -15
 agc tgg gtt ctc ctc gtt gct atg tta aga ggt ctc cag tgt caa gtg 102
 Ser Trp Val Leu Leu Val Ala Met Leu Arg Gly Leu Gln Cys Gln Val
 -10 -5 1
 cag ctg gtg gag tct ggg gga acc gcg gg 131
 Gln Leu Val Glu Ser Gly Gly Thr Ala
 5 10

<210> 72
 <211> 217
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 47..217
 <221> sig_peptide
 <222> 47..91
 <223> Von Heijne matrix
 score 10.5
 seq LSLILLLLENVSG/FP

<221> sig_peptide
 <222> 23..82
 <223> Von Heijne matrix
 score 10.3999996185303
 seq FLTLLHCTGSLA/QL

<400> 74
 agagctctgg ggagctctgca cc atg gct tgg acc cca ctc ctc ttc ctc acc 52
 Met Ala Trp Thr Pro Leu Leu Phe Leu Thr
 -20 -15
 ctc ctc ctc cac tgc aca ggg tct ctc gcc cag ctt gtg ctg act caa 100
 Leu Leu Leu His Cys Thr Gly Ser Leu Ala Gln Leu Val Leu Thr Gln
 -10 -5 1 5
 tcg ccc tct gcc tct gcc tcc ctg gga gcc tcg gtc aag ctc acc tgc 148
 Ser Pro Ser Ala Ser Ala Ser Leu Gly Ala Ser Val Lys Leu Thr Cys
 10 15 20
 act ctg agc agt ggg cac agc aac tac ggc atc gct tgg tat cag cag 196
 Thr Leu Ser Ser Gly His Ser Asn Tyr Gly Ile Ala Trp Tyr Gln Gln
 25 30 35
 cag cca gag aag ggc cct cga ttc ttg atg aaa gtt aac agt gat ggc 244
 Gln Pro Glu Lys Gly Pro Arg Phe Leu Met Lys Val Asn Ser Asp Gly
 40 45 50
 agc cac atg aag gcg gac ggg atc cct gat cgc ttc tca ggc tcc agc 292
 Ser His Met Lys Ala Asp Gly Ile Pro Asp Arg Phe Ser Gly Ser Ser
 55 60 65 70
 tct ggg gct gag cgc tac ctc tcc atc tcc agc ctc a 329
 Ser Gly Ala Glu Arg Tyr Leu Ser Ile Ser Ser Leu
 75 80

<210> 75
 <211> 314
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 259..312

<221> sig_peptide
 <222> 259..300
 <223> Von Heijne matrix
 score 10.3999996185303
 seq PLALFFLLSVALA/IQ

<400> 75
 taggggtgaga gatggggatc tagttttatt cttctgcata tggatatcca gttttccag 60
 taacatttat tgaagagact ggcctttccc caatgagtgt tcttggcacc tttgtcaaaa 120
 gtcagttggc cgtagatatg tggattaatt tctgtgttcc ctgttttgtt ccattggcct 180
 atgtgtctgt ttttatgaca gtaccaggtt gtttttggtta ctacagcttt gtagtttact 240
 ttgaggtctg ttagtgtg atg cct cta gct ttg ttc ttt ttg ctc agt gtt 291
 Met Pro Leu Ala Leu Phe Phe Leu Leu Ser Val
 -10 -5
 gct ttg gct att cag ggt cag gg 314
 Ala Leu Ala Ile Gln Gly Gln

1

<210> 76
<211> 447
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 59..445

<221> sig_peptide
<222> 59..115
<223> Von Heijne matrix
score 10.3999996185303
seq XFCLLAVAPGAHS/QV

<400> 76
atcatccaac aaccacatcc cttctctaca gaagcctctg agaggaaagt tcttcacc 58
atg gac tgg acc tgg agg rwc ttc tgc ttg ctg gct gta gct cca ggt 106
Met Asp Trp Thr Trp Arg Xaa Phe Cys Leu Leu Ala Val Ala Pro Gly
-15 -10 -5
gct cac tcc cag gtg cag ctg gtg cag tct ggg gct gag gtg aag aag 154
Ala His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
1 5 10
cct ggg gcc tca gtg aag gtt tcc tgc aag gca tct gga tac acc ttc 202
Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
15 20 25
acc agc cac tat atg cac tgg gtg cga cag gcc cct gga caa ggg ctt 250
Thr Ser His Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
30 35 40 45
gag tgg atg gga ata atc tac cct gat agt gat acc act aag tac cba 298
Glu Trp Met Gly Ile Ile Tyr Pro Asp Ser Asp Thr Thr Lys Tyr Xaa
50 55 60
cag aac ttc cag ggc aga gtc acc atg act agg gac acg tcc acg agc 346
Gln Asn Phe Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser
65 70 75
aca gtc tac atg gag ctg agc agc ctg aca tct gac gac acg gcc gtg 394
Thr Val Tyr Met Glu Leu Ser Ser Leu Thr Ser Asp Asp Thr Ala Val
80 85 90
tat tat tgt gct aga gag gcg tat agt ggg agc tac cgc ttt gac tac 442
Tyr Tyr Cys Ala Arg Glu Ala Tyr Ser Gly Ser Tyr Arg Phe Asp Tyr
95 100 105
tgg gg 447
Trp
110

<210> 77
<211> 388
<212> DNA
<213> Homo sapiens

<220>
<221> CDS

<222> 16..387

<221> sig_peptide

<222> 16..93

<223> Von Heijne matrix

score 10.3000001907349

seq LLLLVAAPRWVLS/QL

<400> 77

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		Met	Asp	Leu	Met	Cys	Lys	Lys	Met	Arg	His	Leu	Trp	
		-25				-20						-15		
ttc	ctc	ctc	ctg	ctg	gtg	gcg	gct	ccc	aga	tgg	gtc	ctg	tcc	99
Phe	Leu	Leu	Leu	Leu	Val	Ala	Ala	Pro	Arg	Trp	Val	Leu	Ser	
		-10				-5						1		
cag	ctt	cag	gag	tcg	ggc	cca	gga	ctg	gtg	aag	gct	tcg	gag	147
Gln	Leu	Gln	Glu	Ser	Gly	Pro	Gly	Leu	Val	Lys	Ala	Ser	Glu	
	5				10				15					
tcc	ctc	gcc	tgc	agt	gtc	tct	ggg	gac	tcc	atc	agc	agt	ggg	195
Ser	Leu	Ala	Cys	Ser	Val	Ser	Gly	Asp	Ser	Ile	Ser	Ser	Gly	
	20				25				30					
tac	tgg	ggc	tgg	atc	cgg	cag	ccc	cca	ggg	aag	gga	ctg	cag	243
Tyr	Trp	Gly	Trp	Ile	Arg	Gln	Pro	Pro	Gly	Lys	Gly	Leu	Gln	
	35				40				45				50	
ggg	agt	ctt	tgg	aat	cgt	ggc	ggg	ccg	caa	tac	aay	hcc	tcc	291
Gly	Ser	Leu	Trp	Asn	Arg	Gly	Gly	Pro	Gln	Tyr	Asn	Xaa	Ser	
				55				60				65		
aat	cga	gtc	acc	gtg	tcc	gta	gac	acg	tcc	acg	aat	cat	ttc	339
Asn	Arg	Val	Thr	Val	Ser	Val	Asp	Thr	Ser	Thr	Asn	His	Phe	
		70				75						80		
aga	ctg	aat	tcc	gtg	aay	vgh	gga	cac	ggc	aat	tta	tta	ctg	388
Arg	Leu	Asn	Ser	Val	Asn	Xaa	Gly	His	Gly	Asn	Leu	Leu	Leu	
	85					90					95			

<210> 78

<211> 121

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 25..120

<221> sig_peptide

<222> 25..72

<223> Von Heijne matrix

score 10.1999998092651

seq XLXLSVLLGXXXX/KX

<400> 78

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		Met	Arg	Xaa	Xaa	Leu	Xaa	Leu	Ser	Val		
		-15				-10						
ctg	ttr	ggg	sck	rts	tbt	kgc	aag	gmg	gac	ttt	gtg	99

Leu Leu Gly Xaa Xaa Xaa Xaa Lys Xaa Asp Phe Val Gly His Gln Val
 -5 1 5
 ctc cga atc tct gta gcc gat g 121
 Leu Arg Ile Ser Val Ala Asp
 10 15

<210> 79
 <211> 149
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 36..149

<221> sig_peptide
 <222> 36..143
 <223> Von Heijne matrix
 score 10.1999998092651
 seq FLLFFCFVFLRG/QG

<400> 79
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 Met Ala Glu Ser Arg Glu
 -35

gaa ggt gaa agc tgt gtt gag agc cac tgt gtg ctc ttt ttc acc ctg 101
 Glu Gly Glu Ser Cys Val Glu Ser His Cys Val Leu Phe Phe Thr Leu
 -30 -25 -20 -15
 ttt ttt ttg ttg ttt ttt tgt ttt gtt ttt tgt ttg agg gga cag ggg 149
 Phe Phe Leu Leu Phe Phe Cys Phe Val Phe Cys Leu Arg Gly Gln Gly
 -10 -5 1

<210> 80
 <211> 410
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 80..409

<221> sig_peptide
 <222> 80..136
 <223> Von Heijne matrix
 score 10.1000003814697
 seq WLFLVAFLKGVQC/EV

<400> 80
 agctctgaga gaggagccca gccctgggat tttcaggtgt tttcatgtgg tgatcaggac 60
 tgaacagaga gaattcacc atg gag ctt ggg ctg agc tgg ctt ttt ctt gtg 112
 Met Glu Leu Gly Leu Ser Trp Leu Phe Leu Val
 -15 -10
 gct ttt tta aaa ggt gtc cag tgt gag gtg cag ttg ttg gag tct ggg 160
 Ala Phe Leu Lys Gly Val Gln Cys Glu Val Gln Leu Leu Glu Ser Gly

	-5		1		5														
	gga	ggc	ttg	gtc	cag	cct	ggg	ggg	tcc	ctg	aga	ctc	tca	tgt	gca	gcc			208
	Gly	Gly	Leu	Val	Gln	Pro	Gly	Gly	Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala			
	10						15					20							
	tcc	gga	ttc	acc	ttt	agc	tcc	tat	gcc	atg	ctc	tgg	gtc	cgc	cag	gct			256
	Ser	Gly	Phe	Thr	Phe	Ser	Ser	Tyr	Ala	Met	Leu	Trp	Val	Arg	Gln	Ala			
	25					30					35				40				
	cca	ggt	aag	ggg	ctg	gag	tgg	gtc	tca	ggt	att	agt	gct	ggt	gct	gat			304
	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val	Ser	Gly	Ile	Ser	Ala	Gly	Ala	Asp			
					45					50				55					
	gat	aca	tat	gat	gca	gac	tcc	gtg	aag	ggc	cgg	ttc	acc	att	tcc	aga			352
	Asp	Thr	Tyr	Asp	Ala	Asp	Ser	Val	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg			
				60				65					70						
	gac	gat	tcc	aag	aaa	atc	cta	tat	cta	caa	atg	aac	agc	ctg	aga	gcc			400
	Asp	Asp	Ser	Lys	Lys	Ile	Leu	Tyr	Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala			
			75				80					85							
	gag	gac	agg	c															410
	Glu	Asp	Arg																
	90																		

<210> 81
 <211> 219
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 38..217

<221> sig_peptide
 <222> 38..106
 <223> Von Heijne matrix
 score 10.1000003814697
 seq VLGLLVFLTCYA/DD

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					Met	Ala	Val	Ser	Val	Leu									
	cgc	ctg	aca	gtt	gtc	ctg	gga	ctg	ctt	gtc	tta	ttc	ctg	acc	tgc	tat			103
	Arg	Leu	Thr	Val	Val	Leu	Gly	Leu	Leu	Val	Leu	Phe	Leu	Thr	Cys	Tyr			
				-15				-10					-5						
	gca	gac	gac	aaa	cca	gac	aag	cca	gac	gac	aag	cca	gac	gac	tcg	ggc			151
	Ala	Asp	Asp	Lys	Pro	Asp	Lys	Pro	Asp	Asp	Lys	Pro	Asp	Asp	Ser	Gly			
	1				5					10					15				
	aaa	gac	cca	aag	cca	gac	ttc	ccc	aaa	ttc	cta	agc	ctc	ctg	ggc	aca			199
	Lys	Asp	Pro	Lys	Pro	Asp	Phe	Pro	Lys	Phe	Leu	Ser	Leu	Leu	Gly	Thr			
					20				25						30				
	gag	atc	att	gag	aat	gcg	gg												219
	Glu	Ile	Ile	Glu	Asn	Ala													
				35															

<210> 82
 <211> 399

<212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 81..398

<221> sig_peptide
 <222> 81..152
 <223> Von Heijne matrix
 score 10
 seq LLLLQALPSPLSA/RA

<400> 82
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 ggagcaggag caggaggggg atg gag agg aga agg ctc ctg ggt ggc atg gcg 113
 Met Glu Arg Arg Arg Leu Leu Gly Gly Met Ala
 -20 -15
 ctc ctg ctc ctc cag gcg ctg ccc agc ccc ttg tca gcc agg gct gaa 161
 Leu Leu Leu Leu Gln Ala Leu Pro Ser Pro Leu Ser Ala Arg Ala Glu
 -10 -5 1
 ccc ccg cag gat aag gaa gcc tgt gtg ggt acc aac aat caa agc tac 209
 Pro Pro Gln Asp Lys Glu Ala Cys Val Gly Thr Asn Asn Gln Ser Tyr
 5 10 15
 atc tgt gac aca gga cac tgc tgt gga cag tct cag tgc tgy aac tac 257
 Ile Cys Asp Thr Gly His Cys Cys Gly Gln Ser Gln Cys Cys Asn Tyr
 20 25 30 35
 tac tat gaa ctc tgg tgg ttc tgg ctg gtg tgg acc atc atc atc atc 305
 Tyr Tyr Glu Leu Trp Trp Phe Trp Leu Val Trp Thr Ile Ile Ile Ile
 40 45 50
 ctg agc tgc tgc tgt gtt tgc cac cac cgc cga gcc aag cac cgc ctt 353
 Leu Ser Cys Cys Cys Val Cys His His Arg Arg Ala Lys His Arg Leu
 55 60 65
 cag gcc cag cag cgg caa cat gaa atc aac ctg atc gct tac cga g 399
 Gln Ala Gln Gln Arg Gln His Glu Ile Asn Leu Ile Ala Tyr Arg
 70 75 80

<210> 83
 <211> 398
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 288..398

<221> sig_peptide
 <222> 288..368
 <223> Von Heijne matrix
 score 9.89999961853027
 seq LLLLLFSLSLFLC/HE

<400> 83
 cactctacct ctgacagcat gtatatgtgca ccagtagcta acaaaaaactg gtctagtcaa 60

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accaaatggg cacaaaagaa ccaggataacc aaaagttaag ctcatacagc tgcaaaccat 120
atcacttctt ggtaacaatg caagacctca taaacctaaa gaagagaaag aaaagaaaac 180
ttttgttact ttvctttttt gcttgtcact tatatacagg ctatgtgaga atataatttg 240
taggtataac acattaagaa aaagttatct tcattggata gaattga atg gtg gtc 296
                               Met Val Val
                               -25
gct gat agg aat agg gcg tcc tct agc tct tat ctc tgt ctc tta ctc 344
Ala Asp Arg Asn Arg Ala Ser Ser Ser Ser Tyr Leu Cys Leu Leu Leu
                               -20                -15                -10
ttt tct ctt tct ctt ttt ctc tgt cat gag act gtg tgt gac agg gcc 392
Phe Ser Leu Ser Leu Phe Leu Cys His Glu Thr Val Cys Asp Arg Ala
                               -5                1                5
acc tgt 398
Thr Cys
10

```

```

<210> 84
<211> 488
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> 62..487

<221> sig_peptide
<222> 62..118
<223> Von Heijne matrix
      score 9.899999961853027
      seq FLFVVAAATGVQS/QV

```

```

<221> misc_feature
<222> 210,293
<223> n=a, g, c or t
      Oligonucleotide

```

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<400> 84
agcatcacat aacaaccaca ttctctctct aaagaagccc ctgggagcac agctcatcac 60
c atg gac tgg acc tgg agg ttc ctc ttt gtg gtg gca gca gct aca ggt 109
  Met Asp Trp Thr Trp Arg Phe Leu Phe Val Val Ala Ala Ala Thr Gly
                               -15                -10                -5
gtc cag tcc cag gtg cag ctg gtg cag tct ggg gct gag gtg aag aag 157
Val Gln Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
                               1                5                10
cct ggg tcc tcg gtg aag gtc tcc tgc aag gct tct gga ggc acc ttc 205
Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe
15                20                25
agc anc tat gct atc agc tgg gtg cga cag gcc cct gga caa ggg ctt 253
Ser Xaa Tyr Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
30                35                40                45
gag tgg atg gga ggg atc atc cct atc ttt ggt aca gca nac tac gca 301
Glu Trp Met Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Xaa Tyr Ala
50                55                60
cag aag ttc cag ggc aga gtc acs att acc gcg gac gra tcc acg asc 349

```

Gln	Lys	Phe	Gln	Gly	Arg	Val	Thr	Ile	Thr	Ala	Asp	Xaa	Ser	Thr	Xaa	
			65					70					75			
aca	rcc	tac	atg	gag	ctg	agc	agc	ctg	aga	tct	gag	gac	acg	gcc	stg	397
Thr	Xaa	Tyr	Met	Glu	Leu	Ser	Ser	Leu	Arg	Ser	Glu	Asp	Thr	Ala	Xaa	
		80					85					90				
tat	tac	tgt	gcg	aga	ggc	caa	gcc	ccc	ggc	agg	gta	gta	gta	cca	ctt	445
Tyr	Tyr	Cys	Ala	Arg	Gly	Gln	Ala	Pro	Gly	Arg	Val	Val	Val	Pro	Leu	
	95					100					105					
ttc	ctc	tgg	ggc	cag	gga	acc	tgg	tca	ccg	tct	cct	cag	cct	c		488
Phe	Leu	Trp	Gly	Gln	Gly	Thr	Trp	Ser	Pro	Ser	Pro	Gln	Pro			
110					115					120						

<210> 85
 <211> 290
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 30..290

<221> sig_peptide
 <222> 30..164
 <223> Von Heijne matrix
 score 9.89999961853027
 seq LLSLLSFLDETSGLS

<400> 85																		
ctt	ctt	ttt	ttc	ttc	gta	act	cat	ggc	aac	atg	acc	tac	agt	tac	tca	ttt	ttc	53
										Met	Thr	Tyr	Ser	Tyr	Ser	Phe	Phe	
										-45					-40			
agg	cct	gag	ttg	atc	gtt	aat	cat	ctt	aat	tat	gtt	cat	tct	gaa	gcc			101
Arg	Pro	Glu	Leu	Ile	Val	Asn	His	Leu	Asn	Tyr	Val	His	Ser	Glu	Ala			
		-35				-30							-25					
aac	agg	aga	acc	aag	acc	aaa	act	tta	ttg	tct	ctg	ctt	tca	ttt	ctt			149
Asn	Arg	Arg	Thr	Lys	Thr	Lys	Thr	Leu	Leu	Ser	Leu	Leu	Ser	Phe	Leu			
	-20					-15					-10							
gat	gaa	acc	tct	gga	cta	agc	aca	cat	ctt	cct	tgt	tta	tct	ctc	tca			197
Asp	Glu	Thr	Ser	Gly	Leu	Ser	Thr	His	Leu	Pro	Cys	Leu	Ser	Leu	Ser			
-5				1				5					10					
aag	gag	tgt	gga	gtg	ctt	cat	ctg	gac	atc	cac	ggg	aag	aag	gaa	gac			245
Lys	Glu	Cys	Gly	Val	Leu	His	Leu	Asp	Ile	His	Gly	Lys	Lys	Glu	Asp			
	15					20					25							
atg	aga	gat	gag	gtc	ttg	ctg	gcc	ttg	aac	tyc	tgc	acc	cac	agg				290
Met	Arg	Asp	Glu	Val	Leu	Leu	Ala	Leu	Asn	Xaa	Cys	Thr	His	Arg				
	30					35					40							

<210> 86
 <211> 336
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS

<222> 100..336

<221> sig_peptide

<222> 100..156

<223> Von Heijne matrix

score 9.89999961853027

seq ILFLVFLLAGLRS/KA

<400> 86

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ccagatctgt tctgcaacat tcaccgttct ctgcatccag ctctgcttat ctgctgttac      60
cttgacacc agagcagcta taggtatctg ccagragcw atg aaa tca ttc agc      114
                               Met Lys Ser Phe Ser
                               -15
cgg atc ctc ttc ctc gtc ttc ctc ctc gcc ggc ctg agg tcc aag gcc      162
Arg Ile Leu Phe Leu Val Phe Leu Leu Ala Gly Leu Arg Ser Lys Ala
                               -10                               -5                               1
gct ccc tca gcc cct ctg cct ttg ggc tgt ggc ttt ccg gac atg gcc      210
Ala Pro Ser Ala Pro Leu Pro Leu Gly Cys Gly Phe Pro Asp Met Ala
                               5                               10                               15
cac ccc tct gag act tcc cct ctg aag ggt gct tct gaa aat tcc aaa      258
His Pro Ser Glu Thr Ser Pro Leu Lys Gly Ala Ser Glu Asn Ser Lys
                               20                               25                               30
cga gat cgc ctt aac cca gaa ttt cct ggg act cct tac cct gag cct      306
Arg Asp Arg Leu Asn Pro Glu Phe Pro Gly Thr Pro Tyr Pro Glu Pro
                               35                               40                               45                               50
tcc aag cta cct cat acg gtt tcc ctg gaa      336
Ser Lys Leu Pro His Thr Val Ser Leu Glu
                               55                               60
```

<210> 87

<211> 262

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 108..260

<221> sig_peptide

<222> 108..230

<223> Von Heijne matrix

score 9.89999961853027

seq SLCHLGWSAVVQS/QP

<400> 87

```
taggagtgga gtgactgggt gatatgataa ctctatgttt aactttttaaa ggaactgcta      60
gacttttctg aagtgactat gccattttac attaacacca ggagtgt atg agg gtg      116
                               Met Arg Val
                               -40
ccg att ttt cca cat cct cac caa ctc tcg tta tta ttc atc cat tta      164
Pro Ile Phe Pro His Pro His Gln Leu Ser Leu Leu Phe Ile His Leu
                               -35                               -30                               -25
ttt att tat tta ttt aga gaa agg gtc tct ctc tgt cac cta ggc tgg      212
Phe Ile Tyr Leu Phe Arg Glu Arg Val Ser Leu Cys His Leu Gly Trp
```

```

      -20      -15      -10
agt gca gtg gta caa tca cag cca act aca acc ttg acc tcc cgc gct      260
Ser Ala Val Val Gln Ser Gln Pro Thr Thr Thr Leu Thr Ser Arg Ala
      -5              1              5              10
am

```

```

<210> 88
<211> 149
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> 18..149

```

```

<221> sig_peptide
<222> 18..128
<223> Von Heijne matrix
      score 9.89999961853027
      seq FLFVLFCFGGSRA/LL

```

```

<400> 88
ttcggagctt gaccagc atg tgg aag gag agc tct cat ggc tgc aat aac      50
              Met Trp Lys Glu Ser Ser His Gly Cys Asn Asn
              -35              -30
tta ggg agt tcc tac ctg gat gac act ggg gta gga agt ttt ctg ttt      98
Leu Gly Ser Ser Tyr Leu Asp Asp Thr Gly Val Gly Ser Phe Leu Phe
      -25              -20              -15
gtt ttg ttc tgt ttc gga ggg tcc cgt gca ctt ctc ttg cct gga tct      146
Val Leu Phe Cys Phe Gly Gly Ser Arg Ala Leu Leu Leu Pro Gly Ser
      -10              -5              1              5
ggg
Gly

```

```

<210> 89
<211> 315
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> 236..313

```

```

<221> sig_peptide
<222> 236..283
<223> Von Heijne matrix
      score 9.69999980926514
      seq FLCLLFYLIVSCG/AV

```

```

<400> 89
gtaaaagaca aataacttgt atggtttgca aaatgatctg aatatgtgct tttataacat      60
tcagaataca cccaaaagta aacttttaggt ttaatgtaca gtatgttttc tatgtaattg      120
ttttgaataa gtaatamcat ybtacatggc ttaaaaactga aaaacgtatt cctgttactt      180
cttgatgctt ttgagaaatg aataatgttt tctccctttt aaatggtagt acagc atg      238

```



```

                                Met
cac act ttt ctg tgc ttg ctt ttt tat ctc ata gta tct tgt gga gct      286
His Thr Phe Leu Cys Leu Leu Phe Tyr Leu Ile Val Ser Cys Gly Ala
-15                               -10                -5                1
ggt ttc tta aca gtc cct tct ccc caa gg                                315
Val Phe Leu Thr Val Pro Ser Pro Gln
                    5                      10

```

```

<210> 90
<211> 179
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> 24..179

```

```

<221> sig_peptide
<222> 24..140
<223> Von Heijne matrix
      score 9.69999980926514
      seq SIILXLXFPGLG/QA

```

```

<221> misc_feature
<222> 57
<223> n=a, g, c or t
      Oligonucleotide

```

```

<400> 90
agmrctctgg ggcagtctgc acc atg gcc tgg cac ccc act cct cct cct ctt      53
                                Met Ala Trp His Pro Thr Pro Pro Pro Leu
                                -35                -30
csb ncw cct cct cca ctg mac agg gwc tcy ctc cca gcc tgt gct gac      101
Xaa Xaa Pro Pro Pro Leu Xaa Arg Xaa Ser Leu Pro Ala Cys Ala Asp
                    -25                -20                -15
tca atc atc ctc tgm ctc tgm ttc cct ggg atc ctc ggw caa gct cac      149
Ser Ile Ile Leu Xaa Leu Xaa Phe Pro Gly Ile Leu Gly Gln Ala His
                    -10                -5                1
ctg mac tct gag cag tgg aca cag tac cta                                179
Leu Xaa Ser Glu Gln Trp Thr Gln Tyr Leu
      5                      10

```

```

<210> 91
<211> 423
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> 311..421

```

```

<221> sig_peptide
<222> 311..373
<223> Von Heijne matrix

```

score 9.69999980926514
seq LHLILLSGTCFT/WI

<400> 91
gactctatag srcaaatggt taagaacata tacttgggag tcagttgatc tgggttcaaa 60
ttctagctgt gctactttct acctatgctg tattggacaa atgatactgt gtatctgttt 120
cttcaaccgt aagttgggta tattaatatc cttacctcaa aaggatcatga tgattaagt 180
agtbaatgca tgtaaaatgc cttctgtgcc gggcagtcag aaaccactca ataaatattg 240
attattctca ccaaagatgt gcttcctgac ctcaaaagcc tgtcagccta atataaagac 300
agtgtgacaa atg cca atc ctg cct cag gac atc ttg cac ttg ctg atc 349
Met Pro Ile Leu Pro Gln Asp Ile Leu His Leu Leu Ile
-20 -15 -10
ctt ctg tct gga aca tgc ttc act tgg att ctt ttg tgg ctt cca ctc 397
Leu Leu Ser Gly Thr Cys Phe Thr Trp Ile Leu Leu Trp Leu Pro Leu
-5 1 5
tcc cct ctg ttg ggc ctg aaa tgc ta 423
Ser Pro Leu Leu Gly Leu Lys Cys
10 15

<210> 92
<211> 316
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 62..316

<221> sig_peptide
<222> 62..121
<223> Von Heijne matrix
score 9.60000038146973
seq LLALLLCGRPGRG/QT

<221> misc_feature
<222> 264,266
<223> n=a, g, c or t
Oligonucleotide

<400> 92
accgcagctc cagagccctg cgggaggact cagagtcagg gacacagcag cgtccggcga 60
g atg aag gcg ctc ggg gct gtc ctg ctt gcb ctc ttg ctg tgc ggg cgg 109
Met Lys Ala Leu Gly Ala Val Leu Leu Ala Leu Leu Leu Cys Gly Arg
-20 -15 -10 -5
cca ggg aga ggg cag aca cag cag gag gaa gag gaa gag gac gag gac 157
Pro Gly Arg Gly Gln Thr Gln Gln Glu Glu Glu Glu Glu Asp Glu Asp
1 5 10
cac ggg cca gat gac tac gac gag gaa gat gag gat gag gtt gaa gag 205
His Gly Pro Asp Asp Tyr Asp Glu Glu Asp Glu Asp Glu Val Glu Glu
15 20 25
gag gag acc aac agg ctc cct ggt ggc agg agc aga gtg ctg ctg cgg 253
Glu Glu Thr Asn Arg Leu Pro Gly Gly Arg Ser Arg Val Leu Leu Arg
30 35 40
tgc tac acc tnk nag tcc ctg ccc agg gac gag cgc tgc aac ctg acg 301

Cys Tyr Thr Xaa Xaa Ser Leu Pro Arg Asp Glu Arg Cys Asn Leu Thr
 45 50 55 60
 cag aac tgc tca cat
 Gln Asn Cys Ser His
 65

316

<210> 93
 <211> 508
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 245..508

<221> sig_peptide
 <222> 245..289
 <223> Von Heijne matrix
 score 9.60000038146973
 seq EYVLLLFLALCSA/KP

<400> 93
 agtactaaca tggactaatc tgtgggagca gtttattcca gtatcaccca ggggtgcagcc 60
 acaccaggac tgtgttgaag ggtgtttttt ttcttttaaa tgtaatacct cctcatcttt 120
 tcttcttaca cagtgtctga gaacatttac attatagata agtagtacat ggtggataac 180
 ttctactttt aggaggacta ctctcttctg acagtcctag actggctctc tacactaaga 240
 cacc atg aag gag tat gtg ctc cta tta ttc ctg gct ttg tgc tct gcc 289
 Met Lys Glu Tyr Val Leu Leu Leu Phe Leu Ala Leu Cys Ser Ala
 -15 -10 -5
 aaa ccc ttc ttt agc cct tca cac atc gca ctg aag aat atg atg ctg 337
 Lys Pro Phe Phe Ser Pro Ser His Ile Ala Leu Lys Asn Met Met Leu
 1 5 10 15
 aag gat atg gaa gac aca gat gat gat gat gat gat gat gat gat 385
 Lys Asp Met Glu Asp Thr Asp Asp Asp Asp Asp Asp Asp Asp Asp
 20 25 30
 gat gat gat gag gac aac tct ctt ttt cca aca aga gag cca aga agc 433
 Asp Asp Asp Glu Asp Asn Ser Leu Phe Pro Thr Arg Glu Pro Arg Ser
 35 40 45
 cat ttt ttt cca ttt gat ctg ttt cca atg tgt cca ttt gga tgt cag 481
 His Phe Phe Pro Phe Asp Leu Phe Pro Met Cys Pro Phe Gly Cys Gln
 50 55 60
 tgc tat tca cga gtt gta cat tgc tca 508
 Cys Tyr Ser Arg Val Val His Cys Ser
 65 70

<210> 94
 <211> 321
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 36..320

<221> sig_peptide
 <222> 36..92
 <223> Von Heijne matrix
 score 9.60000038146973
 seq FLLLVAAPRWAMS/QV

<400> 94
 actttctgag aggcctggac ctccctgcaca agaac atg aaa cac ctg tgg ttc 53
 Met Lys His Leu Trp Phe
 -15
 ttc ctc ctc ctg gtg gca gct ccc aga tgg gcc atg tct cag gtg caa 101
 Phe Leu Leu Leu Val Ala Ala Pro Arg Trp Ala Met Ser Gln Val Gln
 -10 -5 1
 ctg cag gaa tcg ggc ccg aga ctg gtg aaa cct tcg ggg acc ctg tcc 149
 Leu Gln Glu Ser Gly Pro Arg Leu Val Lys Pro Ser Gly Thr Leu Ser
 5 10 15
 ctc acc tgc agt gtc tct ggt ggc tcc atg gcc act agt gac tgg tgg 197
 Leu Thr Cys Ser Val Ser Gly Gly Ser Met Ala Thr Ser Asp Trp Trp
 20 25 30 35
 agt tgg ttt cga cag acm ccg gag aag ggt ctg gag tgg att ggg gaa 245
 Ser Trp Phe Arg Gln Thr Pro Glu Lys Gly Leu Glu Trp Ile Gly Glu
 40 45 50
 atc ttt cag act ggg ccc acc aat tac aac ccg tcc ctc aag agc cgc 293
 Ile Phe Gln Thr Gly Pro Thr Asn Tyr Asn Pro Ser Leu Lys Ser Arg
 55 60 65
 gtc tcc atg tca gtg gac atg tcc aag a 321
 Val Ser Met Ser Val Asp Met Ser Lys
 70 75

<210> 95
 <211> 402
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 15..401

<221> sig_peptide
 <222> 15..92
 <223> Von Heijne matrix
 score 9.5
 seq FLLLVAAPRWALS/QL

<400> 95
 gctttctgag agtc atg gat ctc acg tgc aag aaa atg aag cac ctg tgg 50
 Met Asp Leu Thr Cys Lys Lys Met Lys His Leu Trp
 -25 -20 -15
 ttc ttc ctc ctg ctg gtg gcg gct ccc aga tgg gcc ctg tcc caa ctg 98
 Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp Ala Leu Ser Gln Leu
 -10 -5 1
 cag ctg cag gag tcg ggc cca gga ctg gtg aag cct tcg gag acc ctg 146
 Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu Thr Leu
 5 10 15

tcc ctc acg tgc act gtc tct ggt gaa tcc atc acc act aat tca ttc	194
Ser Leu Thr Cys Thr Val Ser Gly Glu Ser Ile Thr Thr Asn Ser Phe	
20 25 30	
tgc tgg gcc tgg atc cgc cag ccc ccg ggg aag ggg ctg gaa tgg ctt	242
Cys Trp Ala Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Leu	
35 40 45 50	
ggg act gta tgt tat ggt ggg acc acc tac krc aac kcg tcc ctg aag	290
Gly Thr Val Cys Tyr Gly Gly Thr Thr Tyr Xaa Asn Xaa Ser Leu Lys	
55 60 65	
agt cga gtc aag tta tcg ttg gac acg tcc acg aat cag ttc tcc ctg	338
Ser Arg Val Lys Leu Ser Leu Asp Thr Ser Thr Asn Gln Phe Ser Leu	
70 75 80	
aag gtc acc tct atg acc gcc gga gac gcg gct gtc cat tac tgt gcg	386
Lys Val Thr Ser Met Thr Ala Gly Asp Ala Ala Val His Tyr Cys Ala	
85 90 95	
ggg ctg cgt gtt agt g	402
Gly Leu Arg Val Ser	
100	

<210> 96
 <211> 315
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 118..315

<221> sig_peptide
 <222> 118..306
 <223> Von Heijne matrix
 score 9.5
 seq VLLFLILLYMSWS/AS

<400> 96	
agagacacac ttggacgrtt cctgcagraa tcagtgaaggc agtctcctcc caggggcttg	60
gsgcctggct cgaggcgagg ctgccggccc ggacgctgac tgcccagtgc cacagac	117
atg gcc aac ggg acc aac gcc tct gcc cca tac tac agc tat gaa tac	165
Met Ala Asn Gly Thr Asn Ala Ser Ala Pro Tyr Tyr Ser Tyr Glu Tyr	
-60 -55 -50	
tac ctg gac tat ctg gac ctc att ccc gtg gac gag aag aag ctg aaa	213
Tyr Leu Asp Tyr Leu Asp Leu Ile Pro Val Asp Glu Lys Lys Leu Lys	
-45 -40 -35	
gcc cac aaa cat tcc atc gtg atc gca ttc tgg gtg agc ctg gct gcc	261
Ala His Lys His Ser Ile Val Ile Ala Phe Trp Val Ser Leu Ala Ala	
-30 -25 -20	
ttc gtg gtg ctg ctc ttc ctc atc ttg ctc tac atg tcc tgg tcc gcs	309
Phe Val Val Leu Leu Phe Leu Ile Leu Leu Tyr Met Ser Trp Ser Ala	
-15 -10 -5 1	
tcc ccg	315
Ser Pro	

<210> 97
 <211> 460

<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 62..460

<221> sig_peptide
<222> 62..118
<223> Von Heijne matrix
score 9.39999961853027
seq FLFVVAATGVQS/QX

<400> 97
agcatcacat aacaaccasa ttcctcctct aaagaagccc ctgggagcac agctcatcac 60
c atg gac tgg acc tgg agg ttc ctc ttt gtg gtg gca gct aca ggt 109
Met Asp Trp Thr Trp Arg Phe Leu Phe Val Val Ala Ala Ala Thr Gly
-15 -10 -5
gtc cag tcm cag gks cas ctg gwg cag tct ggg gct gag gtg aag aag 157
Val Gln Ser Gln Xaa Xaa Leu Xaa Gln Ser Gly Ala Glu Val Lys Lys
1 5 10
cct ggg tcc tcg gtg aaa gtc tcc tgc arg gcy tct gga ggc atc ytc 205
Pro Gly Ser Ser Val Lys Val Ser Cys Xaa Ala Ser Gly Gly Ile Xaa
15 20 25
agc asc tat agc ttc aac tgg gtg cgm cag gcc cct gga cag ggg ttt 253
Ser Xaa Tyr Ser Phe Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Phe
30 35 40 45
gag tgg ttg gga agg atc atc ccc atc ctc ggt ata aca aac tac gca 301
Glu Trp Leu Gly Arg Ile Ile Pro Ile Leu Gly Ile Thr Asn Tyr Ala
50 55 60
gag aag ttt cgg ggc aga ctc acg atc acc gtg gac aaa tcc acg cgt 349
Glu Lys Phe Arg Gly Arg Leu Thr Ile Thr Val Asp Lys Ser Thr Arg
65 70 75
gtt gtt tac atg gag cag agc agt ctg aca tct gcg gac acg gcc gta 397
Val Val Tyr Met Glu Gln Ser Ser Leu Thr Ser Ala Asp Thr Ala Val
80 85 90
tat tat tgt gcg aaa ccg act atg act tcg gaa cta cgg gtc tac tat 445
Tyr Tyr Cys Ala Lys Pro Thr Met Thr Ser Glu Leu Arg Val Tyr Tyr
95 100 105
cag wct aca cta tgg 460
Gln Xaa Thr Leu Trp
110

<210> 98
<211> 230
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 140..229

<221> sig_peptide
<222> 140..205

<223> Von Heijne matrix
 score 9.39999961853027
 seq LLLLSAFTSQTVS/GQ

<400> 98
 aacagaacaa tatcaaataag ctaacttcac ccccaaccac agtccttgct gttggcattt 60
 actcaactag tctttaattc ctgttttgac aaactttata aggtgctaca agacagatga 120
 tttttcacca tctaccata atg tgg aac aga tat ttt gtc ttc tat ctc ctg 172
 Met Trp Asn Arg Tyr Phe Val Phe Tyr Leu Leu
 -20 -15
 ctt ttg tca gcg ttt acg agt caa aca gta tcc gga caa aga aag aaa 220
 Leu Leu Ser Ala Phe Thr Ser Gln Thr Val Ser Gly Gln Arg Lys Lys
 -10 -5 1 5
 gga ccc cgg g 230
 Gly Pro Arg

<210> 99
 <211> 467
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 40..465

<221> sig_peptide
 <222> 40..96
 <223> Von Heijne matrix
 score 9.39999961853027
 seq FLLLVAAPRWLS/QL

<400> 99
 aaatactttc tgagagccct ggacctcctg tgcaagaac atg aaa cac ctg ggg 54
 Met Lys His Leu Gly
 -15
 ttc ttc ctc ctg ctg gtg gca gct ccc aga tgg gtc ctg tcc cag ctg 102
 Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp Val Leu Ser Gln Leu
 -10 -5 1
 cag ctc cag gag tcc ggc tca gga ctg gag aag cct tca cag acc ctg 150
 Gln Leu Gln Glu Ser Gly Ser Gly Leu Glu Lys Pro Ser Gln Thr Leu
 5 10 15
 tcc ctc acc tgc tct gtc tct ggt ggc tcc atc agt agt gat gat ttg 198
 Ser Leu Thr Cys Ser Val Ser Gly Gly Ser Ile Ser Ser Asp Asp Leu
 20 25 30
 tcg tgg agc tgg atc cga cag ccg cca ggg aag ggc ctg gag tgg att 246
 Ser Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile
 35 40 45 50
 ggc tac att tat caa aat gag agg acc ctc tac aac ccg tcc ctc aag 294
 Gly Tyr Ile Tyr Gln Asn Glu Arg Thr Leu Tyr Asn Pro Ser Leu Lys
 55 60 65
 agt cga gcc gcc att tca gtg gac agg tcc aag aac cag ttc tcc ctg 342
 Ser Arg Ala Ala Ile Ser Val Asp Arg Ser Lys Asn Gln Phe Ser Leu
 70 75 80
 aaa ctg acc tct gtg acc gcc gcg gac atg gcc gta tat tac tgt gcc 390

Lys	Leu	Thr	Ser	Val	Thr	Ala	Ala	Asp	Met	Ala	Val	Tyr	Tyr	Cys	Ala	
	85					90					95					
acc	agt	gtc	atg	awt	tcc	ttt	ggg	ggc	gtt	ctc	gtc	cct	aat	ctg	ttt	438
Thr	Ser	Val	Met	Xaa	Ser	Phe	Gly	Gly	Val	Leu	Val	Pro	Asn	Leu	Phe	
	100					105					110					
ttg	act	act	ggg	gcc	agg	gaa	tct	cgt	ca							467
Leu	Thr	Thr	Gly	Ala	Arg	Glu	Ser	Arg								
115					120											

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<221> sig_peptide
 <222> 39..95
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 score 9.30000019073486
 seq FLLLVAGPRWVLS/QV

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						Met	Lys	His	Leu	Trp	Phe						
ttc	ctc	ctg	ctg	gtg	gca	ggt	ccc	aga	tgg	gtc	ctg	tcc	cag	gtg	cag		104
Phe	Leu	Leu	Leu	Val	Ala	Gly	Pro	Arg	Trp	Val	Leu	Ser	Gln	Val	Gln		
ctg	sdg	gag	tcg	ggc	cca	aga	ctg	gtg	aag	cct	tca	cag	acc	ctg	tcc		152
Leu	Xaa	Glu	Ser	Gly	Pro	Arg	Leu	Val	Lys	Pro	Ser	Gln	Thr	Leu	Ser		
	5					10					15						
ctc	acc	tgc	act	gta	tct	ggg	gcc	tcc	gtc	agc	agt	cgt	ggg	tac	tat		200
Leu	Thr	Cys	Thr	Val	Ser	Gly	Ala	Ser	Val	Ser	Ser	Arg	Gly	Tyr	Tyr		
20					25				30						35		
tgg	acc	tgg	atc	cgc	cag	ctc	cca	ggg	aag	ggc	ctg	gag	tgg	att	ggc		248
Trp	Thr	Trp	Ile	Arg	Gln	Leu	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Ile	Gly		
				40				45						50			
tac	atc	tgk	tac	act	ggg	agc	acc	ttc	tac	aac	ccg	tcc	ctc	aag	agt		296
Tyr	Ile	Xaa	Tyr	Thr	Gly	Ser	Thr	Phe	Tyr	Asn	Pro	Ser	Leu	Lys	Ser		
				55				60					65				
cga	tta	acc	ata	tca	ata	gac	acg	tct	aag	aat	cag	ttc	tcc	ctg	aac		344
Arg	Leu	Thr	Ile	Ser	Ile	Asp	Thr	Ser	Lys	Asn	Gln	Phe	Ser	Leu	Asn		
				70			75					80					
ctg	agg	tct	gtg	act	acc	gcg	gac	acg	gcc	gtc	tat	tac	tgt	gcg	aga		392
Leu	Arg	Ser	Val	Thr	Thr	Ala	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala	Arg		
	85					90					95						
gac	cat	ttc	gat	ctt	cta	ttc	gac	ccc	tgg	ggc	cag	gga	acc	ctg	gtc		440
Asp	His	Phe	Asp	Leu	Phe	Asp	Pro	Trp	Gly	Gln	Gly	Thr	Leu	Val			
100					105				110					115			
acc	gtc	tcc	tct	gcm	tcc	acc	aag	ggc	cca	tcg	gtc	ttc	ccc	ctg	gca		488
Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe	Pro	Leu	Ala		

120 125 130 504
 scc tcc tcc aag agc a
 Xaa Ser Ser Lys Ser
 135

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 <213> Homo sapiens

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 <222> 148..336

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 <222> 148..270
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 gccaggcctg gaaggatgag aggctccgc tctccaccac aagcaacgaa gcctgcaagc 120
 tgttcgatgc cacgctgacc cagggtat atg gcc tgc cga gag agg ccg cgg ccc 174
 Met Ala Cys Arg Glu Arg Pro Arg Pro
 -40 -35
 ctt ctg tgg agg tct agg gga agg ttt ttt aat tgg gga aag ctg ttt 222
 Leu Leu Trp Arg Ser Arg Gly Arg Phe Phe Asn Trp Gly Lys Leu Phe
 -30 -25 -20
 ttt tgt ttt gtt ttg mtt ttg ttt tgt ttt gtt ttt gag gcg gag tct 270
 Phe Cys Phe Val Leu Xaa Leu Phe Cys Phe Val Phe Glu Ala Glu Ser
 -15 -10 -5
 cgc tct gtc gcc cag gct gga gtg cag tgg cgc tat ttc ggc tca cta 318
 Arg Ser Val Ala Gln Ala Gly Val Gln Trp Arg Tyr Phe Gly Ser Leu
 1 5 10 15
 caa gct ttg cct ccc tgg 336
 Gln Ala Leu Pro Pro Trp
 20

<210> 102
 <211> 289
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 214..288

<221> sig_peptide
 <222> 214..276
 <223> Von Heijne matrix
 score 9.19999980926514
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atattgagtt gatttgtgta tatgggtggag acaggggtcta gtcttgggtct tctgcatgtg 120
actttccaat tttccagca ccatttattg gagaaactgt ctttttccca gtgcatgttc 180
ttggcacctt tggtgaaaaa cagttggcca tag atg cat gaa ttt att tct ggg 234
Met His Glu Phe Ile Ser Gly
-20 -15
ttc ttt att ctc ttt cat tgg tct ctg tgt ttg tgt tta tgc caa tac 282
Phe Phe Ile Leu Phe His Trp Ser Leu Cys Leu Cys Leu Cys Gln Tyr
-10 -5 1
cat gcc g 289
His Ala

<210> 103
<211> 383
<212> DNA
<213> Homo sapiens

<220>
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<222> 252..383
<221> sig_peptide
<222> 252..377
<223> Von Heijne matrix
score 9.19999980926514
seq LLVCLFAVTSILC/SS

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tattctacct ctcccttgct ctttcagac caggcttggg acataacact aacacccttt 120
tcctttcatt tcattctcttg tccttcagtc attcctaaac attgacaybc attgagttcc 180
ttggctctgg ccatagtcct ttctcccttt cccctctggg gcatcaaata gtgattacag 240
tatccacagg g atg gca tat gcc att tca cca ttt cac agt tcc tgg aat 290
Met Ala Tyr Ala Ile Ser Pro Phe His Ser Ser Trp Asn
-40 -35 -30
cca ctt ttc act tct cat aaa gct tca gca agc cat tct cat ctt ggg 338
Pro Leu Phe Thr Ser His Lys Ala Ser Ala Ser His Ser His Leu Gly
-25 -20 -15
ttg ctt gtt tgc cta ttt gct gtt aca tcc att ctc tgc tcc tca 383
Leu Leu Val Cys Leu Phe Ala Val Thr Ser Ile Leu Cys Ser Ser
-10 -5 1

<210> 104
<211> 211
<212> DNA
<213> Homo sapiens

<220>
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<222> 30..209

<221> sig_peptide
<222> 30..74

<223> Von Heijne matrix
score 9.19999980926514
seq PVLLLALLGFILP/LP

<221> misc_feature

<222> 83

<223> n=a, g, c or t
Oligonucleotide

<400> 104

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-15 -10	
ctc ctg ggg ttc atc ctc cca ctg cca ggn agt gca rgc gct gss tck	101
Leu Leu Gly Phe Ile Leu Pro Leu Pro Gly Ser Ala Xaa Ala Xaa Ser	
-5 1 5	
gcc agt ttg gga cag ttc agc atg tgt gga agg tgt ccg acm tgc ccc	149
Ala Ser Leu Gly Gln Phe Ser Met Cys Gly Arg Cys Pro Thr Cys Pro	
10 15 20 25	
ggc aat gga ccc cta aga aca cca gct gcg aca sgg vtt rgg gtg cca	197
Gly Asn Gly Pro Leu Arg Thr Pro Ala Ala Thr Xaa Xaa Xaa Val Pro	
30 35 40	
gga cac gtt gat gc	211
Gly His Val Asp	
45	

<210> 105

<211> 492

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> 29..490

<221> sig_peptide

<222> 29..97

<223> Von Heijne matrix
score 9.10000038146973
seq SLLLFSLMCETSA/FY

<400> 105

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Met Ala Thr Ala Met Asp Trp Leu	
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ccg tgg tct tta ctg ctt ttc tcc ctg atg tgt gaa aca agc gcc ttc	100
Pro Trp Ser Leu Leu Leu Phe Ser Leu Met Cys Glu Thr Ser Ala Phe	
-15 -10 -5 1	
tat gtg cct ggg gtc gcg cct atc aac ttc cac cag aac gat ccc gta	148
Tyr Val Pro Gly Val Ala Pro Ile Asn Phe His Gln Asn Asp Pro Val	
5 10 15	
gaa atc aag gct gtg aag ctc acc agc tct cga acc cag cta cct tat	196
Glu Ile Lys Ala Val Lys Leu Thr Ser Ser Arg Thr Gln Leu Pro Tyr	
20 25 30	

gaa tac tat tca ctg ccc ttc tgc cag ccc agc aag ata acc tac aag 244
 Glu Tyr Tyr Ser Leu Pro Phe Cys Gln Pro Ser Lys Ile Thr Tyr Lys
 35 40 45
 gca gag aat ctg gga gag gtg ctg aga ggg gac cgg att gtc aac acc 292
 Ala Glu Asn Leu Gly Glu Val Leu Arg Gly Asp Arg Ile Val Asn Thr
 50 55 60 65
 cct ttc cag gtt ctc atg aac agc gag aag aag tgt gaa gtt ctg tgc 340
 Pro Phe Gln Val Leu Met Asn Ser Glu Lys Lys Cys Glu Val Leu Cys
 70 75 80
 agc cag tcc aac aag cca gtg acc ctg aca gtg gag cag agc cga ctc 388
 Ser Gln Ser Asn Lys Pro Val Thr Leu Thr Val Glu Gln Ser Arg Leu
 85 90 95
 gtg gcc gag cgg atc aca gaa gac tac tac gtc cac ctc att gct gac 436
 Val Ala Glu Arg Ile Thr Glu Asp Tyr Tyr Val His Leu Ile Ala Asp
 100 105 110
 aac ctg cct gtg gcc acc ggc tgg agc tct act cca acc gag aca gcg 484
 Asn Leu Pro Val Ala Thr Gly Trp Ser Ser Thr Pro Thr Glu Thr Ala
 115 120 125
 atg aca ag 492
 Met Thr
 130

<210> 106
 <211> 126
 <212> DNA
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<220>
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 <222> 41..124
 <221> sig_peptide
 <222> 41..94
 <223> Von Heijne matrix
 score 9.10000038146973
 seq LISLLQCAHVS LG/LQ

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 Met Pro Ser Pro Cys
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 ctg atc tct ctt ctt caa tgt gct cat gtg tcc ctt ggc tta cag tat 103
 Leu Ile Ser Leu Leu Gln Cys Ala His Val Ser Leu Gly Leu Gln Tyr
 -10 -5 1
 cca tgc stt ctc ctt ctc cct cc 126
 Pro Cys Xaa Leu Leu Leu Pro
 5 10

<210> 107
 <211> 242
 <212> DNA
 <213> Homo sapiens

<220>

<221> CDS
<222> 82..240

<221> sig_peptide
<222> 82..132
<223> Von Heijne matrix
score 9.10000038146973
seq LVLA AFCLGIASA/VP

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gacggctgct ggttttgaaa c atg aat ctt tcg ctc gtc ctg gct gcc ttt 111
Met Asn Leu Ser Leu Val Leu Ala Ala Phe
-15 -10
tgc ttg gga ata gcc tcc gct gtt cca aaa ttt gac caa aat ttg gat 159
Cys Leu Gly Ile Ala Ser Ala Val Pro Lys Phe Asp Gln Asn Leu Asp
-5 1 5
aca aag tgg tac cag tgg aag gca aca cac aga aga tta tat ggc gcg 207
Thr Lys Trp Tyr Gln Trp Lys Ala Thr His Arg Arg Leu Tyr Gly Ala
10 15 20 25
aat gaa gaa gga tgg agg aga gca gcg tgg gag gg 242
Asn Glu Glu Gly Trp Arg Arg Ala Ala Trp Glu
30 35

<210> 108
<211> 336
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 81..335

<221> sig_peptide
<222> 81..137
<223> Von Heijne matrix
score 9
seq WVFLVAIFTGVHC/EV

<400> 108
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ctgaacacag accaccaacc atg gag ttt ggc ctt aat tgg gtt ttc ctt gtt 113
Met Glu Phe Gly Leu Asn Trp Val Phe Leu Val
-15 -10
gct att ttt aca ggt gtc cac tgt gag gtg cag ttg gtg gag tct ggg 161
Ala Ile Phe Thr Gly Val His Cys Glu Val Gln Leu Val Glu Ser Gly
-5 1 5
gga gac ctg gta cag cca ggg cgg tcc ctg aga ctc tcc tgt aca gct 209
Gly Asp Leu Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Thr Ala
10 15 20
tct gga ttc acc ttt ggt gat tat gcc atg acc tgg ttc cgc cag gct 257
Ser Gly Phe Thr Phe Gly Asp Tyr Ala Met Thr Trp Phe Arg Gln Ala
25 30 35 40
tca ggg aag cga ctg gag tgg cta ggt ttc att aga aat aga ggt tcs 305

Ser Gly Lys Arg Leu Glu Trp Leu Gly Phe Ile Arg Asn Arg Gly Ser
45 50 55

ggt ggg tca gca gag tac ggc gcg tct gtg a 336
Gly Gly Ser Ala Glu Tyr Gly Ala Ser Val
60 65

<210> 109
<211> 160
<212> DNA
<213> Homo sapiens

<220>
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<222> 6..158

<221> sig_peptide
<222> 6..56
<223> Von Heijne matrix
score 9
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Met Lys Asn Cys Leu Leu Ile Leu Leu Met Leu Leu Leu Phe Ala
-15 -10 -5
ata cac ata aac cgt atg aat gta agg aat gtg gga aat act tta gtc 98
Ile His Ile Asn Arg Met Asn Val Arg Asn Val Gly Asn Thr Leu Val
1 5 10
gta gtg caa atc tta ttc agc atc aga gta ttc ata ctg gag aga aac 146
Val Val Gln Ile Leu Phe Ser Ile Arg Val Phe Ile Leu Glu Arg Asn
15 20 25 30
cct ttg aat gtg gg 160
Pro Leu Asn Val

<210> 110
<211> 527
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 81..527

<221> sig_peptide
<222> 81..137
<223> Von Heijne matrix
score 9
seq WIFLLAILKGVQC/EV

<221> misc_feature
<222> 307..308,466..467
<223> n=a, g, c or t
Oligonucleotide

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ctgaacacag aggactcacc atg gag ttg gga ctg agc tgg att ttc ctt ttg      113
                Met Glu Leu Gly Leu Ser Trp Ile Phe Leu Leu
                        -15                                -10

gct att tta aaa ggt gtc cag tgt gaa gtg cag ctg gtg gag tct ggg      161
Ala Ile Leu Lys Gly Val Gln Cys Glu Val Gln Leu Val Glu Ser Gly
                -5                                1                                5

gga ggc ttg gta cag cct ggc agg tcc ctg aga ctc tcc tgt gca gcc      209
Gly Gly Leu Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Ala Ala
                10                                15                                20

tct gga ttc acc ttt gat gat tac gcc atg cac tgg gtc cgg caa gct      257
Ser Gly Phe Thr Phe Asp Tyr Ala Met His Trp Val Arg Gln Ala
                25                                30                                35                                40

cca ggg aag ggc ctg gag tgg gtc tca gga att act tgg aat agt ggt      305
Pro Gly Lys Gly Leu Glu Trp Val Ser Gly Ile Thr Trp Asn Ser Gly
                45                                50                                55

ann ata ggc tac gcg gac tct gtg aag ggc cga ttc acc atc tcc aga      353
Xaa Ile Gly Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg
                60                                65                                70

gac aac gcc aag aac tcc ctg tat ttg caa atg aac agt ctg aga act      401
Asp Asn Ala Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Thr
                75                                80                                85

gag gac acg gcc ttc tat ttc tgt gca aaa gct cgc ggg ctc ttt agc      449
Glu Asp Thr Ala Phe Tyr Phe Cys Ala Lys Ala Arg Gly Leu Phe Ser
                90                                95                                100

gat acc tgg ccc tac vnn cac tac gct atg gac gtc tgg ggc caa ggg      497
Asp Thr Trp Pro Tyr Xaa His Tyr Ala Met Asp Val Trp Gly Gln Gly
                105                                110                                115                                120

acc acg gtc acc gtc tcc tca gcc tcc acc      527
Thr Thr Val Thr Val Ser Ser Ala Ser Thr
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<210> 111
<211> 154
<212> DNA
<213> Homo sapiens
  
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<220>
<221> CDS
<222> 80..154
  
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<221> sig_peptide
<222> 80..121
<223> Von Heijne matrix
      score 8.89999961853027
      seq LLVFFVLWTCSLA/LL
  
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taccacaggg ctctctgc atg ctc ctt gtt ttc ttt gtg ctc tgg act tgc      112
                Met Leu Leu Val Phe Phe Val Leu Trp Thr Cys
                        -10                                -5

tca ctt gca ctg ctt gct tct tcc cca atc gcm gcc yac cca      154
  
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Ser Leu Ala Leu Leu Ala Ser Ser Pro Ile Ala Ala Xaa Pro
 1 5 10

<210> 112
 <211> 441
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 59..439

<221> sig_peptide
 <222> 59..115
 <223> Von Heijne matrix
 score 8.89999961853027
 seq ILLLVAAATDASS/QM

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 atg gac tgg acc tgg aga atc ctc ctc ttg gtg gca gca gcc aca gat 106
 Met Asp Trp Thr Trp Arg Ile Leu Leu Leu Val Ala Ala Ala Thr Asp
 -15 -10 -5
 gcc tcc tcc cag atg cag ctg ttg cag tct ggg cct gaa gtg aag aag 154
 Ala Ser Ser Gln Met Gln Leu Leu Gln Ser Gly Pro Glu Val Lys Lys
 1 5 10
 act ggg tcc tca gtg aaa ctt tcc tgc acg gcc tcc ggc gac acc ctc 202
 Thr Gly Ser Ser Val Lys Leu Ser Cys Thr Ala Ser Gly Asp Thr Leu
 15 20 25
 gcc tac cac tac ctg cac tgg gtg cga cag gcc ccc gga caa gcg ctt 250
 Ala Tyr His Tyr Leu His Trp Val Arg Gln Ala Pro Gly Gln Ala Leu
 30 35 40 45
 gag tgg atg gga tgg atc aca cct ttc agt gga gac acc aac ttc gca 298
 Glu Trp Met Gly Trp Ile Thr Pro Phe Ser Gly Asp Thr Asn Phe Ala
 50 55 60
 cag cga ttc cag gac aga ctc acc ttc acc agg gac agg tct atg agc 346
 Gln Arg Phe Gln Asp Arg Leu Thr Phe Thr Arg Asp Arg Ser Met Ser
 65 70 75
 aca gtc tac atg acc ctg acc agc ctg ata tct gaa gac aca gcc atg 394
 Thr Val Tyr Met Thr Leu Thr Ser Leu Ile Ser Glu Asp Thr Ala Met
 80 85 90
 tat tac tgt gcc act gat gga cgt cgc acc aac cgt ctt ttt gaa ca 441
 Tyr Tyr Cys Ala Thr Asp Gly Arg Arg Thr Asn Arg Leu Phe Glu
 95 100 105

<210> 113
 <211> 369
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 164..367

<221> sig_peptide
 <222> 164..217
 <223> Von Heijne matrix
 score 8.80000019073486
 seq LGCLLWLLTHIKA/QD

<221> misc_feature
 <222> 290..292
 <223> n=a, g, c or t
 Oligonucleotide

<400> 113
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 tccaaagact ccgatgttgg tcatggactt gggaagacag tcttcccttg gcgtttgatc 120
 actgcggaga tgccttcctt gatcattcac ccacattccc ttg atg gca ggt caa 175
 Met Ala Gly Gln
 -15
 ttg ctg gga tgc ctg ctt tgg ctg ctc acc cac att aaa gcc cag gac 223
 Leu Leu Gly Cys Leu Leu Trp Leu Leu Thr His Ile Lys Ala Gln Asp
 -10 -5 1
 tca gtc agg gat gcc tac tgg aag act ggt agc tgc cca cct cca ttt 271
 Ser Val Arg Asp Ala Tyr Trp Lys Thr Gly Ser Cys Pro Pro Pro Phe
 5 10 15
 ctc cat gtg tct acc ttc nnn kkt aaa ctt acc ttc tcc act aag ggc 319
 Leu His Val Ser Thr Phe Xaa Xaa Lys Leu Thr Phe Ser Thr Lys Gly
 20 25 30
 aac ctt ctg cat tcc att cct ctc tct tcc ccc tta gcc tgt gtt ctt 367
 Asn Leu Leu His Ser Ile Pro Leu Ser Ser Pro Leu Ala Cys Val Leu
 35 40 45 50
 ag 369

<210> 114
 <211> 334
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 20..334

<221> sig_peptide
 <222> 20..292
 <223> Von Heijne matrix
 score 8.80000019073486
 seq LFLMLLGELGVFA/SY

<221> misc_feature
 <222> 295
 <223> n=a, g, c or t
 Oligonucleotide

<400> 114
 agctctgaat tgggaaggg atg aag gag gct gtg cct ccg ggt tgc acg aag 52
 Met Lys Glu Ala Val Pro Pro Gly Cys Thr Lys

1
2
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                                -90                                -85
agt ccg agt cat ttc tca gaa ggt ttt gat agg tgg gcc tta gag gag      100
Ser Pro Ser His Phe Ser Glu Gly Phe Asp Arg Trp Ala Leu Glu Glu
-80                                -75                                -65
acg ccg ccg gaa aac ctg att ggc gcc ctc ttg gcg atc ttc ggg cac      148
Thr Pro Pro Glu Asn Leu Ile Gly Ala Leu Leu Ala Ile Phe Gly His
                                -60                                -55                                -50
ctc gtg gtc agc att gca ctt aac ctc cag aag tac tgc cac atc cgc      196
Leu Val Val Ser Ile Ala Leu Asn Leu Gln Lys Tyr Cys His Ile Arg
                                -45                                -40                                -35
ctg gca ggc tcc aag gat ccc cgg gcc tat ttc aag acc aag aca tgg      244
Leu Ala Gly Ser Lys Asp Pro Arg Ala Tyr Phe Lys Thr Lys Thr Trp
                                -30                                -25                                -20
tgg ctg ggc ctg ttc ctg atg ctt ctg ggc gag ctg ggt gtg ttc gcm      292
Trp Leu Gly Leu Phe Leu Met Leu Leu Gly Glu Leu Gly Val Phe Ala
                                -15                                -10                                -5
tcn tac gcc ttc gcg ccg ctg tca ctc atc gtg ccc ctc agc      334
Ser Tyr Ala Phe Ala Pro Leu Ser Leu Ile Val Pro Leu Ser
1                                5                                10

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 score 8.80000019073486
 seq LLSCWALLGTTFG/CG

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<400> 115
acaccctgc cagcggcacc atg gct ttc ctc tgg ctc ctc tcc tgc tgg gcc      53
                                Met Ala Phe Leu Trp Leu Leu Ser Cys Trp Ala
                                -15                                -10
ctc ctg ggt acc acc ttc ggc tgc ggg gtc ccc gcc atc cac cct ggc      101
Leu Leu Gly Thr Thr Phe Gly Cys Gly Val Pro Ala Ile His Pro Gly
                                -5                                1                                5
tgc caa ctg agc ccg ccg ctc cct ccg acc ctg ctc ccc aca gag cgc      149
Cys Gln Leu Ser Pro Arg Leu Pro Pro Thr Leu Leu Pro Thr Glu Arg
10                                15                                20                                25
ggg g
Gly

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<210> 116
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<221> sig_peptide
 <222> 47..106
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 score 8.80000019073486
 seq LWLFFVLNLGSFA/FS

<400> 116
 taccagtaac ttctttcatg gttcaataaa atcatagctt tagttt atg gca cct 55
 Met Ala Pro
 -20
 ttt caa aac ttc ctt tgg ctt ttc ttt gtg ctt aat tta ggw agt ttt 103
 Phe Gln Asn Phe Leu Trp Leu Phe Phe Val Leu Asn Leu Gly Ser Phe
 -15 -10 -5
 gct ttt agc tca mtt ccd aat tct ctt ttt tac aca att cat ttt ggt 151
 Ala Phe Ser Ser Xaa Pro Asn Ser Leu Phe Tyr Thr Ile His Phe Gly
 1 5 10 15
 cct aat ttc ttt act tta cta tat aaa caa ggt gct gaa atg tgt gtg 199
 Pro Asn Phe Phe Thr Leu Leu Tyr Lys Gln Gly Ala Glu Met Cys Val
 20 25 30
 tat gta ttt aac ttc ctc tac cca ttt gct ctt ggt tat ttc ttc agt 247
 Tyr Val Phe Asn Phe Leu Tyr Pro Phe Ala Leu Gly Tyr Phe Phe Ser
 35 40 45
 tat gat att ctg gat ttg cca gtc akt gtc cgt cct cct agc ggg 292
 Tyr Asp Ile Leu Asp Leu Pro Val Xaa Val Arg Pro Pro Ser Gly
 50 55 60

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 score 8.69999980926514
 seq LLLSVAFNQLVFA/LY

<400> 117
 tttctcatca atttcttgct tctctggcaa cctcaacctc tgattcctga ggccaataaa 60
 actgaaactt tctgcttgag ctcttggttt gccaggctga tggggctgag gtgcaccctc 120
 tgaggaaaag ctgtaaatac atg gat ttt acc caa tgc cat tcc ctt ctt tta 173
 Met Asp Phe Thr Gln Cys His Ser Leu Leu Leu
 -35 -30 -25
 agg gtt gaa tat tct cca gtg tct gtc tgc ttt tta tta ctt tcc gtt 221
 Arg Val Glu Tyr Ser Pro Val Ser Val Cys Phe Leu Leu Leu Ser Val
 -20 -15 -10
 gcc ttc aat cag ttg gtt ttt gct ttg tat cca ata caa gct acw btc 269

Ala	Phe	Asn	Gln	Leu	Val	Phe	Ala	Leu	Tyr	Pro	Ile	Gln	Ala	Thr	Xaa	
		-5						1				5				
tgt	ttc	tct	dda	gtt	tct	ctc	cct	ttc	ccc	gct	ca					304
Cys	Phe	Ser	Xaa	Val	Ser	Leu	Pro	Phe	Pro	Ala						
	10					15										

<210> 118
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 <212> DNA
 <213> Homo sapiens

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 <222> 76..144

<221> sig_peptide
 <222> 76..120
 <223> Von Heijne matrix
 score 8.5
 seq LLLLACGVPSLWP/FA

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gtgaaggtag	gagtgttggg	gccctgaccc	ccgcaggagg	gatgggcgga	ttcgaggact											60
ggctgcctgc	ccatc atg	ctc ttg	ctc ctg	ctg gcc	tgt ggt	gtt ccc	agc									111
		Met	Leu	Leu	Leu	Leu	Ala	Cys	Gly	Val	Pro	Ser				
		-15				-10				-5						
ctg tgg	ccc ttt	gcw ctt	gct ctc	tta aag	acc c											145
Leu	Trp	Pro	Phe	Ala	Leu	Ala	Leu	Leu	Lys	Thr						
	1					5										

<210> 119
 <211> 288
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 160..288

<221> sig_peptide
 <222> 160..228
 <223> Von Heijne matrix
 score 8.5
 seq SFLLLHLCQVLLS/RR

<400> 119																
tcttttagtcc	tgtttatatg	atgaatcaca	tttattgatt	tgcatatgtt	gaaccatcct											60
tgtatcccag	ggataaagcc	tacttgattg	taatggataa	gcttcatgat	gtgctgctga											120
atttggtttg	ccagtatttt	gttaaggatt	tttacatca	atg ttc	att gag	aat										174
				Met	Phe	Ile	Glu	Asn								
				-20												
att ggv	ctg aag	ttt tct	ttt ttg	ttg ttg	cat ctc	tgc cag	gtt ttg									222
Ile	Gly	Leu	Lys	Phe	Ser	Phe	Leu	Leu	Leu	His	Leu	Cys	Gln	Val	Leu	
	-15					-10						-5				

cta tca aga cga gct ggt acc att cct act gaa aca att cca aaa aaa	270
Leu Ser Arg Arg Ala Gly Thr Ile Pro Thr Glu Thr Ile Pro Lys Lys	
1 5 10	
ttg agg agg aga gac ggg	288
Leu Arg Arg Arg Asp Gly	
15 20	

<210> 120
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 <222> 71..385

<221> sig_peptide
 <222> 71..142
 <223> Von Heijne matrix
 score 8.5
 seq XALLMGFLMVCLG/AF

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aattctcttg gagcaagcag ggaagcagag gaggcagcagg gtcagggtgc tgggttccta	60
aggtgcaagg atg cag aac aga act ggc ctc att ctc tgt gct ytt gcc	109
Met Gln Asn Arg Thr Gly Leu Ile Leu Cys Ala Xaa Ala	
-20 -15	
ctc ctg atg ggt ttc ctg atg gtc tgc ctg ggg gcc ttc ttc att tcc	157
Leu Leu Met Gly Phe Leu Met Val Cys Leu Gly Ala Phe Phe Ile Ser	
-10 -5 1 5	
tgg ggc tcc ata ttc gac tgt cag ggg agc ctg att gcg gcc tat ttg	205
Trp Gly Ser Ile Phe Asp Cys Gln Gly Ser Leu Ile Ala Ala Tyr Leu	
10 15 20	
ctt ctg cct ctg ggg ttt gtg atc ctt ctg agt gga att ttc tgg agc	253
Leu Leu Pro Leu Gly Phe Val Ile Leu Leu Ser Gly Ile Phe Trp Ser	
25 30 35	
aac tat cgc cag gtg act gaa agc aaa gga gtg ttg agg cac atg ctc	301
Asn Tyr Arg Gln Val Thr Glu Ser Lys Gly Val Leu Arg His Met Leu	
40 45 50	
cga caa cac ctt gct cat ggg gcc ctg ccc gtg gcc aca gta gac agt	349
Arg Gln His Leu Ala His Gly Ala Leu Pro Val Ala Thr Val Asp Ser	
55 60 65	
gct gct ctt ctg aaa atc atg tgt aag car ttg ctt t	386
Ala Ala Leu Leu Lys Ile Met Cys Lys Gln Leu Leu	
70 75 80	

<210> 121
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 <221> CDS
 <222> 34..189

<221> sig_peptide
 <222> 34..165
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 score 8.5
 seq LTCTSSLLSFALG/RS

<400> 121
 atcttgaaaa cggaataa aaacagcaga cct atg aag gtc gaa ggg gaa gaa 54
 Met Lys Val Glu Gly Glu Glu
 -40
 aag ctg tat cga ttg ttg aga tct ggc gac ttg ttt aaa ttt cat cag 102
 Lys Leu Tyr Arg Leu Leu Arg Ser Gly Asp Leu Phe Lys Phe His Gln
 -35 -30 -25
 cct cac ttc tat gaa ctc tca ggc ctc acg tgt acc agc tct ctg ctc 150
 Pro His Phe Tyr Glu Leu Ser Gly Leu Thr Cys Thr Ser Ser Leu Leu
 -20 -15 -10
 tcc ttt gcc ttg gga cgt tcc atc cct gga agt ttc cca g 190
 Ser Phe Ala Leu Gly Arg Ser Ile Pro Gly Ser Phe Pro
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<400> 122
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 Met Glu Ser Arg Thr Leu Leu
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 ctg ctg ttc tcg gga gcc gtg gcc ctg atc cag acc tgg gca ggt gag 100
 Leu Leu Phe Ser Gly Ala Val Ala Leu Ile Gln Thr Trp Ala Gly Glu
 -10 -5 1
 tgc ggg gtc ggg agg gaa aag gcc tct gcg gga agg agc gag ggg ccc 148
 Cys Gly Val Gly Arg Glu Lys Ala Ser Ala Gly Arg Ser Glu Gly Pro
 5 10 15 20
 gcc cgg agg agt aaa tct gca cat ata kbt aat tac aga tta caa tta 196
 Ala Arg Arg Ser Lys Ser Ala His Ile Xaa Asn Tyr Arg Leu Gln Leu
 25 30 35
 caa tca agg cag ggg 211
 Gln Ser Arg Gln Gly
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score 8.39999961853027
seq SVPLLCFWSLCYC/FA

<221> misc_feature
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Oligonucleotide

<400> 123
agcgagtcct tgcctcccg cggctcagga cgagggcaga tctcgttctg gggcaagccg 60
ttgacactcg ctccctgcc cggcccgggc tccgtgccgc caagttttca tttccacct 120
tctctgcctc cagtcccca gccctggcc gagagaagg tcttaccggc cgggattgct 180
ggaaacnaa gaggtggttt ttgttttta aaacttctgt ttcttgggag ggggtgtggc 240
ggggcagg atg agc aac tcc gtt cct ctg ctc tgt ttc tgg agc ctc tgc 290
Met Ser Asn Ser Val Pro Leu Leu Cys Phe Trp Ser Leu Cys
-15 -10 -5
tat tgc ttt gct gcg ggg agc ccc gta cct ttt ggt cca gag gga cgg 338
Tyr Cys Phe Ala Ala Gly Ser Pro Val Pro Phe Gly Pro Glu Gly Arg
1 5 10
ctg gaa gat aag ctc 353
Leu Glu Asp Lys Leu
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<210> 124
<211> 249
<212> DNA
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cagccggatt tcccagccaa acgcagagag ag atg ccc tgg acc atc ttg ctc 113
Met Pro Trp Thr Ile Leu Leu
-10

ttt gca gct ggc tcc ttg gcg atc cca gca cca tcc atc cgg gtg gtg	161
Phe Ala Ala Gly Ser Leu Ala Ile Pro Ala Pro Ser Ile Arg Val Val	
-5 1 5	
ccc ccg tac cca agc agc caa gag gac ccc atc cac atc gca tgc atg	209
Pro Pro Tyr Pro Ser Ser Gln Glu Asp Pro Ile His Ile Ala Cys Met	
10 15 20 25	
gcc gct ggg aac ttc ccg ggg gcg aat ttc aca ctg tat c	249
Ala Ala Gly Asn Phe Pro Gly Ala Asn Phe Thr Leu Tyr	
30 35	

<210> 125
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<220>
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<221> sig_peptide
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ccctctgtcc ccgcggctgg gtctcgtctg ctccggttcc tgggctccta attcttggtc	120
cagcttcttc caggtcagtg tgcgggcctt ccacgctgcc agcgggaacac tgga atg	177
Met	
gcg gaa ggg gaa cgg gtc tgc gcg tct gtk gtt ccc agc gct ctg cga	225
Ala Glu Gly Glu Arg Val Cys Ala Ser Val Val Pro Ser Ala Leu Arg	
-60 -55 -50	
acg ctg aaa agg agg agc aac ctg tcc aga atc ccc gca gga cag gaa	273
Thr Leu Lys Arg Arg Ser Asn Leu Ser Arg Ile Pro Ala Gly Gln Glu	
-45 -40 -35	
aag gag ggg aaa tct cga cat gtt gct ccc cct ttt cgc ttt ttc cct	321
Lys Glu Gly Lys Ser Arg His Val Ala Pro Pro Phe Arg Phe Phe Pro	
-30 -25 -20	
ttt tcc ggt ttt ttg ttt ttt ggt ttt ctt ttt ccc gtc ttt tct ttc	369
Phe Ser Gly Phe Leu Phe Phe Gly Phe Leu Phe Pro Val Phe Ser Phe	
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ccc tcc	375
Pro Ser	

<210> 126
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 score 8.39999961853027
 seq MFCLAAILASASA/QR

<221> misc_feature
 <222> 404
 <223> n=a, g, c or t
 Oligonucleotide

<400> 126
 tcaataccca tgtgaacagt ttcgtggagg gttttaagta ttttccactg gctggctttg 60
 ggtataagta cctttccttc ttctgtcggt aaccacgccg aggggagaaa actatgcccc 120
 cgtgaaagtc cccactctgt ttcggttggg gaatactgga gcttaacctc ttggaggggg 180
 ttgttcata ccaagggtcc ttccgtaggt atttctaatt gg atg ttc tgc ctg 234
 Met Phe Cys Leu
 -10
 gca gca att tta gcc tca gca tct gcc caa cgg ttt cct tct gcc ttt 282
 Ala Ala Ile Leu Ala Ser Ala Ser Ala Gln Arg Phe Pro Ser Ala Phe
 -5 1 5
 tct cct tca cct tty yga tgg ctt yrg car tgt aas act gcc acc tcc 330
 Ser Pro Ser Pro Phe Xaa Trp Leu Xaa Gln Cys Xaa Thr Ala Thr Ser
 10 15 20
 ttg ggt ttt trc act gtg tgy art aac tcc ata att tcc ttg tgg tat 378
 Leu Gly Phe Xaa Thr Val Cys Xaa Asn Ser Ile Ile Ser Leu Trp Tyr
 25 30 35
 tta ayg ggr gtt ccc cca gag gtt ang gaa ctc cct ttc ttt cca tat 426
 Leu Xaa Gly Val Pro Pro Glu Val Xaa Glu Leu Pro Phe Phe Pro Tyr
 40 45 50 55
 tgc agc atg gg 437
 Cys Ser Met

<210> 127
 <211> 304
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 24..302

<221> sig_peptide
 <222> 24..74
 <223> Von Heijne matrix
 score 8.39999961853027
 seq TLLLLLSEALALT/QT

<400> 127
 ctcaggactc agaggctggg atc atg gta gat gga acc ctc ctt tta ctc ctc 53
 Met Val Asp Gly Thr Leu Leu Leu Leu Leu
 -15 -10
 tcg gaa gcc ctg gcc ctt acc car acc tgg gcg ggc tcc cac tcc tkr 101
 Ser Glu Ala Leu Ala Leu Thr Gln Thr Trp Ala Gly Ser His Ser Xaa

	-5		1		5												
	aag	tat	ttc	cac	act	tcc	gtg	tcc	cgg	mcc	ggc	cgc	ggg	gag	ccc	cgc	149
	Lys	Tyr	Phe	His	Thr	Ser	Val	Ser	Arg	Xaa	Gly	Arg	Gly	Glu	Pro	Arg	
	10					15					20				25		
	ttc	atc	tct	gtg	ggc	tac	gtg	gac	gac	acc	cgg	tca	gag	tat	tgg	gac	197
	Phe	Ile	Ser	Val	Gly	Tyr	Val	Asp	Asp	Thr	Arg	Ser	Glu	Tyr	Trp	Asp	
					30					35					40		
	cgg	gag	aca	cgg	agc	gcc	agg	gac	acc	gca	cag	att	ttc	cga	gtg	aac	245
	Arg	Glu	Thr	Arg	Ser	Ala	Arg	Asp	Thr	Ala	Gln	Ile	Phe	Arg	Val	Asn	
					45				50				55				
	ctg	cgg	acg	ctg	cgc	ggc	tac	tac	aat	cag	agc	gag	gcc	ggg	tct	cam	293
	Leu	Arg	Thr	Leu	Arg	Gly	Tyr	Tyr	Asn	Gln	Ser	Glu	Ala	Gly	Ser	Xaa	
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	acc	ctg	cag	tg													304
	Thr	Leu	Gln														
	75																

<210> 128
 <211> 244
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> CDS
 <222> 19..243

 <221> sig_peptide
 <222> 19..99
 <223> Von Heijne matrix
 score 8.39999961853027
 seq LVLISLISLSIAWS/MV

 <221> misc_feature
 <222> 112
 <223> n=a, g, c or t
 Oligonucleotide

<400> 128	
gcgattaggt tttaatgt atg aat ttc agg ggg cca caa acg ttc agt ctt	51
	Met Asn Phe Arg Gly Pro Gln Thr Phe Ser Leu
	-25 -20
tca cac agc ctt gtg tta tcc cta atc agt ctc tcc att gca tgg tct	99
Ser His Ser Leu Val Leu Ser Leu Ile Ser Leu Ser Ile Ala Trp Ser	
	-15 -10 -5
atg gtc gaa atg nbc act tct gca agc tac aar caa aag ttt gcc ctt	147
Met Val Glu Met Xaa Thr Ser Ala Ser Tyr Lys Gln Lys Phe Ala Leu	
	1 5 10 15
aga atc cta gtt gtg cag ttg ccc aca tgg gtg gaa tgt cca gta aac	195
Arg Ile Leu Val Val Gln Leu Pro Thr Trp Val Glu Cys Pro Val Asn	
	20 25 30
cac agg tgt gca cta ggg aga aag aat tgt tct att agg acc cag cca c	244
His Arg Cys Ala Leu Gly Arg Lys Asn Cys Ser Ile Arg Thr Gln Pro	
	35 40 45

<210> 129
 <211> 232
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 156..230

<221> sig_peptide
 <222> 156..215
 <223> Von Heijne matrix
 score 8.39999961853027
 seq SCICLFLPSLIHS/FP

<400> 129
 ctacaggaag gaaaagtgtg acagctttga aaaagaaaga gggtaaaata ttttaaccac 60
 ccttggtgtc atttgtggca gcctatagca ttagagcctt tgagaacaga tctttccaga 120
 ttctgcttaa gtccagggat tctgtgaccg cagaa atg act ggc atc tcc atc 173
 Met Thr Gly Ile Ser Ile
 -20 -15
 tgc tcg tgc atc tgt ttg ttt ctt cct tca ttg att cac tca ttc ccc 221
 Cys Ser Cys Ile Cys Leu Phe Leu Pro Ser Leu Ile His Ser Phe Pro
 -10 -5 1
 ccg ccc tgc gg 232
 Pro Pro Cys
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<210> 130
 <211> 312
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 17..310

<221> sig_peptide
 <222> 17..94
 <223> Von Heijne matrix
 score 8.30000019073486
 seq FLLLVAAPRWQL/QE

<400> 130
 atgctttctg agagtc atg gac ctc ctg tgc aag aac atg aag cac ctg tgg 52
 Met Asp Leu Leu Cys Lys Asn Met Lys His Leu Trp
 -25 -20 -15
 ttc ttc ctc ctg ctg gtg gcg gct ccc aga tgg gtc cag ctg cag gag 100
 Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp Val Gln Leu Gln Glu
 -10 -5 1
 tcg ggc cca cgc ctg gtg agg cct ccg gag acc ctg aag cct tcg gag 148
 Ser Gly Pro Arg Leu Val Arg Pro Pro Glu Thr Leu Lys Pro Ser Glu
 5 10 15
 acc ctg tcc ctc acc tgc act att tct ggt gac tcc atg agc agt gct 196

Thr	Leu	Ser	Leu	Thr	Cys	Thr	Ile	Ser	Gly	Asp	Ser	Met	Ser	Ser	Ala	
20					25				30							
tct	tac	tat	tgg	gcc	tgg	atc	cgc	cag	ccc	cca	ggc	aag	ggc	ctg	gaa	244
Ser	Tyr	Tyr	Trp	Ala	Trp	Ile	Arg	Gln	Pro	Pro	Gly	Lys	Gly	Leu	Glu	
35				40				45						50		
ttc	att	ggg	cgt	gcc	tta	tat	agt	ggg	acc	acc	gac	tac	aat	ccg	tcc	292
Phe	Ile	Gly	Arg	Ala	Leu	Tyr	Ser	Gly	Thr	Thr	Asp	Tyr	Asn	Pro	Ser	
			55					60					65			
ctc	agc	agt	cga	atc	acc	ct										312
Leu	Ser	Ser	Arg	Ile	Thr											
			70													

<210> 131
 <211> 276
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 119..274
 <221> sig_peptide
 <222> 119..253
 <223> Von Heijne matrix
 score 8.19999980926514
 seq PLSLSLCLSLCHT/HT

<400> 131	
gccttcattct ctccattctt gcgctgctgc cggtgcgcc atccagcacc cagactccag	60
caccggccga ggacccccac tccggctgca gggaccctgt cccagcgaga ccgcaggc	118
atg tca tcc gaa aag tca gga ctc cca gac tca gtc cct cac act tct	166
Met Ser Ser Glu Lys Ser Gly Leu Pro Asp Ser Val Pro His Thr Ser	
-45 -40 -35 -30	
ccg ccg ccc tac aat gcc cct cag cct cca gcc gaa ccc cca gcc ccg	214
Pro Pro Pro Tyr Asn Ala Pro Gln Pro Pro Ala Glu Pro Pro Ala Pro	
-25 -20 -15	
cct ctc tct ctc tct ctc tgt ctc tct ctc tgt cac aca cac aca cac	262
Pro Leu Ser Leu Ser Leu Cys Leu Ser Leu Cys His Thr His Thr His	
-10 -5 1	
aca cac aca cac ac	276
Thr His Thr His	
5	

<210> 132
 <211> 174
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 35..172

<221> sig_peptide
 <222> 35..118

<223> Von Heijne matrix
 score 8.19999980926514
 seq LVSLLMQPEGALG/EE

<400> 132
 actctgctga gctcctctgc acctgcccag gacc atg acg cct gct ctg cgc tgc 55
 Met Thr Pro Ala Leu Arg Cys
 -25

gca ttc gct ctg gcc ata gcg ggc ctc gtg tcg ctg ctg atg cag ccc 103
 Ala Phe Ala Leu Ala Ile Ala Gly Leu Val Ser Leu Leu Met Gln Pro
 -20 -15 -10

gag ggc gcc ctc ggc gag gag gct gca agt gcc gca gcc cag ggc cgc 151
 Glu Gly Ala Leu Gly Glu Glu Ala Ala Ser Ala Ala Ala Gln Gly Arg
 -5 1 5 10

cag ttg gct gaa ctt agg ctc ca 174
 Gln Leu Ala Glu Leu Arg Leu
 15

<210> 133

<211> 344

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 133..342

<221> sig_peptide

<222> 133..246

<223> Von Heijne matrix
 score 8.19999980926514
 seq LLLIFLSFPYTLC/IL

<400> 133
 gcctttcact tgcacaaaca ctgttattat gatcacttat ccaactgaca tttttcagac 60
 cttttaactt caactgttct tttttcctgt aaatcttaat tttctttttt tttctcccaa 120
 tttttctcct ac atg tct gga ctc ttc cca gtt cct gtc aga gta aat gtt 171
 Met Ser Gly Leu Phe Pro Val Pro Val Arg Val Asn Val
 -35 -30

gat att gcc cag aac ata act tgc tct tcc ttt tct ctc ctt ctc att 219
 Asp Ile Ala Gln Asn Ile Thr Cys Ser Ser Phe Ser Leu Leu Leu Ile
 -25 -20 -15 -10

ttt ctt tct ttc ccc tac acc ctc tgt ata ctc tat aga gta aaa tca 267
 Phe Leu Ser Phe Pro Tyr Thr Leu Cys Ile Leu Tyr Arg Val Lys Ser
 -5 1 5

tat aca ccc acg gag tca ata act gcc ttt aat cta aca att ggg wga 315
 Tyr Thr Pro Thr Glu Ser Ile Thr Ala Phe Asn Leu Thr Ile Gly Xaa
 10 15 20

ttc cca tat ctt taw wtt tcw acc ccg gg 344
 Phe Pro Tyr Leu Xaa Xaa Ser Thr Pro
 25 30

<210> 134

<211> 244

<212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 128..244

<221> sig_peptide
 <222> 128..226
 <223> Von Heijne matrix
 score 8.19999980926514
 seq HALSLCLCTCAFA/FL

<400> 134
 aagcaagaga ggggtgttca ggatgataaa gtcctggttg atgaaggcag atgcctgcag 60
 ctcttccttg gggcagggct ggcttccata ggggtgcttg ttgggccctt tggaaggggg 120
 tgtgcgg atg tgc agg gct gct tgt atc att aga atg gct gtt aga att 169
 Met Cys Arg Ala Ala Cys Ile Ile Arg Met Ala Val Arg Ile
 -30 -25 -20
 tca ttc ttt ctt tct tac cat gct ctg tct ctc tgc ctt tgt aca tgt 217
 Ser Phe Phe Leu Ser Tyr His Ala Leu Ser Leu Cys Leu Cys Thr Cys
 -15 -10 -5
 gcg ttt gca ttt ctc tcc ctc ctc ggg 244
 Ala Phe Ala Phe Leu Ser Leu Leu Gly
 1 5

<210> 135
 <211> 217
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 40..216

<221> sig_peptide
 <222> 40..90
 <223> Von Heijne matrix
 score 8.19999980926514
 seq LLXALGFLXQVNP/XP

<400> 135
 attaaaccac caccagstcc ccaagccacc ccttcagcc atg aag ttc ctg ctc 54
 Met Lys Phe Leu Leu
 -15
 ctg gma gcc ctc gga ttc ctg amc cag gtg aat ccc arc cca att sma 102
 Leu Xaa Ala Leu Gly Phe Leu Xaa Gln Val Asn Pro Xaa Pro Ile Xaa
 -10 -5 1
 ggd ggg tca aaa atg tgt gag twa cac ccc agg ata ctg cag gac atg 150
 Gly Gly Ser Lys Met Cys Glu Xaa His Pro Arg Ile Leu Gln Asp Met
 5 10 15 20
 ttg cca ctg ggg gga gac agc att gtt cat gtg caa cgc tks cag aaa 198
 Leu Pro Leu Gly Gly Asp Ser Ile Val His Val Gln Arg Xaa Gln Lys
 25 30 35

atg ctg cat cag yta ctc c
Met Leu His Gln Leu Leu
40

217

<210> 136
<211> 428
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 114..428

<221> sig_peptide
<222> 114..239
<223> Von Heijne matrix
score 8.10000038146973
seq LFCFLLLCLSAAS/LL

<400> 136
aggcgtctgt gtgcgccgcc aagtcggtgg ggcggggacg cgaggtgtgg atggggggtc 60
gccttgacct ctgcctcagc cagtagcgca gtctcggcct cgccgttacg gag atg 116
Met
gtg ccc tgg gtg cgg acg atg ggg cag aag ctg aag cag cgg ctg cga 164
Val Pro Trp Val Arg Thr Met Gly Gln Lys Leu Lys Gln Arg Leu Arg
-40 -35 -30
ctg gac gtg gga cgc gag atc tgc cgc cag tac ccg ctg ttc tgc ttc 212
Leu Asp Val Gly Arg Glu Ile Cys Arg Gln Tyr Pro Leu Phe Cys Phe
-25 -20 -15 -10
ctg ctg ctc tgt ctc agc gcc gcc tcc ctg ctt ctt aac agg tat att 260
Leu Leu Leu Cys Leu Ser Ala Ala Ser Leu Leu Leu Asn Arg Tyr Ile
-5 1 5
cat att tta atg atc ttc tgg tca ttt gtt gct gga gtt gtc aca ttt 308
His Ile Leu Met Ile Phe Trp Ser Phe Val Ala Gly Val Val Thr Phe
10 15 20
tac tgc tca cta gga cct gat tct ctc tta cca aat ata ttc ttc aca 356
Tyr Cys Ser Leu Gly Pro Asp Ser Leu Leu Pro Asn Ile Phe Phe Thr
25 30 35
ata aaa tac aaa ccc aag cag tta gga ctt cag gaa tta ttt cct caa 404
Ile Lys Tyr Lys Pro Lys Gln Leu Gly Leu Gln Glu Leu Phe Pro Gln
40 45 50 55
ggg cat agc tgt gct gtt tgt ggt 428
Gly His Ser Cys Ala Val Cys Gly
60

<210> 137
<211> 434
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 305..433

<221> sig_peptide
 <222> 305..406
 <223> Von Heijne matrix
 score 8.10000038146973
 seq LLCLFXLFFFSFL/KR

<400> 137
 tttctgtcca ttctccctca ccaccctgac gcaggctctg ggaatgtgct gaaggtgcag 60
 cagctgctcc acatttgtag cgaacacttt gactccaaag agaaggagga agacaaagac 120
 aagaaggaaa agaaagacaa ggacaagaag gaagcccctg ctgacatggg agcacatcag 180
 ggagtggctg ttctggggat tgcccttatt gctatggggg aggagattgg tgcagagatg 240
 gcattacgaa cttttggcca cttggtgagt atagcatgaa gaaaattgga atatactggt 300
 tttg atg gcc tgg ggt tcc cca ggg aag att ttt ctg atg ggt ttt ctt 349
 Met Ala Trp Gly Ser Pro Gly Lys Ile Phe Leu Met Gly Phe Leu
 -30 -25 -20
 ggt gga gag ctg gtc ttt ttg ctg tgc ctt ttc ttw ctt ttt ttc ttt 397
 Gly Gly Glu Leu Val Phe Leu Leu Cys Leu Phe Xaa Leu Phe Phe Phe
 -15 -10 -5
 tct ttt ttg aag cgg agt ttt gct cta gag tgc aat g 434
 Ser Phe Leu Lys Arg Ser Phe Ala Leu Glu Cys Asn
 1 5

<210> 138
 <211> 395
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 310..393

<221> sig_peptide
 <222> 310..357
 <223> Von Heijne matrix
 score 8.10000038146973
 seq SILLLLAPPLPSA/VS

<221> misc_feature
 <222> 189
 <223> n=a, g, c or t
 Oligonucleotide

<400> 138
 aaaagctctg taaacatata ataaatggaa ttccattgac attcaagcct tacgtatttc 60
 cagagcttct tcgacttatc ctgcctcccc tactttaatt ctgttaaagt agttgaacac 120
 cattcttctc ataatagttc tccctcsatt cttcagtgat tyccttgtgt ttataggata 180
 aagtccacnt gttatttttg cagtcagttc aagatccaca aatcagtcct tacccttaca 240
 tccttatttc tcaactgctg tctaataatag tctttataacc agtcaggctg gtctgttcac 300
 tattcctga atg ttt ttc tcc att ctt ttg tta ttg gca ccc ccg cta ccc 351
 Met Phe Phe Ser Ile Leu Leu Leu Ala Pro Pro Leu Pro
 -15 -10 -5
 tct gca gtg tct ttg cta cct ttc ttc tac tgt gtg cag gg 395
 Ser Ala Val Ser Leu Leu Pro Phe Phe Phe Tyr Cys Val Gln
 1 5 10

<210> 139
 <211> 268
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 141..266

<221> sig_peptide
 <222> 141..206
 <223> Von Heijne matrix
 score 8.10000038146973
 seq LLVCSWLSISLHA/HT

<400> 139
 caactctgct gttttgtagg aagccacatg gaggtcattt acggttacta gttatcttag 60
 tcagcttggg cagccattaa aaaataatac tgtagacgga gtggccaaa cgagagaaat 120
 ttatttctta tagttttggc atg gta gat ttc atc ctg agg tct ctt ctc ttg 173
 Met Val Asp Phe Ile Leu Arg Ser Leu Leu Leu
 -20 -15
 gtt tgt agt tgg ctg tca atc tcc ctg cat gct cac acg acc gct ttt 221
 Val Cys Ser Trp Leu Ser Ile Ser Leu His Ala His Thr Thr Ala Phe
 -10 -5 1 5
 tgt aca tac agt aag aaa ata cac act gtc atg tca ttt ttt tgt aa 268
 Cys Thr Tyr Ser Lys Lys Ile His Thr Val Met Ser Phe Phe Cys
 10 15 20

<210> 140
 <211> 170
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 93..170

<221> sig_peptide
 <222> 93..140
 <223> Von Heijne matrix
 score 8.10000038146973
 seq LLYFLCVSSYVTS/FF

<400> 140
 ttttgactga tatcaaattc taggtggacc gagattttct ttcagtcttt caaagatatt 60
 actctattgc cttctatctt gcatagtttc tg atg aga agt ctg ttg tat ttc 113
 Met Arg Ser Leu Leu Tyr Phe
 -15 -10
 tta tgt gtt tct tca tat gta aca tct ttt ttc ttt ttt ttt ttt 161
 Leu Cys Val Ser Ser Tyr Val Thr Ser Phe Phe Phe Phe Phe Phe
 -5 1 5
 ttt ttt ttt 170
 Phe Phe Phe

10

<210> 141
<211> 396
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 192..395

<221> sig_peptide
<222> 192..236
<223> Von Heijne matrix
score 8
seq FISFLCLIALAGT/SS

<400> 141
gattctcagc ttagttgctg ttggtgtata ggagagctac tgatttgtgt acattaattt 60
tgtatccgga aactttgttg aattatttta tcagttctag gagctttttg gaggagtctt 120
tagggttctc taggtataca atcatatcat cagcaaacag tgacaattcg acttcctctt 180
tatggatttg t atg ccc ttt att tct ttc ctt tgt ctg att gct ctg gct 230
Met Pro Phe Ile Ser Phe Leu Cys Leu Ile Ala Leu Ala
-15 -10 -5
ggg act tcc agt act atg ttg aga agt gct ctg gct ggg act tcc agt 278
Gly Thr Ser Ser Thr Met Leu Arg Ser Ala Leu Ala Gly Thr Ser Ser
1 5 10
act atg tkg arg aga agt ggt gam agt ggg wat cct kgh ctk gty cma 326
Thr Met Xaa Xaa Arg Ser Gly Xaa Ser Gly Xaa Pro Xaa Leu Val Xaa
15 20 25 30
gtc ctm aga ggg aat gct ttc agc ttt ttc cca ttc agt ctg atg twg 374
Val Leu Arg Gly Asn Ala Phe Ser Phe Phe Pro Phe Ser Leu Met Xaa
35 40 45
gct atg ggt tgt cat aga tgg c 396
Ala Met Gly Cys His Arg Trp
50

<210> 142
<211> 357
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 292..357

<221> sig_peptide
<222> 292..339
<223> Von Heijne matrix
score 8
seq FLLGAIFIALSSS/RI

<400> 142
cgtgcctgcg caatgggtgt cgggtccgct ttttcccaat ccggacgtaa tcgtggtttt 60

tggtctgcaa taggcggctt agagggaggg gctttttcgc ctatacctac tgtagcttct	120
ccacgtatgg accctaaagg ctactgctgc tactacgggg ctagacagtt actgtctcag	180
ctctaggatg tgcgttcttc cactagaagc tcttctgagg gaggtaatta aaaaacagtg	240
gaatggaaaa acagtgtgtg agtcatcctg taatatgctc cttgtcaaca a atg tat	297
	Met Tyr
	-15

aca ttc ctg cta ggt gcc ata ttc att gct tta agc tca agt cgc atc	345
Thr Phe Leu Leu Gly Ala Ile Phe Ile Ala Leu Ser Ser Ser Arg Ile	
	-10 -5 1

tta cta gtg aag	357
Leu Leu Val Lys	
	5

<210> 143
 <211> 159
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 26..157

<221> sig_peptide
 <222> 26..151
 <223> Von Heijne matrix
 score 7.90000009536743
 seq LVCVCVCVCVCXC/XR

<400> 143	
tgtgtgtgtg tgtgtctgcg tgtgt atg tgt ttg tgt ccc tgc tgg gat gtg	52
	Met Cys Leu Cys Pro Cys Trp Asp Val
	-40 -35
ttt act gtg ttt gtg tgt gtc tct gtg tgt gtg tct gtg tct gtc cct	100
Phe Thr Val Phe Val Cys Val Ser Val Cys Val Ser Val Ser Val Pro	
	-30 -25 -20
gtc ggg atg tat tta gtg tgt gtg tgt gtg tgt gtg tgt stc	148
Val Gly Met Tyr Leu Val Cys Val Cys Val Cys Val Cys Xaa	
	-15 -10 -5
tgc gyg cgt gg	159
Cys Xaa Arg	
	1

<210> 144
 <211> 433
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 282..431

<221> sig_peptide
 <222> 282..383
 <223> Von Heijne matrix

score 7.90000009536743
seq LFSLLMLTQSPLA/GQ

<221> misc_feature
<222> 132,149
<223> n=a, g, c or t
Oligonucleotide

<400> 144
aaaataaggt atctggcaaa agaatatatg aaagagtatg aagaactctc cttgaaagct 60
gtggcccca ttggccatgg ctgcagagcc gatgtcccgg ccaatccagg cgggatcccc 120
ttgaagcmgg knsmwhbtcy kragscwknc cmabtctccg ggggcaastc ttttccttc 180
cctgtgaccc kcttcggaca gttgaccatc tcaacaccta gtggttaaaa agaagagcat 240
ggacggcctg gggcctgcac tggctgtgct gggagtttgt c atg ttg ata gct aag 296
Met Leu Ile Ala Lys
-30

cag gcc cag ccc caa ggc ctc act gcc atc tgc ttc cct ctc aca cct 344
Gln Ala Gln Pro Gln Gly Leu Thr Ala Ile Cys Phe Pro Leu Thr Pro
-25 -20 -15
ctc ttc tcc ctc ctc atg ctc act cag agc ccc ctt gca ggt cag gaa 392
Leu Phe Ser Leu Leu Met Leu Thr Gln Ser Pro Leu Ala Gly Gln Glu
-10 -5 1
gga aga gaa gga ggg aaa gaa cgg tac ttg ttg gtg att ca 433
Gly Arg Glu Gly Gly Lys Glu Arg Tyr Leu Leu Val Ile
5 10 15

<210> 145
<211> 200
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 15..200

<221> sig_peptide
<222> 15..92
<223> Von Heijne matrix
score 7.90000009536743
seq RVCLLSLSLFLWA/NR

<400> 145
aatacgccag gaac atg cta agg acc tgg agc tct cta ccc tgg acc cgt 50
Met Leu Arg Thr Trp Ser Ser Leu Pro Trp Thr Arg
-25 -20 -15
ttt cgg gtt tgc ttg ctc tct ctc tct ctc ttt ctc tgg gct aat cgt 98
Phe Arg Val Cys Leu Leu Ser Leu Ser Leu Phe Leu Trp Ala Asn Arg
-10 -5 1
tta gag gac agt cgc tcc tgc caa cct aat ccc atg agc ctg act acc 146
Leu Glu Asp Ser Arg Ser Cys Gln Pro Asn Pro Met Ser Leu Thr Thr
5 10 15
ttg ccg ggc cac agg ctc aaa gaa gca gtg tgg ctg cca gca ccc tca 194
Leu Pro Gly His Arg Leu Lys Glu Ala Val Trp Leu Pro Ala Pro Ser
20 25 30

ctt ggg 200
 Leu Gly
 35

<210> 146
 <211> 297
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 80..295

<221> sig_peptide
 <222> 80..166
 <223> Von Heijne matrix
 score 7.90000009536743
 seq LVVXWLLPXQCSC/ER

<400> 146
 aacaccccag cccaagtcca tccccggtcc cttggcagca gtgcgcatcc acaaagccag 60
 cggcacaatt taattactg atg gcc cct ttc cta cga cag gtg gat rtg tgg 112
 Met Ala Pro Phe Leu Arg Gln Val Asp Xaa Trp
 -25 -20
 gga gca cag gcc ggt ctg gtg gtb gsm tgg tta cta cca tgs caa tgc 160
 Gly Ala Gln Ala Gly Leu Val Val Xaa Trp Leu Leu Pro Xaa Gln Cys
 -15 -10 -5
 agc tgt gaa cga tca gag caa tat ctg agc acc tgt ctc cca cag cac 208
 Ser Cys Glu Arg Ser Glu Gln Tyr Leu Ser Thr Cys Leu Pro Gln His
 1 5 10
 tca agc atc aag cag tcg tgc atc aag cat cca gca ggc ccg atc ccc 256
 Ser Ser Ile Lys Gln Ser Cys Ile Lys His Pro Ala Gly Pro Ile Pro
 15 20 25 30
 gca ggc cac cta cag gga aag gcc aca gct gcg ccc ctg gg 297
 Ala Gly His Leu Gln Gly Lys Ala Thr Ala Ala Pro Leu
 35 40

<210> 147
 <211> 300
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 80..298

<221> sig_peptide
 <222> 80..136
 <223> Von Heijne matrix
 score 7.90000009536743
 seq WLFLVAILKGVRC/EV

<400> 147
 agctctgaga gaggagccca gccctgggat cttcaggtgt tttcactcgg tgatcaggac 60

tgcacagaga gaactcacc atg gag ttt ggg ctg aag tgg ctt ttt ctt gtg	112
Met Glu Phe Gly Leu Lys Trp Leu Phe Leu Val	
-15 -10	
gca att tta aaa ggt gtc cgg tgt gaa gtg aag ctg gtg gag tct ggg	160
Ala Ile Leu Lys Gly Val Arg Cys Glu Val Lys Leu Val Glu Ser Gly	
-5 1 5	
gga ggc ctg gtg cag ccg ggg ggg tcc ctg aga ctc tcc tgt gta gga	208
Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Val Gly	
10 15 20	
tct gga ttc gtc ttc gat aaa tat ggc ata agt tgg gtg cgc cag gca	256
Ser Gly Phe Val Phe Asp Lys Tyr Gly Ile Ser Trp Val Arg Gln Ala	
25 30 35 40	
cca gga aag ggc cta cag tgg gtc gcg ggg atc ggt ggc ggg gg	300
Pro Gly Lys Gly Leu Gln Trp Val Ala Gly Ile Gly Gly Gly	
45 50	

<210> 148
 <211> 405
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 21..404

<221> sig_peptide
 <222> 21..68
 <223> Von Heijne matrix
 score 7.90000009536743
 seq AMLVLVVSPWSAA/RG

<400> 148	
gcggtcttcc agcagggaaa atg gcg ctg gcc atg ctg gtc ttg gtg gtt tcg	53
Met Ala Leu Ala Met Leu Val Leu Val Val Ser	
-15 -10	
ccg tgg tct gcg gcc ccg gga gtg ctt cga aac tac tgg gag cga ctg	101
Pro Trp Ser Ala Ala Arg Gly Val Leu Arg Asn Tyr Trp Glu Arg Leu	
-5 1 5 10	
cta ccg aag ctt ccg cag agc ccg ggc ttt ccc agt cct ccg tgg	149
Leu Arg Lys Leu Pro Gln Ser Arg Pro Gly Phe Pro Ser Pro Pro Trp	
15 20 25	
gga cca gca tta gca gta cag ggc cca gcc atg ttt aca gag cca gca	197
Gly Pro Ala Leu Ala Val Gln Gly Pro Ala Met Phe Thr Glu Pro Ala	
30 35 40	
aat gat acc agt gga agt aaa gag aat tcc agc ctt ttg gac agt atc	245
Asn Asp Thr Ser Gly Ser Lys Glu Asn Ser Ser Leu Leu Asp Ser Ile	
45 50 55	
ttt tgg atg gca gct ccc aaa aat aga cgc acc att gaa gtt aac ccg	293
Phe Trp Met Ala Ala Pro Lys Asn Arg Arg Thr Ile Glu Val Asn Arg	
60 65 70 75	
tgt agg aga aga aat ccg cag aag ctt att aaa gtt aag aac aac ata	341
Cys Arg Arg Arg Asn Pro Gln Lys Leu Ile Lys Val Lys Asn Asn Ile	
80 85 90	
gac gtt tgt cct gaa tgt ggt cac ctg aaa cag aaa srt gtc ctt tgt	389

Asp Val Cys Pro Glu Cys Gly His Leu Lys Gln Lys Xaa Val Leu Cys
 95 100 105

gct act gct atg aaa a 405
 Ala Thr Ala Met Lys
 110

<210> 149
 <211> 146
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 56..145

<221> sig_peptide
 <222> 56..115
 <223> Von Heijne matrix
 score 7.80000019073486
 seq LLLFPLSLFTLG/FL

<400> 149
 aaaccttctg actactaacc ttagatccc tttagttcct tagcagtatt cacia atg 58
 Met
 -20

ttt ttc tac tca cac ttt tta ctt ctt ttt ccc ctc tcg tta ctt ttc 106
 Phe Phe Tyr Ser His Phe Leu Leu Leu Phe Pro Leu Ser Leu Leu Phe
 -15 -10 -5

aca ctt gga ttt ttg ttt gtc ttt ttt ttt ttt ttt t 146
 Thr Leu Gly Phe Leu Phe Val Phe Phe Phe Phe Phe
 1 5 10

<210> 150
 <211> 408
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 105..407

<221> sig_peptide
 <222> 105..242
 <223> Von Heijne matrix
 score 7.80000019073486
 seq LVLLGTRVPLSGG/GP

<400> 150
 aaacagggcc attggcaaag ctgggggtacc agtcacccag ccacgctcta gggtggttagc 60
 caagaagacg gaccccgagt gggaggcaga gagacaagag gtgg atg aag cag agc 116
 Met Lys Gln Ser
 -45

aag cgt gas atg gtg aag aga aga cgg agc ccc gcg ctg gga gag gaa 164
 Lys Arg Xaa Met Val Lys Arg Arg Arg Ser Pro Ala Leu Gly Glu Glu

	-40		-35		-30	
cgc ttc agt ccg agt tcc att ctg cac cca agg ctc ccc ttg gtc ctc						212
Arg Phe Ser Pro Ser Ser Ile Leu His Pro Arg Leu Pro Leu Val Leu						
-25		-20		-15		
ctg gga acc agg gtg ccc ctt agt ggt ggt ggc cca gga gaa ccc gac						260
Leu Gly Thr Arg Val Pro Leu Ser Gly Gly Gly Pro Gly Glu Pro Asp						
-10		-5		1	5	
caa ggc agg agc gcc ccc tcc tgg aag agc ctc gct tca acg cat mat						308
Gln Gly Arg Ser Ala Pro Ser Trp Lys Ser Leu Ala Ser Thr His Xaa						
	10		15		20	
cat tcc cgg ccg gca gca ggg gcg acg cca gca agg cct gcg act cag						356
His Ser Arg Pro Ala Ala Gly Ala Thr Pro Ala Arg Pro Ala Thr Gln						
	25		30		35	
agc cag ctt ggc ccg ttc gcc ccg ccc ctt ccc ggt gtc cgc ccc gcc						404
Ser Gln Leu Gly Pro Phe Ala Pro Pro Leu Pro Gly Val Arg Pro Ala						
	40		45		50	
cca t						408
Pro						
55						

<210> 151
 <211> 166
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 69..164

<221> sig_peptide
 <222> 69..122
 <223> Von Heijne matrix
 score 7.80000019073486
 seq LCVLSLLVSFKSA/CL

<400> 151	
cacattttct acttaaaagc aamgttacaa agcctgtgga attgctctga cttagaaaga	60
acttgatc atg ctt ttg gag tct cta tgt gtt ctc tct ctg ttg gtt agt	110
Met Leu Leu Glu Ser Leu Cys Val Leu Ser Leu Leu Val Ser	
-15	-10
ttt aaa tca gcc tgc ctc aca agg gag cct gca ttt gat tcc caa gcc	158
Phe Lys Ser Ala Cys Leu Thr Arg Glu Pro Ala Phe Asp Ser Gln Ala	
	1
	5
	10
cgc ccg gg	166
Arg Pro	

<210> 152
 <211> 382
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 99..380

<221> sig_peptide
 <222> 99..236
 <223> Von Heijne matrix
 score 7.80000019073486
 seq LLYLSFAALGVVA/LR

<400> 152
 ttttacacac acacatacat acacacacac agctaattga gtttttaaagt aatattcttg 60
 ctaatcccta ctgaattgta gcttggtgtt gtttctga atg gtt ttt gga tat tgg 116
 Met Val Phe Gly Tyr Trp
 -45
 aag cag ccg ctg att acc ctt gca aag aaa tct gta aaa tgt gca cgt 164
 Lys Gln Pro Leu Ile Thr Leu Ala Lys Lys Ser Val Lys Cys Ala Arg
 -40 -35 -30 -25
 gaa tgt ctg aga tgc tct ctc agg cct cta gtc ctt ctg tat ctt tcc 212
 Glu Cys Leu Arg Cys Ser Leu Arg Pro Leu Val Leu Leu Tyr Leu Ser
 -20 -15 -10
 ttt gca gcc ctg ggt gta gta gca ctc agg agt gtt gaa tca ccc ctg 260
 Phe Ala Ala Leu Gly Val Val Ala Leu Arg Ser Val Glu Ser Pro Leu
 -5 1 5
 gcc gag acc cac tcc tgc tgg ctc agc ctg ggc atg tgt gtg ctc cag 308
 Ala Glu Thr His Ser Cys Trp Leu Ser Leu Gly Met Cys Val Leu Gln
 10 15 20
 tgt gaa cag cag tgg gtt cca acc cca gtc tcc ttt ctc tgt ggc ctc 356
 Cys Glu Gln Gln Trp Val Pro Thr Pro Val Ser Phe Leu Cys Gly Leu
 25 30 35 40
 tct ggc tcc agc acc atc atc gtt ag 382
 Ser Gly Ser Ser Thr Ile Ile Val
 45

<210> 153
 <211> 208
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 10..207

<221> sig_peptide
 <222> 10..81
 <223> Von Heijne matrix
 score 7.80000019073486
 seq CVYVVCLVSCVLC/VV

<400> 153
 tgcaatgtc atg tgt gtt gtg tgc agt gtg cat ggt gtg tgt tgt gta tat 51
 Met Cys Val Val Cys Ser Val His Gly Val Cys Cys Val Tyr
 -20 -15
 gtg gtg tgc ctg gtg tgc tgt gtt ttg tgt gtc gtg tgt cct gtg tgt 99
 Val Val Cys Leu Val Ser Cys Val Leu Cys Val Val Cys Pro Val Cys
 -10 -5 1 5
 tgg gtt atg tgt tgt gtg tgg tgc atc tgt gtg tgt gtg tgg tgt gtc 147

Trp Val Met Cys Cys Val Trp Cys Ile Cys Val Cys Val Trp Cys Val
 10 15 20
 tgt tgt atg tgt tgt gtg ttg tca tgt gtt gtg tca cat ggg ttg tgt 195
 Cys Cys Met Cys Cys Val Leu Ser Cys Val Val Ser His Gly Leu Cys
 25 30 35
 ggt gtg tca tgg g 208
 Gly Val Ser Trp
 40

<210> 154
 <211> 251
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 73..249

<221> sig_peptide
 <222> 73..129
 <223> Von Heijne matrix
 score 7.80000019073486
 seq WVFLVAVLEVVC/EI

<400> 154
 agagaggagc ctcagcccta gactccaagg cctttccact tggatgacag cactgagcac 60
 agaggactca cc atg gaa ctg ggg ctg tcc tgg gtc ttc ctt gtt gct gtt 111
 Met Glu Leu Gly Leu Ser Trp Val Phe Leu Val Ala Val
 -15 -10
 tta gaa gtt gtc cag tgt gaa att caa ctg att gac gcc ggg gga ggc 159
 Leu Glu Val Val Gln Cys Glu Ile Gln Leu Ile Asp Ala Gly Gly Gly
 -5 1 5 10
 cac gtc cag gcg ggg ggg tca ctg aga ctc tcc tgt gtt gcc tct gac 207
 His Val Gln Ala Gly Gly Ser Leu Arg Leu Ser Cys Val Ala Ser Asp
 15 20 25
 ttc ctg ttt aga agc tat tgg atg acc tgg gtc cgc cat ccg gg 251
 Phe Leu Phe Arg Ser Tyr Trp Met Thr Trp Val Arg His Pro
 30 35 40

<210> 155
 <211> 147
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 24..146

<221> sig_peptide
 <222> 24..140
 <223> Von Heijne matrix
 score 7.80000019073486
 seq ILLFLFLILFIWH/IR

<400> 155
ggattttgtc aaatgctttt tct atg tcg att ttg ctg agg gtt tta ggc ata 53
Met Ser Ile Leu Leu Arg Val Leu Gly Ile
-35 -30
aag gga tgc tgg att ttg tca aat cct ttt tct gca tgt att gag atg 101
Lys Gly Cys Trp Ile Leu Ser Asn Pro Phe Ser Ala Cys Ile Glu Met
-25 -20 -15
atc ttg tta ttt ttg ttt tta att ctg ttt ata tgg cac att cgg g 147
Ile Leu Leu Phe Leu Phe Leu Ile Leu Phe Ile Trp His Ile Arg
-10 -5 1

<210> 156
<211> 141
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 61..141
<221> sig_peptide
<222> 61..135
<223> Von Heijne matrix
score 7.69999980926514
seq LVPILLIGWIVG/CT

<400> 156
gctggataac aaaagaaaga ggtaagcgtg gcctgaccta gccacccacc aacaggaata 60
atg gct gaa aaa gcg ggg tct aca ttt tca cac ctt ctg gtt cct att 108
Met Ala Glu Lys Ala Gly Ser Thr Phe Ser His Leu Leu Val Pro Ile
-25 -20 -15 -10
ctt ctc ctg att ggc tgg att gtg ggc tgc acc 141
Leu Leu Leu Ile Gly Trp Ile Val Gly Cys Thr
-5 1

<210> 157
<211> 115
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 12..113
<221> sig_peptide
<222> 12..68
<223> Von Heijne matrix
score 7.69999980926514
seq RLYLWMCLAAALA/SF

<400> 157
ctcaagaagc c atg gcg gaa tcc agg ggc cgt ctg tac ctt tgg atg tgc 50
Met Ala Glu Ser Arg Gly Arg Leu Tyr Leu Trp Met Cys
-15 -10


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<400> 159
aggaggggcc gtcagggngg gatacagcct ggaaggtgcg tgtggggctg ggtctcggag      60
tgggagacgt ggagtgcagg taatgcatgt ccatgggtaca caaattcaca aggtttgtaa      120
atg aga aaa gac gtg agg ttc ctt ttg ttc ttt acc tgt ggc ctc cct      168
Met Arg Lys Asp Val Arg Phe Leu Leu Phe Phe Thr Cys Gly Leu Pro
-20          -15          -10          -5
gcc cta cac ggg gac tct agg gtg gaa tgt agc aaa gcc cat cca cca      216
Ala Leu His Gly Asp Ser Arg Val Glu Cys Ser Lys Ala His Pro Pro
1          5          10
gcc atg tac tac cc      230
Ala Met Tyr Tyr
15

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<210> 160
<211> 346
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> 202..345

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<221> sig_peptide
<222> 202..282
<223> Von Heijne matrix
      score 7.59999990463257
      seq WTLISISLSVFWS/EP

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<400> 160
ttcttctaca tacagctacc caactagccc acaccattta ttgaatacag agtagtcttt      60
tccctgttgg ttatittttct taactttgtt aaagatcaga tatctgtagg tgtgcagctt      120
tatttctggg ttttctgttc cgttccattg gtctatgtgt ctgtttttgt accagtacca      180
tgctgttctg gcaccagtac c atg cta ttt tgg tta cca tct cca tct gag      231
                        Met Leu Phe Trp Leu Pro Ser Pro Ser Glu
                        -25          -20
acc act tca gcc tgg act tta ttg tcc ata tca cta tca gta ttt tgg      279
Thr Thr Ser Ala Trp Thr Leu Leu Ser Ile Ser Leu Ser Val Phe Trp
-15          -10          -5
tca gag cca ttc aat aag tct cta gga agt tcc aaa cta cca tgt cat      327
Ser Glu Pro Phe Asn Lys Ser Leu Gly Ser Ser Lys Leu Pro Cys His
1          5          10          15
ttt ttt tct ata aaa cgg g      346
Phe Phe Ser Ile Lys Arg
20

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<210> 161
<211> 388
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> 194..388

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<221> sig_peptide
 <222> 194..334
 <223> Von Heijne matrix
 score 7.59999990463257
 seq LXLGEGLTFLCLC/QV

<221> misc_feature
 <222> 352
 <223> n=a, g, c or t
 Oligonucleotide

<400> 161
 agtgagagct tagtcttggt actatttggt tttgtttctt actgtttgtc tgtttatggt 60
 tgggtgcaag aaaattgtgt tgtaaattat cccttgcttt ctctattagt taatagcctt 120
 ccccttctgt agtaaagtaa msagsctttt kcctgttcaa atattttagg cttgtttttt 180
 gttttgattg tac atg cct gtg tgt ttt tat tcc tta att tgt ttc ttt 229
 Met Pro Val Cys Phe Tyr Ser Leu Ile Cys Phe Phe
 -45 -40
 att tat ttc tgt ttg tta tct cca aga gaa aca ata gaa gag gtg gcc 277
 Ile Tyr Phe Cys Leu Leu Ser Pro Arg Glu Thr Ile Glu Glu Val Ala
 -35 -30 -25 -20
 ctc ttc cag ttt tct ctg cth mtc ttg gga gag ggt ctc acc ttt ctt 325
 Leu Phe Gln Phe Ser Leu Leu Xaa Leu Gly Glu Gly Leu Thr Phe Leu
 -15 -10 -5
 tgc ctc tgc cag gta atg acg aat aan atg caa ctg ctg ttc ttg agt 373
 Cys Leu Cys Gln Val Met Thr Asn Xaa Met Gln Leu Leu Phe Leu Ser
 1 5 10
 ggg gta gtc tgt ggg 388
 Gly Val Val Cys Gly
 15

<210> 162
 <211> 235
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 172..234

<221> sig_peptide
 <222> 172..210
 <223> Von Heijne matrix
 score 7.5
 seq MAPLLLSLSCSFS/CH

<400> 162
 cccctccaaa tctcatgttg agatttgatc cctaagtgtg gagatggggc ctgggtgggag 60
 atattcggat catgagggca gatccctcac taatggcctg gtgccctccc tgtggaaatg 120
 agtaagttct cactcttttg gttcacctga gagctgtttg tttaaaagag c atg gca 177
 Met Ala
 ccc ctc ctt ctc tct ctg tct tgc tcc ttt tct tgc cat gtg aca ctc 225
 Pro Leu Leu Leu Ser Leu Ser Cys Ser Phe Ser Cys His Val Thr Leu

Leu	Ile	Ser	Glu	Leu	Leu	Leu	Leu	Arg	Ser	Val	Thr	Ser	His	Asn	Thr	
			-10					-5					1			
atg	atg	aga	gct	tta	tca	agc	cag	atg	ctt	agt	cag	agc	ttt	cca	aga	148
Met	Met	Arg	Ala	Leu	Ser	Ser	Gln	Met	Leu	Ser	Gln	Ser	Phe	Pro	Arg	
	5					10				15						
ccc	agc	ttt	ggt	ttt	atc	agc	aaa	atc	cat	cct	tcc	cac	ccc	ccc	aa	195
Pro	Ser	Phe	Gly	Phe	Ile	Ser	Lys	Ile	His	Pro	Ser	His	Pro	Pro		
20					25				30							

<210> 165
 <211> 256
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 34..255
 <221> sig_peptide
 <222> 34..186
 <223> Von Heijne matrix
 score 7.5
 seq VVSLTFLLGMTWG/FA

<221> misc_feature
 <222> 18
 <223> n=a, g, c or t
 Oligonucleotide

<400> 165																
tatttatgtg	acctgtgngg	gtattttgga	gtc	atg	ttt	ttt	ctg	aac	att	gcc						54
				Met	Phe	Phe	Leu	Asn	Ile	Ala						
				-50				-45								
atg	ttc	att	gtg	gta	atg	gtg	cag	atc	tgt	ggg	agg	aat	ggc	aag	aga	102
Met	Phe	Ile	Val	Val	Met	Val	Gln	Ile	Cys	Gly	Arg	Asn	Gly	Lys	Arg	
			-40					-35					-30			
agc	aac	cgg	acc	ctg	aga	gaa	gaa	gtg	tta	agg	aac	ctg	cgc	agt	gtg	150
Ser	Asn	Arg	Thr	Leu	Arg	Glu	Glu	Val	Leu	Arg	Asn	Leu	Arg	Ser	Val	
			-25					-20				-15				
gtt	agc	ttg	acc	ttt	ctg	ttg	ggc	atg	aca	tgg	ggt	ttt	gca	ttc	ttt	198
Val	Ser	Leu	Thr	Phe	Leu	Leu	Gly	Met	Thr	Trp	Gly	Phe	Ala	Phe	Phe	
		-10					-5				1					
gcc	tgg	gga	ccc	tta	aat	atc	ccc	ttc	atg	tac	ctc	ttc	tcc	atc	ttc	246
Ala	Trp	Gly	Pro	Leu	Asn	Ile	Pro	Phe	Met	Tyr	Leu	Phe	Ser	Ile	Phe	
5				10					15					20		
aat	tca	tta	c													256
Asn	Ser	Leu														

<210> 166
 <211> 209
 <212> DNA
 <213> Homo sapiens

<220>

<221> CDS
<222> 36..209

<221> sig_peptide
<222> 36..86
<223> Von Heijne matrix
score 7.5
seq FLFLFLXXLIVA/VT

<400> 166
cttttttdtc ckgcacaagg gattttccggg tcagg atg aac aaa cac ttc ttg 53
Met Asn Lys His Phe Leu
-15
ttc ctc ttc ctc ctt dac kgc ctc att gtg gca gtg aca tca ctt cag 101
Phe Leu Phe Leu Leu Xaa Xaa Leu Ile Val Ala Val Thr Ser Leu Gln
-10 -5 1 5
tgc ata aca tgc cac ctt cgc aca cgg aca gac cgc tgt aga aga ggc 149
Cys Ile Thr Cys His Leu Arg Thr Arg Thr Asp Arg Cys Arg Arg Gly
10 15 20
ttt ggt gdc tgt act gct cag aag ggc gag gca tgc atg ctc tta agg 197
Phe Gly Xaa Cys Thr Ala Gln Lys Gly Glu Ala Cys Met Leu Leu Arg
25 30 35
att cac cag cgc 209
Ile His Gln Arg
40

<210> 167
<211> 184
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 44..184

<221> sig_peptide
<222> 44..148
<223> Von Heijne matrix
score 7.5
seq LLLTSHFLGESLG/GG

<400> 167
taaagtcctg tgtatgacat gacatagtat ttgctgaatt taa atg tac ata aag 55
Met Tyr Ile Lys
-35
atg gag tct gtc acc ttg tca cca gcc cca gtc ttc ccc gtc cct gca 103
Met Glu Ser Val Thr Leu Ser Pro Ala Pro Val Phe Pro Val Pro Ala
-30 -25 -20
car ctc ctt tta ctg aca tcc cat ttt cta ggc gag tcc ctt ggt gga 151
Gln Leu Leu Leu Leu Thr Ser His Phe Leu Gly Glu Ser Leu Gly Gly
-15 -10 -5 1
ggc aca ctg ctt gtc cca ctc ctc ccc cca ggg 184
Gly Thr Leu Leu Val Pro Leu Leu Pro Pro Gly
5 10

<210> 168
 <211> 218
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 97..216

<221> sig_peptide
 <222> 97..177
 <223> Von Heijne matrix
 score 7.40000009536743
 seq ILLLTICAAGIXG/TR

<400> 168
 ccttccctcc gcgcacaggc tgccggctca ccgcttgcta atggcagccg gggctctccct 60
 gggacagcaa gacctccgct caggcccctc tttcga atg ckc cam gcm ctc ctg 114
 Met Xaa Xaa Ala Leu Leu
 -25
 cga tct aga atg att cag ggc agg atc ctg ctc ctg acc atc tgc gct 162
 Arg Ser Arg Met Ile Gln Gly Arg Ile Leu Leu Leu Thr Ile Cys Ala
 -20 -15 -10
 gcc ggc att rgt ggg act cgt cag ttt ggc tat aac ctc tct atc atc 210
 Ala Gly Ile Xaa Gly Thr Arg Gln Phe Gly Tyr Asn Leu Ser Ile Ile
 -5 1 5 10
 aat gac cc 218
 Asn Asp

<210> 169
 <211> 480
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 317..478

<221> sig_peptide
 <222> 317..457
 <223> Von Heijne matrix
 score 7.40000009536743
 seq SCLFSXAWLXCXC/HG

<400> 169
 gtctcgtggg ctgggtcccca gcgggtccct ccccgaacag ctgctgctcc agggaggaag 60
 cggcgyrrgt gmtgtccagc ttcccgggtgc tgaaaaccgg agggctcgtc atccaccact 120
 accatgtaag ggccatgaga agggctcatc ctggcgcasg cggacatgga ggaggactta 180
 ttccagctaa ggcagctgcc ggttgtgaaa ttccgtcgca caggcgagag tgcaagggtca 240
 gaggacgaca cggcttcagg agagcatgaa gtccagattg aaggggtcca cgtgggccta 300
 gaggtgtggt agctgg atg atg ggg cak ctg tgc cca agg agt ttg cca atc 352
 Met Met Gly Xaa Leu Cys Pro Arg Ser Leu Pro Ile
 -45 -40

cca ccg atg ata ctt tca tgg tgg aag atg cag tgg aag cca ttg gct	400
Pro Pro Met Ile Leu Ser Trp Trp Lys Met Gln Trp Lys Pro Leu Ala	
-35 -30 -25 -20	
ttg gaa aat ttc agt gga agc tgt ctg ttc tca mtg gct tgg ctt kga	448
Leu Glu Asn Phe Ser Gly Ser Cys Leu Phe Ser Xaa Ala Trp Leu Xaa	
-15 -10 -5	
tgc tsa tgc cat gga gat gat gat ctc agc at	480
Cys Xaa Cys His Gly Asp Asp Asp Leu Ser	
1 5	

<210> 170
 <211> 280
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 135..278
 <221> sig_peptide
 <222> 135..179
 <223> Von Heijne matrix
 score 7.40000009536743
 seq LLQLLAFLGNS/VE

<221> misc_feature
 <222> 104
 <223> n=a, g, c or t
 Oligonucleotide

<400> 170	
ttctttgggc tcgggggctc ccggagcagg gcgagagctc gcgtcgccgg aaaggaagac	60
gggaagaaag ggcaggcggc tcggcgggcg tcttctccac tccntgccgc gccccgtggc	120
tgcaggggagc cggc atg ggg ctt ctc cag ttg cta gct ttc agt ttc tta	170
Met Gly Leu Leu Gln Leu Leu Ala Phe Ser Phe Leu	
-15 -10 -5	
ggt aat tcc gtg gaa acg gtg cgg gga ggc gga cgg act tgg gca tgg	218
Gly Asn Ser Val Glu Thr Val Arg Gly Gly Gly Arg Thr Trp Ala Trp	
1 5 10	
gga agg aaa acc caa aag ctg ctt gct cac ctt cgt ggg atc ctg ggg	266
Gly Arg Lys Thr Gln Lys Leu Leu Ala His Leu Arg Gly Ile Leu Gly	
15 20 25	
gct tgg gas agg ga	280
Ala Trp Xaa Arg	
30	

<210> 171
 <211> 103
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 28..102

<221> sig_peptide
 <222> 28..69
 <223> Von Heijne matrix
 score 7.40000009536743
 seq LVLVHSSLSKTLs/QK

<400> 171
 actgggatgc agaggctgca gtgagcc atg ttg gtg ctg gtg cac tcc agc ctg 54
 Met Leu Val Leu Val His Ser Ser Leu
 -10
 agc aag acc ttg tct cag aaa aaa aaa aag ttc aca aas ccc acc agg g 103
 Ser Lys Thr Leu Ser Gln Lys Lys Lys Lys Phe Thr Xaa Pro Thr Arg
 -5 1 5 10

<210> 172
 <211> 218
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 73..216

<221> sig_peptide
 <222> 73..129
 <223> Von Heijne matrix
 score 7.40000009536743
 seq LILVISCLLLAFE/CV

<400> 172
 caattttgtt gatcttttca aaaaaccagc tcctggattc attaatTTTT tgaagggttt 60
 tttgatgtct ct atg tcc ttc agt tct gct ctg att tta gtt att tct tgc 111
 Met Ser Phe Ser Ser Ala Leu Ile Leu Val Ile Ser Cys
 -15 -10
 ctt ctg cta gct ttt gaa tgt gtt tgc tct tgc ttt tct ggt tct ttt 159
 Leu Leu Leu Ala Phe Glu Cys Val Cys Ser Cys Phe Ser Gly Ser Phe
 -5 1 5 10
 aat tgt gat gtt agg gtg tca att tcg gat ctt tcc tgc ttt ctc ttg 207
 Asn Cys Asp Val Arg Val Ser Ile Ser Asp Leu Ser Cys Phe Leu Leu
 15 20 25
 tgg ggc aag gg 218
 Trp Gly Lys

<210> 173
 <211> 380
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 295..378

<221> sig_peptide

<222> 295..360
 <223> Von Heijne matrix
 score 7.40000009536743
 seq CLXVFLLTDRTLS/CR

<400> 173
 tattggttat tctagttata cattagtcta aatttttttc aaagttttca acttctttgc 60
 ctttggtttg aatttcctcc tgtagcttgg agtagtttga tcatctgaag ctttcttctc 120
 tcaactcatc aaagtcattc tccatccagc tttgttccat tgctggtgag gaactgtgtt 180
 ccttcggagg aggagaggtg ctctgctttt ttgagtttcc agtttttctg ctctgttttt 240
 tccccatctt tgtggtttta tctacttttg gtctttgatg ctggtgatgt acag atg 297
 Met
 ggt ttt tgg tgt gga tgt cct ttc tgt ttg twa gtt ttc ctt cta aca 345
 Gly Phe Trp Cys Gly Cys Pro Phe Cys Leu Xaa Val Phe Leu Leu Thr
 -20 -15 -10
 gac agg acc ctc agc tgc agg tct gtt gga gtt gc 380
 Asp Arg Thr Leu Ser Cys Arg Ser Val Gly Val
 -5 1 5

<210> 174
 <211> 139
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 59..139

<221> sig_peptide
 <222> 59..103
 <223> Von Heijne matrix
 score 7.30000019073486
 seq LLSLSLWGISTLS/ST

<400> 174
 ataacagaat gatttacatt cctttgggta tataccagc gatgggat atgtgtca 58
 atg gta tta ctg tct tta agt ctt tgg ggc atc tcc aca ctg tct tcc 106
 Met Val Leu Leu Ser Leu Ser Leu Trp Gly Ile Ser Thr Leu Ser Ser
 -15 -10 -5 1
 aca aca att gaa cta att tac acc ccc atc ggg 139
 Thr Thr Ile Glu Leu Ile Tyr Thr Pro Ile Gly
 5 10

<210> 175
 <211> 122
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 38..121

<221> sig_peptide
 <222> 38..112

<223> Von Heijne matrix
 score 7.30000019073486
 seq LLHVHSFLPPVFS/TQ

<400> 175
 ctacctgtcc ttgcgcacca cccttgtctg ggccttc atg gcc tct ctc ctg agt 55
 Met Ala Ser Leu Leu Ser
 -25 -20
 ggc ttt act agc ttc tgt ctt ttg cac gtt cac tct ttc ctc cct cca 103
 Gly Phe Thr Ser Phe Cys Leu Leu His Val His Ser Phe Leu Pro Pro
 -15 -10 -5
 gtg ttt tcc acc cag aat g 122
 Val Phe Ser Thr Gln Asn
 1

<210> 176
 <211> 300
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 175..300

<221> sig_peptide
 <222> 175..264
 <223> Von Heijne matrix
 score 7.30000019073486
 seq AILLXXWEAGSEA/VR

<221> misc_feature
 <222> 51..52,63,239
 <223> n=a, g, c or t
 Oligonucleotide

<400> 176
 aaaaactcta aaagaaggac gcatttttagg taagatctag tggctagatc nncaggggtg 60
 gcnkcgttct tgtggaaatc agtcaagaaa gatcggtatc gcggttattt atgcaaatca 120
 tctgggtgga ttgtgtacgg agttaaactg cgccttctgg accgggtctg aaca atg 177
 Met
 -30
 gag act gcg cta saa tka acg cca cag aaa agg caa gtt atg ttt ctt 225
 Glu Thr Ala Leu Xaa Xaa Thr Pro Gln Lys Arg Gln Val Met Phe Leu
 -25 -20 -15
 gct ata ttg ttg cnt twg tgg gag gct ggc tct gag gca gth agg tat 273
 Ala Ile Leu Leu Xaa Xaa Trp Glu Ala Gly Ser Glu Ala Val Arg Tyr
 -10 -5 1
 tcc ata cca gaa gaa aca gaa agt ggc 300
 Ser Ile Pro Glu Glu Thr Glu Ser Gly
 5 10

<210> 177
 <211> 466
 <212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 268..465

<221> sig_peptide

<222> 268..372

<223> Von Heijne matrix

score 7.30000019073486

seq LDLLGSSSPPTSA/SQ

<400> 177

cttaaacttt	attatgttgk	kttcacaaag	agcagccttt	gttgactttg	aaatcattgc	60
ttcagtattc	tagaaaatct	tgtttttgtt	aaacatgggc	agtaacttac	tatttttgta	120
tagttgttgt	wcatcktacc	cccaccctgt	tttaaaaata	aaaagtagtt	gtcagattac	180
tttggtttta	gaagtacctt	ttcacttgcc	ttagaatctt	cattactttg	agcctacact	240
ccacctctta	ttggaacttc	atgaaga	atg atg ttg gat ttc gct ctg tgc ccc			294
			Met Met Leu Asp Phe Ala Leu Ser Pro			
			-35	-30		
agg cta gag cgc agt ggt ctg atc atg gct tgc tgt acc ctt gac ctc						342
Arg Leu Glu Arg Ser Gly Leu Ile Met Ala Cys Cys Thr Leu Asp Leu						
-25		-20		-15		
ctg ggt tca agc agt cct ccc acc tca gcc tcc cag gtg gct ggg act						390
Leu Gly Ser Ser Ser Pro Pro Thr Ser Ala Ser Gln Val Ala Gly Thr						
-10		-5		1	5	
ggg cat gtg cca cca cac cca gct agt ttt ttt tac ttt ktt gta wga						438
Gly His Val Pro Pro His Pro Ala Ser Phe Phe Tyr Phe Xaa Val Xaa						
	10		15		20	
cag gtc tac tat gtt tcg cag ctg atc t						466
Gln Val Tyr Tyr Val Ser Gln Leu Ile						
	25		30			

<210> 178

<211> 222

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 30..221

<221> sig_peptide

<222> 30..95

<223> Von Heijne matrix

score 7.19999980926514

seq QVFFLVFPDGVPR/QP

<400> 178

acgtcggacc	cggaggccct	gaatgcccc	atg cgc acc cca cag ctc gcg ctc	53	
			Met Arg Thr Pro Gln Leu Ala Leu		
			-20	-15	
ctg caa gtg ttc ttt ctg gtg ttc ccc gat ggc gtc cgg cct cag ccc					101
Leu Gln Val Phe Phe Leu Val Phe Pro Asp Gly Val Arg Pro Gln Pro					

				-10				-5					1			
tct	tcc	tcc	cca	tca	ggg	gca	gtg	ccc	acg	tct	ttg	gag	ctg	cag	cga	149
Ser	Ser	Ser	Pro	Ser	Gly	Ala	Val	Pro	Thr	Ser	Leu	Glu	Leu	Gln	Arg	
	5						10					15				
ggg	acg	gat	ggc	gga	acc	ctc	cag	tcc	cct	tca	gag	gcg	act	gca	act	197
Gly	Thr	Asp	Gly	Gly	Thr	Leu	Gln	Ser	Pro	Ser	Glu	Ala	Thr	Ala	Thr	
	20					25					30					
cgc	ccg	gcc	gtg	ccc	gga	ctc	cgg	g								222
Arg	Pro	Ala	Val	Pro	Gly	Leu	Arg									
35					40											

<210> 179
 <211> 171
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 33..170

<221> sig_peptide
 <222> 33..95
 <223> Von Heijne matrix
 score 7.19999980926514
 seq SWPLLA AVSGLRG/LE

<400> 179																
ccttttgcct	tcaaccttcg	agccgccacg	ta	atg	cca	cgt	ccc	cgc	gca	tgc						53
				Met	Pro	Arg	Pro	Arg	Ala	Cys						
				-20						-15						
gca	tct	tgg	ccg	ctg	ctg	gcg	gct	gtt	tcc	ggg	ctt	aga	ggg	ctg	gag	101
Ala	Ser	Trp	Pro	Leu	Leu	Ala	Ala	Val	Ser	Gly	Leu	Arg	Gly	Leu	Glu	
				-10				-5						1		
tgg	ccg	ccg	agt	tgg	agg	cgg	gtg	gtg	gca	gca	gta	gga	gtg	tgt	aga	149
Trp	Pro	Pro	Ser	Trp	Arg	Arg	Val	Val	Ala	Ala	Val	Gly	Val	Cys	Arg	
	5					10						15				
gtg	cgg	gat	tgg	ggg	ccc	cgg	g									171
Val	Arg	Asp	Trp	Gly	Pro	Arg										
	20					25										

<210> 180
 <211> 245
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 177..245

<221> sig_peptide
 <222> 177..227
 <223> Von Heijne matrix
 score 7.19999980926514
 seq FLLISVLTVIWF/WK

<400> 180
 tgtaattttc cttgccaaaa agcttagttt catcttttat aaatataccta taatgccaaag 60
 ttgattgcat ggtcagagtg aatctgtgct gtaccawat tcagtagcct tctcctatcc 120
 aacaaagtgt tttgtaaata ggaggtaaat gaatgagtgg atggatggag ggatga atg 179
 Met
 aat gga att ttc ttg ctc ttg atc tct gtc tta aca gtg att tgg ttt 227
 Asn Gly Ile Phe Leu Leu Leu Ile Ser Val Leu Thr Val Ile Trp Phe
 -15 -10 -5
 tgg aag aca cac ccg ggg 245
 Trp Lys Thr His Pro Gly
 1 5

<210> 181
 <211> 241
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 160..240

<221> sig_peptide
 <222> 160..213
 <223> Von Heijne matrix
 score 7.19999980926514
 seq XLLCIIXLYLIRG/SE

<400> 181
 gttgactttt ctctctgctg aggcagaaaa atgcttccat agtccatgca gcaatgttta 60
 aaacaaggga ttctgttccc ccctevcctt ttgtgtaggc tggtaataa actctgtgtt 120
 tywtacatt gtcgtgaawa ttcagagtgc tccctgcga atg gtt ttc cta gta 174
 Met Val Phe Leu Val
 -15
 kct ctg ttg tgt atc att kct ctt tat ttg att cgt ggt tct gag tgg 222
 Xaa Leu Leu Cys Ile Ile Xaa Leu Tyr Leu Ile Arg Gly Ser Glu Trp
 -10 -5 1
 amc cta cca ccg aac tgg g 241
 Xaa Leu Pro Pro Asn Trp
 5

<210> 182
 <211> 263
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 103..261

<221> sig_peptide
 <222> 103..156
 <223> Von Heijne matrix
 score 7.19999980926514

seq LFFLLRIALASWA/LF

```
<400> 182
gggttatcta acctgttcca ttgttccgtg tatcagtttc tgtaccgata ccatgctggt      60
ttggttactg tagtcttgta gtatagttta aagtcagata gc atg atg act cta      114
                                   Met Met Thr Leu
                                   -15
gct ttg ttc ttt ttg ctt agg att gct ttg gct agt tgg gct ctc ttt      162
Ala Leu Phe Phe Leu Leu Arg Ile Ala Leu Ala Ser Trp Ala Leu Phe
                                   -10      -5      1
tgg atc cat atg aat ttt aga aga gct ttt ttc cac tta cgg tgg ttt      210
Trp Ile His Met Asn Phe Arg Arg Ala Phe Phe His Leu Arg Trp Phe
                                   5      10      15
gat atc aat agc act gaa tct gta aat tgc ttt ggg cag tat ggc cta      258
Asp Ile Asn Ser Thr Glu Ser Val Asn Cys Phe Gly Gln Tyr Gly Leu
                                   20      25      30
gcg gg      263
Ala
35
```

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<210> 183
<211> 170
<212> DNA
<213> Homo sapiens
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<220>
<221> CDS
<222> 60..170

<221> sig_peptide
<222> 60..146
<223> Von Heijne matrix
score 7.09999990463257
seq SLLVFCLNDLSNA/VX
```

```
<400> 183
ttccatgtgg agatgrraag aatatatatt ctgtgggttat tgggtagagt gttctatag      59
atg tct att agg tct aat tgg tct agt gtc gaa tct aag tct aga att      107
Met Ser Ile Arg Ser Asn Trp Ser Ser Val Glu Ser Lys Ser Arg Ile
                                   -25      -20      -15
tct tta tta gtt ttc tgc ctc aat gat ctw tck aat gcw gtc arg wgg      155
Ser Leu Leu Val Phe Cys Leu Asn Asp Leu Ser Asn Ala Val Xaa Xaa
                                   -10      -5      1
ggm att gaa rtc ccc      170
Gly Ile Glu Xaa Pro
5
```

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<210> 184
<211> 443
<212> DNA
<213> Homo sapiens
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<220>
<221> CDS
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<222> 83..442

<221> sig_peptide

<222> 83..130

<223> Von Heijne matrix

score 7.09999990463257

seq IPLFLGVLAYCTG/SV

<400> 184

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ctttccagca aggggataag agaggcctgg aagaacctgc ccagcctggg cctcaggaag      60
cagcatcgga ggtgcctcag cc atg gca tgg atc cct ctc ttc ctc ggc gtc      112
                               Met Ala Trp Ile Pro Leu Phe Leu Gly Val
                               -15                               -10
ctt gct tac tgc aca gga tcc gtg gcc tcc tat gag ctg act cac cca      160
Leu Ala Tyr Cys Thr Gly Ser Val Ala Ser Tyr Glu Leu Thr His Pro
-5                               1                               5                               10
ccc tca gtg tcc gtg tcc cca gga cag aca gcc agc atc acc tgc tct      208
Pro Ser Val Ser Val Ser Pro Gly Gln Thr Ala Ser Ile Thr Cys Ser
                               15                               20                               25
gga gat aaa ttg ggg gat aaa tat gct tgc tgg tat cag cag aag cca      256
Gly Asp Lys Leu Gly Asp Lys Tyr Ala Cys Trp Tyr Gln Gln Lys Pro
                               30                               35                               40
ggc cag tcc cct gtg ctg gtc atc tat caa gat agc aag cgg ccc tca      304
Gly Gln Ser Pro Val Leu Val Ile Tyr Gln Asp Ser Lys Arg Pro Ser
                               45                               50                               55
ggg atc cct gag cga ttc tct ggc tcc aac tct ggg aac aca gcc act      352
Gly Ile Pro Glu Arg Phe Ser Gly Ser Asn Ser Gly Asn Thr Ala Thr
                               60                               65                               70
ctg acc atc agc ggg acc cag gct atg gat gag gct gac tat tac tgt      400
Leu Thr Ile Ser Gly Thr Gln Ala Met Asp Glu Ala Asp Tyr Tyr Cys
75                               80                               85                               90
cag gcg tgg gac agc agc act gtg gta ttc ggc gga ggg acc a      443
Gln Ala Trp Asp Ser Ser Thr Val Val Phe Gly Gly Gly Thr
                               95                               100
```

<210> 185

<211> 427

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 332..427

<221> sig_peptide

<222> 332..418

<223> Von Heijne matrix

score 7.09999990463257

seq FCFXLCFGRSSLG/CR

<400> 185

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taagtttata yhtctgaatc tgaaatcaga atatatatat ttaatttttc aatttttaaaa      60
atgttacctt gtgtgagaca aaacaaaaca gtgactagaa ccctccttgt gggctaaatt      120
tgagtttgct tcttcataat gttttaaatg cttcacaaac atttttcttt ggtatatga      180
```

gcaaaatgaa ttgaagtata ttactgagt gatgattatt gaggaaaaac tcaaagatct	240
gctgtaagca ctagagttga aggactagcc caacagctcc tcaggcacct ttgggtatat	300
tgagttgccc cccctgactt tgaacacatc t atg gtc tgt gtc atc ttc aaa	352

Met Val Cys Val Ile Phe Lys

-25

gag ctc atg gaa ttt gaa ttc cct ggg ttt tgt ttt tgh ctt tgt ttt	400
Glu Leu Met Glu Phe Glu Phe Pro Gly Phe Cys Phe Xaa Leu Cys Phe	
-20 -15 -10	

gga cgg agc tcg ctc tgt tgc cga rac	427
Gly Arg Ser Ser Leu Cys Cys Arg Xaa	
-5 1	

<210> 186
 <211> 365
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 130..363

<221> sig_peptide
 <222> 130..219
 <223> Von Heijne matrix
 score 7.09999990463257
 seq SCLALXTLAVVYA/AL

<400> 186	
aacgagtctt tgggaacgtg gtccaccag ggatgtaaaa ctgtgcttac cgatgcatcc	60
catacgaaat gcttatgtga tcgtctctct accttcgcca ttttggtca gcaacctaga	120
gaaataatc atg gaa tcc tct ggc aca cct tca gtt acc cta ata gta ggc	171

Met Glu Ser Ser Gly Thr Pro Ser Val Thr Leu Ile Val Gly

-30 -25 -20

agt ggt ctt tct tgc ttg gcc ttg atb acc cta gca gtt gtc tat gca	219
Ser Gly Leu Ser Cys Leu Ala Leu Xaa Thr Leu Ala Val Val Tyr Ala	
-15 -10 -5	

gca tta tgg mgg tac ata cgc tct gag aga tcc ata ata cta att aac	267
Ala Leu Trp Arg Tyr Ile Arg Ser Glu Arg Ser Ile Ile Leu Ile Asn	
1 5 10 15	

ttc tgc ctg tct atc atc tca tcc aat atc ctc ata ctg gtt gga cag	315
Phe Cys Leu Ser Ile Ile Ser Ser Asn Ile Leu Ile Leu Val Gly Gln	
20 25 30	

act cag aca cat aat aaa gag tat ctg cac aac cac cac tgc att ttt	363
Thr Gln Thr His Asn Lys Glu Tyr Leu His Asn His His Cys Ile Phe	
35 40 45	

gc 365

<210> 187
 <211> 260
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS

<222> 86..259

<221> sig_peptide

<222> 86..178

<223> Von Heijne matrix

score 7.09999990463257

seq LXFLASSFCFGEA/DS

<221> misc_feature

<222> 143

<223> n=a, g, c or t

Oligonucleotide

<400> 187

ttttggaaca gggtaggcat tttgttttatt gtttgcttgc ttctagggtgt tttcgccatc 60

agggtgtatt ggaggctgac actta atg ggt gtg tgt tgc gcc cag aac tgc 112

Met Gly Val Cys Cys Ala Gln Asn Cys
-30 -25

tgc gtg tgc ggg ktc waa agr aat gcg ctg ntg ttc ttg gct tca agt 160

Ser Val Ser Gly Xaa Xaa Arg Asn Ala Leu Xaa Phe Leu Ala Ser Ser
-20 -15 -10

ttc tgc ttt gga gaa gca gat tca gga agt agg tgt tgc tta aaa ata 208

Phe Cys Phe Gly Glu Ala Asp Ser Gly Ser Arg Cys Cys Leu Lys Ile
-5 1 5 10

att ctt ggt ttt tat cta atc aga tat tca ttg att acc tac cag gtg 256

Ile Leu Gly Phe Tyr Leu Ile Arg Tyr Ser Leu Ile Thr Tyr Gln Val
15 20 25

cgt g 260

Arg

<210> 188

<211> 172

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 52..171

<221> sig_peptide

<222> 52..105

<223> Von Heijne matrix

score 7.09999990463257

seq LFFFLKWSHPGWS/AT

<221> misc_feature

<222> 112

<223> n=a, g, c or t

Oligonucleotide

<400> 188

ttaatggaat atattatagt acactagcat gctggaaaaga atgaaaataa t atg aaa 57

Met Lys

att ctt tac ctt ttt ttc ttt ttg aaa tgg agt cac cca ggc tgg agt 105

Ile	Leu	Tyr	Leu	Phe	Phe	Phe	Leu	Lys	Trp	Ser	His	Pro	Gly	Trp	Ser		
-15							-10				-5						
gca	acg	ncg	tgg	tct	tgg	cac	act	gca	acc	tcc	gcc	tcc	ctg	att	caa		153
Ala	Thr	Xaa	Trp	Ser	Trp	His	Thr	Ala	Thr	Ser	Ala	Ser	Leu	Ile	Gln		
1			5					10					15				
gtg	att	ctc	ccg	cct	tgg	g											172
Val	Ile	Leu	Pro	Pro	Trp												
			20														

<210> 189
 <211> 150
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 47..148
 <221> sig_peptide
 <222> 47..124
 <223> Von Heijne matrix
 score 7.09999990463257
 seq LFLSGCFLFLSXC/XI

<400> 189																						
tat	cac	wt	tct	aag	ag	att	ttc	tgg	t	gaa	act	tgt	g	gatt	ttt	ct	tac	atg	aca	cca		55
																			Met	Thr	Pro	
																				-25		
tgt	ttt	ctg	caa	atg	gac	aat	ttg	act	cct	ctt	ttc	cta	tct	gga	tgc							103
Cys	Phe	Leu	Gln	Met	Asp	Asn	Leu	Thr	Pro	Leu	Phe	Leu	Ser	Gly	Cys							
			-20					-15			-10											
ttt	tta	ttt	ctc	tct	cwt	tgc	wtg	att	tat	ttg	gct	agg	att	ttg	gg							150
Phe	Leu	Phe	Leu	Ser	Xaa	Cys	Xaa	Ile	Tyr	Leu	Ala	Arg	Ile	Leu								
		-5				1				5												

<210> 190
 <211> 339
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 195..338
 <221> sig_peptide
 <222> 195..314
 <223> Von Heijne matrix
 score 7
 seq ITCKLCLCEQSXG/QD

<400> 190																						
agt	ctt	gcaa	agt	gtaa	agc	tgt	cag	ccgc	ag	agc	cag	gga	ag	acg	gga	ag	aga	aat	gga		60	
ag	ag	ctc	ctg	tcc	ggt	gtgc	cag	cag	ccc	g	act	ggc	ggt	gag	cg	gag	gag	g	ctack	g	120	
aga	ag	ccc	g	cg	ac	g	gag	ga	acg	cag	gt	ct	g	ct	g	cc	agg	g	att	gag	gag	180

ctgaagacag gctg atg ggc tca gct ggt agg ctc cac tat ctc gsc atg	230
Met Gly Ser Ala Gly Arg Leu His Tyr Leu Xaa Met	
-40 -35 -30	
act gct gaa aat ccc act cct gga gac ctg gct ccg kcc ccc ctc atc	278
Thr Ala Glu Asn Pro Thr Pro Gly Asp Leu Ala Pro Xaa Pro Leu Ile	
-25 -20 -15	
act tgc aaa ctc tgc ctg tgt gag cag tct crt gga caa gat gac cac	326
Thr Cys Lys Leu Cys Leu Cys Glu Gln Ser Xaa Gly Gln Asp Asp His	
-10 -5 1	
act cca gga atg c	339
Thr Pro Gly Met	
5	

<210> 191
 <211> 359
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 96..359

<221> sig_peptide
 <222> 96..242
 <223> Von Heijne matrix
 score 7
 seq VTVLLSAAPCLLS/CF

<221> misc_feature
 <222> 340
 <223> n=a, g, c or t
 Oligonucleotide

<400> 191	
tacaagagtt tttgctgaaa gttttaagtt gataagatgc agagaattgg gggaatgtat	60
aataaatcag gtttcattgt tatattattt accac atg aat cac ctt cct cct	113
Met Asn His Leu Pro Pro	
-45	
aac cat tat agg mgc cat gtg ttc aca tgt cat gtg gac cag tat tta	161
Asn His Tyr Arg Xaa His Val Phe Thr Cys His Val Asp Gln Tyr Leu	
-40 -35 -30	
act gtg gaa acc gcg ggt ggc atg gag aag gag gca gtg tcc gtg act	209
Thr Val Glu Thr Ala Gly Gly Met Glu Lys Glu Ala Val Ser Val Thr	
-25 -20 -15	
gtg ctg ctc tcc gca gcc ccc tgc ctg ctg tcc tgt ttc ctc ggc tcc	257
Val Leu Leu Ser Ala Ala Pro Cys Leu Leu Ser Cys Phe Leu Gly Ser	
-10 -5 1 5	
tcg gtg tct gga ctg gcg ttc tgg gtt tcc cag cag aaa act aaa ggg	305
Ser Val Ser Gly Leu Ala Phe Trp Val Ser Gln Gln Lys Thr Lys Gly	
10 15 20	
cca gag agg tgt aaa aac aca cac cac tbg gca gnt aat aat ttc ccc	353
Pro Glu Arg Cys Lys Asn Thr His Xaa Ala Xaa Asn Asn Phe Pro	
25 30 35	
gcg agg	359

Ala Arg

<210> 192
<211> 264
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 138..263

<221> sig_peptide
<222> 138..257
<223> Von Heijne matrix
score 7
seq FLFMLPLWCSIGT/CT

<400> 192
ttgagcttaa ggccaggtat atgggctcac acttgtaatc tcagtgcctt gggaggctga 60
gggaaaagga tagcttgagt ccaggagttc gagatcatcc tgggcaacat agcaagatcc 120
tgtctctaca aaaccta atg aac aaa att aaa gaa aac aca cac aca cac 170
Met Asn Lys Ile Lys Glu Asn Thr His Thr His
-40 -35 -30
aca cac aca cac aca cac aaa aac aac acc aaa cta gtg tca aac cta 218
Thr His Thr His Thr His Lys Asn Asn Thr Lys Leu Val Ser Asn Leu
-25 -20 -15
ttc ctt ttt atg tta cct ctc tgg tgc tcc att ggc act tgc aca g 264
Phe Leu Phe Met Leu Pro Leu Trp Cys Ser Ile Gly Thr Cys Thr
-10 -5 1

<210> 193
<211> 301
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 147..299

<221> sig_peptide
<222> 147..272
<223> Von Heijne matrix
score 7
seq LFLYSLFTENVLA/HP

<400> 193
tgtattgttt mmmttattta ctagtatgca gatctggttt tcattctttt catattgaat 60
ttcgttatgg gtagaatcat ttgcaaacat ttctagacat tttaaagat ctatttaatt 120
tgtttaagaa tggaaaacat aaaata atg cat gat tct tca ggc aag aat aat 173
Met His Asp Ser Ser Gly Lys Asn Asn
-40 -35
ttc aga aag ata cct gtt gta aat tta att tat ctc tat gta gac ata 221
Phe Arg Lys Ile Pro Val Val Asn Leu Ile Tyr Leu Tyr Val Asp Ile
-30 -25 -20

cat	ata	cat	aaa	tta	ttt	tta	tat	agt	ctc	ttt	aca	gaa	aat	gta	ttg	269
His	Ile	His	Lys	Leu	Phe	Leu	Tyr	Ser	Leu	Phe	Thr	Glu	Asn	Val	Leu	
			-15				-10					-5				
gca	cat	cct	tgc	att	gtt	cta	cgc	cgc	cta	tg						301
Ala	His	Pro	Cys	Ile	Val	Leu	Arg	Arg	Leu							
	1				5											

<210> 194
 <211> 215
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 105..215

<221> sig_peptide
 <222> 105..203
 <223> Von Heijne matrix
 score 7
 seq LFFLFVGPFSCLG/SY

<400> 194																	
gctctgactg	cagcctccca	gggaatgcgc	ggccgagggga	atgcgcgcag	tcacaggccc											60	
tgggagtgag	ctgggtgccg	gcgacctggc	acccgcgcct	ggat atg	ggg cgt	cta										116	
						Met Gly Arg Leu											
						-30											

cat	cgt	ccc	agg	agc	agc	acc	agc	tac	agg	aac	ctg	ccg	cat	ctg	ttt	164
His	Arg	Pro	Arg	Ser	Ser	Thr	Ser	Tyr	Arg	Asn	Leu	Pro	His	Leu	Phe	
			-25					-20						-15		
ctg	ttt	ttc	ctc	ttc	gtg	gga	ccc	ttc	agc	tgc	ctc	ggg	agt	tac	agc	212
Leu	Phe	Phe	Leu	Phe	Val	Gly	Pro	Phe	Ser	Cys	Leu	Gly	Ser	Tyr	Ser	
			-10					-5				1				
cgg																215
Arg																

<210> 195
 <211> 209
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 78..209

<221> sig_peptide
 <222> 78..158
 <223> Von Heijne matrix
 score 7
 seq RLLLLLLLXLPLP/PP

<221> misc_feature
 <222> 73..74
 <223> n=a, g, c or t

Oligonucleotide

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<400> 195
tcattcactg attagatcca gcgctgagag gcagcactgc tccttctctc acgccaactg      60
agtctcttga tcnntac atg caa tcc cag gca gct cgc gaa cac aaa ccc      110
                Met Gln Ser Gln Ala Ala Arg Glu His Lys Pro
                -25                -20
ggg ghc agc cgc cta ctg ctg ctg ctg ctg ctg cwg ctg ccg ctg cct      158
Gly Xaa Ser Arg Leu Leu Leu Leu Leu Leu Leu Xaa Leu Pro Leu Pro
    -15                -10                -5
ccg ccg gkv ctg cga acc cgg gdy ttt tca wgc acc aca ctc acc gcm      206
Pro Pro Xaa Leu Arg Thr Arg Xaa Phe Ser Xaa Thr Thr Leu Thr Ala
1                5                10                15
ggg
Gly
    209

```

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<210> 196
<211> 363
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> 287..361

<221> sig_peptide
<222> 287..331
<223> Von Heijne matrix
      score 7
      seq LWSLACLSPPAVQ/LG

```

```

<400> 196
ttacattgta atatataaat aattatacaa ctcaccataa cgtagaatca gtgggagccc      60
tgagcttggt ttcttgcaac tagatgggcc caactagacc aggtgatggg agacaatgac      120
agatcattag gcattagatt atcataagga gcatacaacc tagatccctt gcatgtgcag      180
ttaataatag gttttgcaat tctatgagga tctaagtcgg cctctgatct gacaaggggc      240
ggastcaggc agtaatggga gcaatgggga gcggttttca atacag atg agg ctt      295
                                Met Arg Leu
                                -15
tgg tca ctt gcc tgc ctt tca cct cct gct gtg cag ctt ggt tcc caa      343
Trp Ser Leu Ala Cys Leu Ser Pro Pro Ala Val Gln Leu Gly Ser Gln
    -10                -5                1
cag gcc acg gac tgg tgg tc
Gln Ala Thr Asp Trp Trp
5                10
    363

```

```

<210> 197
<211> 155
<212> DNA
<213> Homo sapiens

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```

<220>
<221> CDS
<222> 58..153

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<221> sig_peptide
 <222> 58..132
 <223> Von Heijne matrix
 score 7
 seq IFSFFFFITLVRG/SI

<400> 197
 tagtggtatt catagtagta tctgaagacc ttttgtattc ttgtgggatc agttgta 57
 atg tca cct ttg ttt att ctg att gtg ctt att tgg atc ttc tct ttc 105
 Met Ser Pro Leu Phe Ile Leu Ile Val Leu Ile Trp Ile Phe Ser Phe
 -25 -20 -15 -10
 ttt ttc ttt att act cta gtt agg ggg tct atc aat ctt ttt ttt ttt 153
 Phe Phe Phe Ile Thr Leu Val Arg Gly Ser Ile Asn Leu Phe Phe Phe
 -5 1 5
 tt 155

<210> 198
 <211> 135
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 60..134

<221> sig_peptide
 <222> 60..125
 <223> Von Heijne matrix
 score 7
 seq STFLFFLFFSVFC/FF

<400> 198
 ttgcctctta aaaggccaca cttcttaata ctatcaaatt ggctattaag tttcaacaa 59
 atg aat ttg ggg gga cat tca gat cat agc act ttt ctt ttc ttt ctt 107
 Met Asn Leu Gly Gly His Ser Asp His Ser Thr Phe Leu Phe Phe Leu
 -20 -15 -10
 ttt ttt tct gtt ttt tgt ttt ttt ttt t 135
 Phe Phe Ser Val Phe Cys Phe Phe Phe
 -5 1

<210> 199
 <211> 320
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 46..318

<221> sig_peptide
 <222> 46..108
 <223> Von Heijne matrix
 score 6.90000009536743

seq VTFLALVGAVLY/LY

<221> misc_feature

<222> 9

<223> n=a, g, c or t
Oligonucleotide

<400> 199

```

gctggagcng ccgatccgag acgtggcthc ctgggcggca gaacc atg ttg gac ttc      57
                               Met Leu Asp Phe
                               -20
gcg atc ttc gcc gtt acc ttc ttg ctg gcg ttg gtg gga gcc gtg ctc      105
Ala Ile Phe Ala Val Thr Phe Leu Leu Ala Leu Val Gly Ala Val Leu
      -15                               -10                               -5
tac ctc tat ccg gct tcc aga caa gct gca gga att cca ggg att act      153
Tyr Leu Tyr Pro Ala Ser Arg Gln Ala Ala Gly Ile Pro Gly Ile Thr
      1                               5                               10                               15
cca act gaa gaa aaa gat ggt aat ctt cca gat att gtg aat agt gga      201
Pro Thr Glu Glu Lys Asp Gly Asn Leu Pro Asp Ile Val Asn Ser Gly
      20                               25                               30
agt ttg cat gag tbc ctg gtt aat ttg cat gag aga tat ggg cct gtg      249
Ser Leu His Glu Xaa Leu Val Asn Leu His Glu Arg Tyr Gly Pro Val
      35                               40                               45
gtc tcc ttc tgg ttt ggc agg cgc ctc gtg gtt agt ttg ggc act gtt      297
Val Ser Phe Trp Phe Gly Arg Arg Leu Val Val Ser Leu Gly Thr Val
      50                               55                               60
gat gta ctg aag cag cat cgg gg      320
Asp Val Leu Lys Gln His Arg
      65                               70

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<210> 200

<211> 125

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 40..123

<221> sig_peptide

<222> 40..93

<223> Von Heijne matrix
score 6.90000009536743
seq LELLGSSSPPIISA/SQ

<400> 200

```

cttcctcagt caccagcgt ggagtacagt ggcataatc atg gct cac tgc agc      54
                               Met Ala His Cys Ser
                               -15
tta gaa ctc ttg ggc tca agc agt cct ccc atc tca gcc tcc caa agc      102
Leu Glu Leu Leu Gly Ser Ser Ser Pro Pro Ile Ser Ala Ser Gln Ser
      -10                               -5                               1
act gga att aca agc gtg agc ca      125
Thr Gly Ile Thr Ser Val Ser

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5 10

<210> 201
 <211> 210
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 78..209

<221> sig_peptide
 <222> 78..128
 <223> Von Heijne matrix
 score 6.90000009536743
 seq LLLLSLSLFLFFW/RQ

<400> 201
 tcaggttttc ctccttcccg ggtgctctga agtttcacca tgaatcacct tgcaggggct 60
 ctttttattt tttatttg atg ccc agc cag ttg ttg ttg ttg tct ctt tct 110
 Met Pro Ser Gln Leu Leu Leu Leu Ser Leu Ser
 -15 -10
 ctc ttt ttg ttt ttt tgg aga cag agt ctc gtt ttg tgg ccc agg ctg 158
 Leu Phe Leu Phe Phe Trp Arg Gln Ser Leu Val Leu Trp Pro Arg Leu
 -5 1 5 10
 gag tgc agt tgt gtc att gcg gct cac tgc agc ctg acc tcc cag gct 206
 Glu Cys Ser Cys Val Ile Ala Ala His Cys Ser Leu Thr Ser Gln Ala
 15 20 25
 cgg g 210
 Arg

<210> 202
 <211> 338
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 89..337

<221> sig_peptide
 <222> 89..226
 <223> Von Heijne matrix
 score 6.90000009536743
 seq CLFCCXFISSCNS/VF

<221> misc_feature
 <222> 291
 <223> n=a, g, c or t
 Oligonucleotide

<400> 202
 aattataata atatactaaa atatgtacga atatatacta ataattagta tataatgaat 60
 cagtataaaa tatataatat acactaat atg tat act aat aaa tat aca cta 112

	Met	Tyr	Thr	Asn	Lys	Tyr	Thr	Leu	
	-45							-40	
ata tat aac ata cta ata tat aat ata tgt btk drg tat atg tgg ttg									160
Ile Tyr Asn Ile Leu Ile Tyr Asn Ile Cys Xaa Xaa Tyr Met Trp Leu									
	-35							-25	
ata ctc att tat atg tac cta cat att tgc ctc ttt tgt tgc wct ttt									208
Ile Leu Ile Tyr Met Tyr Leu His Ile Cys Leu Phe Cys Cys Xaa Phe									
	-20							-10	
att tct tcc tgc aat tct gtg ttt ccc tgt gtg att atb ttt ctt ctg									256
Ile Ser Ser Cys Asn Ser Val Phe Pro Cys Val Ile Xaa Phe Leu Leu									
	-5				1		5		10
cct gaa gaa ctt ctt twt gtd twt ctd wdw dtg tnt tty wtt gtg aga									304
Pro Glu Glu Leu Leu Xaa Val Xaa Leu Xaa Xaa Xaa Phe Xaa Val Arg									
				15			20		25
tgg agt ctc amt cwg tcg tcc agg ctg gag tgc a									338
Trp Ser Leu Xaa Xaa Ser Ser Arg Leu Glu Cys									
	30						35		

<210> 203

<211> 188

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 84..188

<221> sig_peptide

<222> 84..176

<223> Von Heijne matrix

score 6.90000009536743

seq LWSLIQAVHICLG/RK

<400> 203

tattctctga ttckctgtct tggaatgcat ttaaaatctc tgcctcgatt ctgacctacc 60

tggcatggga acaagaattt aca atg tta ctc acc cac aat gaa gat tac atg 113

Met Leu Leu Thr His Asn Glu Asp Tyr Met

-30

-25

cct ggc aat ttd grc ttw ard daw ttg tgg agc tta att cag gct gtt 161

Pro Gly Asn Xaa Xaa Xaa Xaa Xaa Leu Trp Ser Leu Ile Gln Ala Val

-20

-15

-10

cat atc tgc cta ggc agg aaa aaa aaa 188

His Ile Cys Leu Gly Arg Lys Lys Lys

-5

1

<210> 204

<211> 347

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 81..347

<221> sig_peptide

<222> 81..137

<223> Von Heijne matrix

score 6.90000009536743

seq WVFLVAIIKGVQC/QV

<400> 204

agctctggga gaagagcccc agccccagaa ttcccaggag tttccattcg gtgatcagca 60

ctgaacacag aggactcacc atg gag ttt ggg ctg agc tgg gtt ttc ctt gtt 113

Met Glu Phe Gly Leu Ser Trp Val Phe Leu Val

-15

-10

gct att ata aaa ggt gtc cag tgt cag gtg caa ctg gtg gag tct ggg 161

Ala Ile Ile Lys Gly Val Gln Cys Gln Val Gln Leu Val Glu Ser Gly

-5

1

5

ggg ggc ttg gtc aag cct gga ggg tcc cta aga ctc tcc tgt gca gcc 209

Gly Gly Leu Val Lys Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala

10

15

20

tct gga ttc acc ttc agt gay tac waw atr act kgg att cgc mag gcc 257

Ser Gly Phe Thr Phe Ser Asp Tyr Xaa Xaa Thr Xaa Ile Arg Xaa Ala

25

30

35

40

cma ggg aag ggs ytg rak tgg att yca tam atw acg act agt ggg aat 305

Xaa Gly Lys Gly Leu Xaa Trp Ile Xaa Xaa Ile Thr Thr Ser Gly Asn

45

50

55

acc gca awy tac gca gwc tct gta aag gsc cga ttc acc atc 347

Thr Ala Xaa Tyr Ala Xaa Ser Val Lys Xaa Arg Phe Thr Ile

60

65

70

<210> 205

<211> 440

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 276..440

<221> sig_peptide

<222> 276..326

<223> Von Heijne matrix

score 6.90000009536743

seq FLFVCLXFDESCS/VT

<400> 205

cagtaaattt ttttgwwcat tggttccttc dkcttggact ctctgttagc acacctgac 60

agagttggcc gtgttgtaat tctttccctc tctgctgcaa tgttgtttac ttctacctgs 120

caactawkct ttatacttct cttttttgcc atgaagggaa tacatttttt ctttctgtt 180

gggctataca gtgatcctca tcaacaaatt atcaagaac tgtatgagga aaaggtctct 240

ttttttaaaa gtgaatcagg gctggggagt tagga atg aag agg ttt ttt ttg 293

Met Lys Arg Phe Phe Leu

-15

ttt gtt tgt ttg tww ttt gac gag tct tgc tct gtc acc agg ctg ggg 341

Phe Val Cys Leu Xaa Phe Asp Glu Ser Cys Ser Val Thr Arg Leu Gly

-10

-5

1

5

tgc tgt ggc gcg atc tca gcc cac tgc aam ctc cga ctc cct ggt tca 389

Cys	Cys	Gly	Ala	Ile	Ser	Ala	His	Cys	Xaa	Leu	Arg	Leu	Pro	Gly	Ser	
				10					15					20		
agc	rat	dyt	cct	gcc	tca	acc	tcc	cga	gta	gvy	ggg	att	aca	ggc	atg	437
Ser	Xaa	Xaa	Pro	Ala	Ser	Thr	Ser	Arg	Val	Xaa	Gly	Ile	Thr	Gly	Met	
			25					30					35			
cgc																440
Arg																

<210> 206
 <211> 283
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 162..281

<221> sig_peptide
 <222> 162..275
 <223> Von Heijne matrix
 score 6.90000009536743
 seq CMLFVSFLLLLLG/SR

<400> 206																
aataactccc	tttagcattt	cttgtaggac	aggtctgatg	ttgatgaaat	ctctcatctt											60
gtttgtcaga	gaaagtcttt	atttctcctt	catgcttgaa	ggatgtttcc	accggatata											120
ctatcctagg	gtaaaagttt	ttttccttca	gcactttaaa	t atg tca tgc cac tct												176
				Met Ser Cys His Ser												
				-35												
ctt ctg gcc tgt aag gtt ttc act gaa aag tct cct acc aaa cat att																224
Leu Leu Ala Cys Lys Val Phe Thr Glu Lys Ser Pro Thr Lys His Ile																
	-30					-25				-20						
aga gag cac cat tgt atg tta ttt gtt tct ttt ctc ttg ctg ctt tta																272
Arg Glu His His Cys Met Leu Phe Val Ser Phe Leu Leu Leu Leu																
	-15					-10				-5						
gga tcc cgg gg																283
Gly Ser Arg																
1																

<210> 207
 <211> 264
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 113..262

<221> sig_peptide
 <222> 113..190
 <223> Von Heijne matrix
 score 6.90000009536743
 seq LLSMLSCCQGACC/PS


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<400> 207
gacggcggag agcagagagg gagcgcgcct tggctcgctg gccttggcgg cggctcctca      60
ggagagctgg ggcgccacg agaggatccc tcacccgggt ctctcctcag gg atg aca      118
                                   Met Thr
                                   -25
tca tcc gtc cac ctc ctt gtc ttc aag gac cac ctc ctc tcc atg ctg      166
Ser Ser Val His Leu Leu Val Phe Lys Asp His Leu Leu Ser Met Leu
               -20               -15               -10
agc tgc tgc caa ggg gcc tgc tgc cca tct aca cct cac gag ggc act      214
Ser Cys Cys Gln Gly Ala Cys Cys Pro Ser Thr Pro His Glu Gly Thr
               -5               1               5
agg agc acg gtt tcc tgg atc cca cca aca tac aaa gca gcc aca cag      262
Arg Ser Thr Val Ser Trp Ile Pro Pro Thr Tyr Lys Ala Ala Thr Gln
      10               15               20
gg
264

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<210> 208
<211> 422
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> 352..420

<221> sig_peptide
<222> 352..408
<223> Von Heijne matrix
      score 6.80000019073486
      seq LLSMFVSVHTVQT/AT

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<221> misc_feature
<222> 289..290
<223> n=a, g, c or t
      Oligonucleotide

```

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<400> 208
aaaataaaaag tcttcttgat ttccagtgtg ttccctcctgc acwttttggc ctgtttggac      60
cacagatttg tggcttttta tgaaatacac ctgtagatta atttwcagtt thtwhayggw      120
agtagacagt caaaggctag atcactgtra tgagtagggc ttccacattt aagaaaaagc      180
tgtaatgaag tgaattgaat cttgcttctt ttgggtcacc caaaagcagt gataagtgtc      240
gagtgtgtta ggcacttatt aacaaaagta actcagaatt gctgtctann cctccatc      300
tttttcttc tctccgtgta gttctaaaaa tgaccatcgt atattccttg a atg gta      357
                                   Met Val
aga gcg tct att ctt ctt agc atg ttc tgt gtg tca cac act gtg cag      405
Arg Ala Ser Ile Leu Leu Ser Met Phe Cys Val Ser His Thr Val Gln
      -15               -10               -5
aca gca aca tac aca ca
Thr Ala Thr Tyr Thr
      1
422

```

```

<210> 209
<211> 195
<212> DNA

```

<213> Homo sapiens

<220>

<221> CDS

<222> 39..194

<221> sig_peptide

<222> 39..89

<223> Von Heijne matrix

score 6.80000019073486

seq ALSSFTWWAPACC/AP

<400> 209

agccactgca cctgggctca cagtttaa at cttgagta atg gag aaa aca gcc ttg 56
Met Glu Lys Thr Ala Leu

-15

tca tcc ttt acg tgg tgg gca cct gcc tgc tgt gct cca cgt aca tac 104

Ser Ser Phe Thr Trp Trp Ala Pro Ala Cys Cys Ala Pro Arg Thr Tyr

-10

-5

1

5

gtg gtg tct gca aca act ctg tca gct gtg caa ggt cac tgt cct cta 152

Val Val Ser Ala Thr Thr Leu Ser Ala Val Gln Gly His Cys Pro Leu

10

15

20

cag agt aga aca tcg acc aaa gga aag tta tgg ccg ttt ggg g 195

Gln Ser Arg Thr Ser Thr Lys Gly Lys Leu Trp Pro Phe Gly

25

30

35

<210> 210

<211> 363

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 212..361

<221> sig_peptide

<222> 212..280

<223> Von Heijne matrix

score 6.80000019073486

seq KLLLSGLTQECLG/AL

<400> 210

taattttcat catctaaact gaatgcaa ac agcgcttggc aattaaaatg aagctctcca 60

atgaagtata cttcatcagc tgctgtca ag tcatccattg atactgtttt gcggttttta 120

aattcctttt gtcactgtga ctgctcatca gcaggcaagg aagagcaggc aacaaaagtt 180

gaaaagtgca tgaaggaaaa ctttgaggaa t atg ata ttc aca ttc cag caa 232

Met Ile Phe Thr Phe Gln Gln

-20

att ggg gga aaa ctg cta tta tct ggt tta aca cag gag tgc ctt ggt 280

Ile Gly Gly Lys Leu Leu Ser Gly Leu Thr Gln Glu Cys Leu Gly

-15

-10

-5

gcc ctg cct gag gct aat gtg ttc tgt agg ggt ggc tgc aca gcc aca 328

Ala Leu Pro Glu Ala Asn Val Phe Cys Arg Gly Gly Cys Thr Ala Thr

1

5

10

15

gtc ctg aaa cat ggg aaa gca tct cct gag tcc ag 363
 Val Leu Lys His Gly Lys Ala Ser Pro Glu Ser
 20 25

<210> 211
 <211> 368
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 230..367

<221> sig_peptide
 <222> 230..322
 <223> Von Heijne matrix
 score 6.80000019073486
 seq LLALSPDLQAARG/LM

<400> 211
 acagagaacc ctgcttcaaa gcagaagtag cagttccgga gtccagctgg ctaaaactca 60
 tccchygat aatggcaacc catgccttag aaatcgctgg gctgtttctt ggtggtgttg 120
 gmatgggtgg gsacmrkgwg ggbkgyvack gtcatgcctc agtggdrrag tgctggcctt 180
 cattgaaaac aacatcgtag tttttgaaaa cttctgggaa ggactgttg atg aat tgc 238
 Met Asn Cys
 -30
 gtg agg cag gct aac atc agg atg cag tgc aaa atc tat gat tcc ctg 286
 Val Arg Gln Ala Asn Ile Arg Met Gln Cys Lys Ile Tyr Asp Ser Leu
 -25 -20 -15
 ctg gct ctt tct ccg gac cta cag gca gcc aga ggr ctg atg tgt gct 334
 Leu Ala Leu Ser Pro Asp Leu Gln Ala Ala Arg Gly Leu Met Cys Ala
 -10 -5 1
 gct tcc gtg atg tcc ttc ttg gct ttc atg atg g 368
 Ala Ser Val Met Ser Phe Leu Ala Phe Met Met
 5 10 15

<210> 212
 <211> 448
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 316..447

<221> sig_peptide
 <222> 316..435
 <223> Von Heijne matrix
 score 6.80000019073486
 seq LLKLLISLRSFWA/ET

<400> 212
 ttgtcttggc tatacgggat ctttttttgt cccatatgaa atttaagtag cttttcctaa 60
 ttctgtgaag gaagtcaatg gtagcttgat gggaatagca ttgaatctat aaattacttt 120

```

gggccgatatg gcatttgggc aatattgatt ctctctattc atgagcatgg aatgtttttc 180
catttgttca tgtcctctct tattttgttg agcagtgggt tgtagtcttc cttgaagggg 240
ttcttcacat cccttgtaag ttgtattccc aggtatttta ttctctttgt agcaattttg 300
aatgggagtt cactc atg att tgg ctc tct ttt tgt cta tta ttg gtg tat 351
          Met Ile Trp Leu Ser Phe Cys Leu Leu Leu Val Tyr
          -40          -35          -30
agg aat gct tgt gat ttt tgc aca ttg act tta tat cct ggg act ttg 399
Arg Asn Ala Cys Asp Phe Cys Thr Leu Thr Leu Tyr Pro Gly Thr Leu
          -25          -20          -15
ctg aag ttg ctt atc agc tta agg agt ttt tgg gct gag acg acg ggg g 448
Leu Lys Leu Leu Ile Ser Leu Arg Ser Phe Trp Ala Glu Thr Thr Gly
          -10          -5          1

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<210> 213
<211> 158
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 28..156

<221> sig_peptide
<222> 28..102
<223> Von Heijne matrix
score 6.69999980926514
seq LVGSLHLFLSVLA/SK

```

<400> 213
gcgctgggag ttctcttttt cacttga atg ttt tct tct cca ggg ctg agg acg 54
          Met Phe Ser Ser Pro Gly Leu Arg Thr
          -25          -20
ctc ttt gta ttg gta ggc agc ctg cac ttg ttc ctt tca gtc ctg gca 102
Leu Phe Val Leu Val Gly Ser Leu His Leu Phe Leu Ser Val Leu Ala
          -15          -10          -5
agt aaa agc agg aat tct aaa aag caa cga tta ttc ctc cta gtt cct 150
Ser Lys Ser Arg Asn Ser Lys Lys Gln Arg Leu Phe Leu Leu Val Pro
1          5          10          15
ttg tac ag 158
Leu Tyr

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<210> 214
<211> 193
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 39..191

<221> sig_peptide
<222> 39..107
<223> Von Heijne matrix
score 6.69999980926514

seq NVCSLPAPGLCSG/QP

<400> 214

```

aagaaaagct ttgggtcaac tcagcatcat gtttcgag atg ctg aca gac ggg atc      56
                               Met Leu Thr Asp Gly Ile
                               -20
cta atg aga gtc aat gtg tgc tca ctg cca gct cct ggg ctg tgc tct      104
Leu Met Arg Val Asn Val Cys Ser Leu Pro Ala Pro Gly Leu Cys Ser
      -15                               -10                               -5
ggg cag cca ggt gtg agg gcc tgg cct ggg gtc aca cag ctg act car      152
Gly Gln Pro Gly Val Arg Ala Trp Pro Gly Val Thr Gln Leu Thr Gln
      1                               5                               10                               15
bta gag gaa tgc cca tgg ttc tca gca ttg gaa gga ctg gg      193
Xaa Glu Glu Cys Pro Trp Phe Ser Ala Leu Glu Gly Leu
                               20                               25

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<210> 215

<211> 214

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 67..213

<221> sig_peptide

<222> 67..165

<223> Von Heijne matrix
score 6.69999980926514
seq ILLLSLIFGPCIL/NS

<400> 215

```

aaagttcgag aaaatchaga taggcaccaa caagaacgag aaaataacat cccctggtat      60
caaagc atg ttt aac tgg aac cca tgg cta act act tta atc act ggg      108
      Met Phe Asn Trp Asn Pro Trp Leu Thr Thr Leu Ile Thr Gly
      -30                               -25                               -20
wta gch gga cct ctc ctc atc cta cta tta agt tta att ttt ggg cct      156
Xaa Ala Gly Pro Leu Leu Ile Leu Leu Leu Ser Leu Ile Phe Gly Pro
      -15                               -10                               -5
tgt ata tta aat tcg ttt ctk aat tkt ata aaa caa cgc ata gct tct      204
Cys Ile Leu Asn Ser Phe Leu Asn Xaa Ile Lys Gln Arg Ile Ala Ser
      1                               5                               10
ggc aaa cgg g      214
Gly Lys Arg
      15

```

<210> 216

<211> 327

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 22..327

<221> sig_peptide
 <222> 22..108
 <223> Von Heijne matrix
 score 6.69999980926514
 seq FCALLLSLXXXXP/XX

<400> 216
 ctccgcgttc cagaatccaa g atg gcg gga tcc agg caa agg ggt ctc cgg 51
 Met Ala Gly Ser Arg Gln Arg Gly Leu Arg
 -25 -20
 gcc aga gtt cgg ccg ctg ttc tgc gcc ttg ctg ctg tca ctm sgw hsv 99
 Ala Arg Val Arg Pro Leu Phe Cys Ala Leu Leu Leu Ser Leu Xaa Xaa
 -15 -10 -5
 mty ckt ccg rkg cka cgs cgt gkg agg aga ccc cgc ggt cgc gtt gcc 147
 Xaa Xaa Pro Xaa Xaa Arg Arg Xaa Arg Arg Pro Arg Gly Arg Val Ala
 1 5 10
 aca tcg ccg ttt cga gta saa ata cag ctt caa ggg gcc gca cct ggt 195
 Thr Ser Pro Phe Arg Val Xaa Ile Gln Leu Gln Gly Ala Ala Pro Gly
 15 20 25
 gca gag cga cgg gac cgt gcc ctt ctg ggm cca cgc ggg gaa tgc tat 243
 Ala Glu Arg Arg Asp Arg Ala Leu Leu Gly Pro Arg Gly Glu Cys Tyr
 30 35 40 45
 tcc aag ttc aga tca aat tcg agt agc acc atc ttt aaa aag cya aag 291
 Ser Lys Phe Arg Ser Asn Ser Ser Ser Thr Ile Phe Lys Lys Xaa Lys
 50 55 60
 agg ctc agt gtg gvm aam gac aav agc gga cct ggg 327
 Arg Leu Ser Val Xaa Xaa Asp Xaa Ser Gly Pro Gly
 65 70

<210> 217
 <211> 357
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 70..357

<221> sig_peptide
 <222> 70..126
 <223> Von Heijne matrix
 score 6.69999980926514
 seq WVFLVAILKGVHC/DV

<400> 217
 aggagcccca gccctgggat tcccagctgt ttctgcttgc tgatcaggac tgcacacaga 60
 gaactcacc atg gag ttt ggg ctg agc tgg gtt ttc ctt gtt gct att tta 111
 Met Glu Phe Gly Leu Ser Trp Val Phe Leu Val Ala Ile Leu
 -15 -10
 aaa ggt gtc cac tgt gac gtg cag ctg gtg gag tcc ggg gga ggt tta 159
 Lys Gly Val His Cys Asp Val Gln Leu Val Glu Ser Gly Gly Gly Leu
 -5 1 5 10
 gtt cag cct ggg ggg tcc ctg aga ctc tcc tgt gca gcc tct gga ctc 207

Val	Gln	Pro	Gly	Gly	Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Leu		
			15					20					25				
acc	ctc	agt	aac	gac	tgg	atg	cac	tgg	gtc	cgc	caa	gcc	cca	ggg	aag		255
Thr	Leu	Ser	Asn	Asp	Trp	Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys		
		30					35				40						
ggg	ctg	gtg	tgg	gtc	tca	cac	att	gat	agt	tct	rgg	act	atc	aca	aat		303
Gly	Leu	Val	Trp	Val	Ser	His	Ile	Asp	Ser	Ser	Xaa	Thr	Ile	Thr	Asn		
	45					50					55						
tac	gcg	gac	tcc	gtg	aag	ggc	cga	ttc	acc	atc	tcc	aga	gac	aac	gcc		351
Tyr	Ala	Asp	Ser	Val	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ala		
60					65					70				75			357
aag	tgg																
Lys	Trp																

<210> 218

<211> 189

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 74..187

<221> sig_peptide

<222> 74..118

<223> Von Heijne matrix

score 6.69999980926514

seq LFLGFLACSVAYQ/CH

<400> 218

ttatcaagga	cactgtcttt	tcgccatcat	gtgttcttgg	cccctctgtt	gaaattcaat		60
ctatcataga	caa atg ggt tta ttt ctg ggc ttt cta gcc tgt tct gtt		109				
	Met Gly Leu Phe Leu Gly Phe Leu Ala Cys Ser Val						
	-15	-10	-5				

gca'tac	cag tgc cat tct gct ttt gtt act gta gct tca cag tac act		157
Ala Tyr Gln Cys His Ser Ala Phe Val Thr Val Ala Ser Gln Tyr Thr			
	1	5	10

ttg aaa tca gag act ttg atg ccc gca gcg gg			189
Leu Lys Ser Glu Thr Leu Met Pro Ala Ala			
	15	20	

<210> 219

<211> 353

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 41..352

<221> sig_peptide

<222> 41..187

<223> Von Heijne matrix

score 6.69999980926514

seq FLGLIFFLELATG/IL

<400> 219

```

agttgacttg ccattctgcct tgcaggatgg catccagccc atg tgg gag gac agc      55
                               Met Trp Glu Asp Ser
                               -45
agg aat aaa cgg ggt ggc cgc tgg ctg gtc agc ctg gcc aag cag cag      103
Arg Asn Lys Arg Gly Gly Arg Trp Leu Val Ser Leu Ala Lys Gln Gln
                               -40                               -35                               -30
cgc cac att gag ctg gac cgg ctg tgg ctg gag acg ttc tcc gtg ttc      151
Arg His Ile Glu Leu Asp Arg Leu Trp Leu Glu Thr Phe Ser Val Phe
                               -25                               -20                               -15
ctc ggt ctc atc ttc ttc ctg gag ctg gca aca ggg atc ctg gcc ttt      199
Leu Gly Leu Ile Phe Phe Leu Glu Leu Ala Thr Gly Ile Leu Ala Phe
                               -10                               -5                               1
gtc ttc aag gac tgg att cga gac cag ctc aac ctc ttc atc aac aac      247
Val Phe Lys Asp Trp Ile Arg Asp Gln Leu Asn Leu Phe Ile Asn Asn
5                               10                               15                               20
aac gtc aag gcc tac cgg gac gac att gac ctc cag arc ctc att gac      295
Asn Val Lys Ala Tyr Arg Asp Asp Ile Asp Leu Gln Xaa Leu Ile Asp
                               25                               30                               35
ttt gct cag gaa tac tgg tct tgc tgc gga scc gag gcc cca ata rdt      343
Phe Ala Gln Glu Tyr Trp Ser Cys Cys Gly Xaa Glu Ala Pro Ile Xaa
                               40                               45                               50
gga acc ggg g
Gly Thr Gly
                               55

```

<210> 220

<211> 115

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 12..113

<221> sig_peptide

<222> 12..53

<223> Von Heijne matrix
score 6.59999990463257
seq FLSLSTAFWVYA/MI

<400> 220

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actagcatitt c atg ttt tta tct ctc tct act gca ttc tgg gta gtt tat      50
                               Met Phe Leu Ser Leu Ser Thr Ala Phe Trp Val Val Tyr
                               -10                               -5
gcc atg ata att tat tca gct ctc tct gct gga ttt att att ttc ttt      98
Ala Met Ile Ile Tyr Ser Ala Leu Ser Ala Gly Phe Ile Ile Phe Phe
1                               5                               10                               15
tta gtt gtg ttt aat ct
Leu Val Val Phe Asn
                               20

```


<210> 221
 <211> 142
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 29..142

<221> sig_peptide
 <222> 29..130
 <223> Von Heijne matrix
 score 6.59999990463257
 seq FFLFFCFETGSHS/VT

<400> 221
 cctgccatt gcttcaacct gcacctct atg tac att gtg atg gat cta cct 52
 Met Tyr Ile Val Met Asp Leu Pro
 -30
 cta tgg ctc tcc cat gag gtc caa tct tat att cct tct ttc ttc ctt 100
 Leu Trp Leu Ser His Glu Val Gln Ser Tyr Ile Pro Ser Phe Phe Leu
 -25 -20 -15
 ttt ttt tgc ttt gag act ggg tct cac tct gtc acc cac ggg 142
 Phe Phe Cys Phe Glu Thr Gly Ser His Ser Val Thr His Gly
 -10 -5 1

<210> 222
 <211> 370
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 209..370

<221> sig_peptide
 <222> 209..289
 <223> Von Heijne matrix
 score 6.59999990463257
 seq LAFSFSFFPSSFS/SF

<400> 222
 ttttgatcac atatgactca tgtgacatta gatcacagca tttttgtttt tattattaat 60
 atattgcctt agaactacat tgctaaacct ggtctttgta tctgcgaagt tctaaccatct 120
 tgccacagct tagttagctt tgagagggaa agggtagaat ccatttaagg agacagggtta 180
 aaaaatgata tattttaagca tataggca atg gta gca cat gat tac caa aac 232
 Met Val Ala His Asp Tyr Gln Asn
 -25 -20
 ata att agc ctt ttc ttt ctt gct ttt tca ttt tct ttc ttt cct tct 280
 Ile Ile Ser Leu Phe Phe Leu Ala Phe Ser Phe Ser Phe Phe Pro Ser
 -15 -10 -5
 tca ttt tct tct ttc ttt ctt ktc ttt tct tct ttt ttc tct tct ttc 328
 Ser Phe Ser Ser Phe Phe Leu Xaa Phe Leu Ser Phe Phe Ser Ser Phe
 1 5 10

370

```
<220>  
<221> CDS  
<222> 22..429
```

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<221> sig_peptide
<222> 22..66
<223> Von Heijne matrix
      score 6.59999990463257
      seq ALRALCGFRGVAA/OV
```

<400> 223																	
gcagtc	ctgca	gccggag	taag	g	atg	gcg	gcg	ctg	agg	gct	ttg	tgc	ggc	ttc		51	
					Met	Ala	Ala	Leu	Arg	Ala	Leu	Cys	Gly	Phe			
					-15					-10							
cgg	ggc	gtc	gcg	gcc	cag	gtg	ctg	cgg	mct	ggg	gct	gga	gtc	cga	ttg	99	
Arg	Gly	Val	Ala	Ala	Gln	Val	Leu	Arg	Xaa	Gly	Ala	Gly	Val	Arg	Leu		
-5					1				5					10			
ccg	att	cag	ccc	agc	aga	ggt	gtt	cgg	cag	tgg	cag	cca	gat	gtg	gaa	147	
Pro	Ile	Gln	Pro	Ser	Arg	Gly	Val	Arg	Gln	Trp	Gln	Pro	Asp	Val	Glu		
			15					20					25				
tgg	gca	cag	cag	ttt	ggg	gga	gct	gtt	atg	tac	cca	agc	aaa	gaa	aca	195	
Trp	Ala	Gln	Gln	Phe	Gly	Gly	Ala	Val	Met	Tyr	Pro	Ser	Lys	Glu	Thr		
		30					35					40					
gcc	cac	tgg	aag	cct	cca	cct	tgg	aat	gat	gtg	gac	cct	cca	aag	gac	243	
Ala	His	Trp	Lys	Pro	Pro	Pro	Trp	Asn	Asp	Val	Asp	Pro	Pro	Lys	Asp		
	45					50					55						
aca	att	gtg	aag	aac	att	acc	ctg	aac	ttt	ggg	ccc	caa	cac	cca	gca	291	
Thr	Ile	Val	Lys	Asn	Ile	Thr	Leu	Asn	Phe	Gly	Pro	Gln	His	Pro	Ala		
60				65					70					75			
gcg	cat	ggt	gtc	ctg	cga	cta	gtg	atg	gaa	ttg	agt	ggg	gag	atg	gtg	339	
Ala	His	Gly	Val	Leu	Arg	Leu	Val	Met	Glu	Leu	Ser	Gly	Glu	Met	Val		
			80					85						90			
cgg	aag	tgt	gat	cct	cac	atc	ggg	ctc	ctg	cac	cga	ggc	act	gag	aag	387	
Arg	Lys	Cys	Asp	Pro	His	Ile	Gly	Leu	Leu	His	Arg	Gly	Thr	Glu	Lys		
			95				100						105				
ctc	att	gaa	tac	aag	rcc	tat	ctt	cag	gcc	ctt	cca	tac	ttt	ga		431	
Leu	Ile	Glu	Tyr	Lys	Xaa	Tyr	Leu	Gln	Ala	Leu	Pro	Tyr	Phe				
		110					115					120					

<220>

<221> CDS
 <222> 132..281

<221> sig_peptide
 <222> 132..215
 <223> Von Heijne matrix
 score 6.5
 seq LVFLHLFLXVYL/LV

<400> 224
 atttttaaagt gtttctgtta atgtattcta cttcagttccc ccaaaattcc aactaacgac 60
 atacatgaat aacagatcat gactgctgtt tctacaagcc tttctgctca ctgtgcttcc 120
 acttacaact c atg tta ata tgg tct tcc tct tct ttt cct gca ccc cct 170
 Met Leu Ile Trp Ser Ser Ser Ser Phe Pro Ala Pro Pro
 -25 -20
 ctc ttt ctt gtc ttt ctt cat ctt ttc ctt mwt gtc tat ttg ggt ctt 218
 Leu Phe Leu Val Phe Leu His Leu Phe Leu Xaa Val Tyr Leu Gly Leu
 -15 -10 -5 1
 gtc atg ccc act caa cag tat ctc ctc ctg cag agt cca ttg atg ttc 266
 Val Met Pro Thr Gln Gln Tyr Leu Leu Leu Gln Ser Pro Leu Met Phe
 5 10 15
 aca gac aaa gcc cag c 282
 Thr Asp Lys Ala Gln
 20

<210> 225
 <211> 198
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 26..196
 <221> sig_peptide
 <222> 26..163
 <223> Von Heijne matrix
 score 6.5
 seq WLFFLMLSCTPP/DR

<400> 225
 actttttgctt tatgttcagg ggtcc atg tgt agg atg tgc agg ttt gtt aca 52
 Met Cys Arg Met Cys Arg Phe Val Thr
 -45 -40
 tgg ata aac gtg tgc cat ggt gat ttg ctg cac aga tca tcc cgt cgc 100
 Trp Ile Asn Val Cys His Gly Asp Leu Leu His Arg Ser Ser Arg Arg
 -35 -30 -25
 ctg ggt gtg aag ccg agc acg cat tgg cta ttc ttc ctg atg ctc tcc 148
 Leu Gly Val Lys Pro Ser Thr His Trp Leu Phe Phe Leu Met Leu Ser
 -20 -15 -10
 ctt tgc acc cct cct gac aga ccc tgg tgt gtg ttg ttc ccc ccg ctg 196
 Leu Cys Thr Pro Pro Asp Arg Pro Trp Cys Val Leu Phe Pro Pro Leu
 -5 1 5 10
 gg 198

<210> 226
 <211> 141
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 21..140

<221> sig_peptide
 <222> 21..113
 <223> Von Heijne matrix
 score 6.5
 seq LSLSLPLSLXLLX/XP

<400> 226
 gcagttgagr dsacttggtatg tsa acg caa gaa gca ggc ttg aty ttt ttt 53
 Met Xaa Thr Gln Glu Ala Gly Leu Ile Phe Phe
 -30 -25
 tct ccc ccc ttc tct ctc tct ctc tct ctc tct cty cct ctc tcc ctc 101
 Ser Pro Pro Phe Ser Leu Ser Leu Ser Leu Ser Leu Pro Leu Ser Leu
 -20 -15 -10 -5
 tyt ctc ctc tst sac cca cac tca cgc aca cct caa agg g 141
 Xaa Leu Leu Xaa Xaa Pro His Ser Arg Thr Pro Gln Arg
 1 5

<210> 227
 <211> 206
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 77..205

<221> sig_peptide
 <222> 77..115
 <223> Von Heijne matrix
 score 6.5
 seq MEFLLLWSLXSNG/KR

<400> 227
 awcaartact tggttaagcrt ttacgatgtg ccaggttctg tgctaggtgc tgagtgtaca 60
 ttgttggarcc aaacag atg gag ttc ctg cta ttg tgg agt ttg cmg tct aat 112
 Met Glu Phe Leu Leu Leu Trp Ser Leu Xaa Ser Asn
 -10 -5
 ggg aag aga ggc cag gca tgg cgg ctc atg cct gtw gtc cca gca gtt 160
 Gly Lys Arg Gly Gln Ala Trp Arg Leu Met Pro Val Val Pro Ala Val
 1 5 10 15
 tgg gag cct gag gca ggt gga ttg ctt cag ctc ggg ggt tct agg g 206
 Trp Glu Pro Glu Ala Gly Gly Leu Leu Gln Leu Gly Gly Ser Arg
 20 25 30

<210> 228
 <211> 480
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 216..479

<221> sig_peptide
 <222> 216..326
 <223> Von Heijne matrix
 score 6.5
 seq LLVFFLIVRTLSC/RS

<400> 228
 gcatcccccck ktagctcaga gaagtttggt rdgaccgatc ttctgaagcc tacttctgtc 60
 aactcatcaa agtcattctc catccagctt tgttccatta tgggtgagga gctacgatcc 120
 tttggaggag aagaggcact ctgattttta gaattttcag cttttctgct ctggtttcgc 180
 cccatctttg tggttttatc taccttcggg ctttg atg atg gtg acc tac aga 233
 Met Met Val Thr Tyr Arg
 -35
 tgg ggt ttt ggt gtg gat gtc mtt ttt gtt gct gtt gat gct att cct 281
 Trp Gly Phe Gly Val Asp Val Xaa Phe Val Ala Val Asp Ala Ile Pro
 -30 -25 -20
 ttc tgt ttg tta gtt ttc ttt cta ata gtc agg acc ctc agc tgc agg 329
 Phe Cys Leu Leu Val Phe Phe Leu Ile Val Arg Thr Leu Ser Cys Arg
 -15 -10 -5 1
 tct gtt gga gta tgc tgg agg tcc act cca gac cct gtt tgc cta ggt 377
 Ser Val Gly Val Cys Trp Arg Ser Thr Pro Asp Pro Val Cys Leu Gly
 5 10 15
 atc acc agc aga ggc tgc aga aca gaa ata ttg cag aac agc aaa tgt 425
 Ile Thr Ser Arg Gly Cys Arg Thr Glu Ile Leu Gln Asn Ser Lys Cys
 20 25 30
 tgc tcc ctg atc ctt cct ctg gaa gct tcg tct caa agg ggc act gaa 473
 Cys Ser Leu Ile Leu Pro Leu Glu Ala Ser Ser Gln Arg Gly Thr Glu
 35 40 45
 tgt atg a 480
 Cys Met
 50

<210> 229
 <211> 144
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 43..144

<221> sig_peptide
 <222> 43..99
 <223> Von Heijne matrix
 score 6.5

seq EIFLPFSLSPANA/QS

<400> 229
tccagatgtg atttgggtatt tcatactttg ttgcttttgt aa atg ctg tac cca 54
Met Leu Tyr Pro
ctg cct gag ata ttc tta cct ttt tct ttg tcc cca gca aat gcc cag 102
Leu Pro Glu Ile Phe Leu Pro Phe Ser Leu Ser Pro Ala Asn Ala Gln
-15 -10 -5 1
tca aaa ttt agc ctt tat ttt ttt ccc ttg gtg aag ccg ggg 144
Ser Lys Phe Ser Leu Tyr Phe Phe Pro Leu Val Lys Pro Gly
5 10 15

<210> 230
<211> 457
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 314..457
<221> sig_peptide
<222> 314..394
<223> Von Heijne matrix
score 6.40000009536743
seq RLLCLXFXRLLLG/TS

<221> misc_feature
<222> 118,258..259,303,440
<223> n=a, g, c or t
Oligonucleotide

<400> 230
agctccgcgg taatggaggg tagggatggg tgctgaagta tcaggctctg gctctagctt 60
tagctctggc actggaactg cgtcggagtc tgggtctgag tctggcagcc cgaagccntg 120
grmcaccttt tcttgattct ctaaggcggg ggctgcctgc gtccaagcag ctggtttgca 180
gcgttccaac gctgggaggg agttccctta cctgggggtcc agtctgtaaa gttgtcgccg 240
ctttctaggg acccgccnnd scggctggga ctcttccatg cgtgagtatt actgarstgc 300
tsnaagggtcc ggc atg tcc ctg gaa cct gcc tcg gsc ctc ttg ggt gtg 349
Met Ser Leu Glu Pro Ala Ser Xaa Leu Leu Gly Val
-25 -20
cgg cgg aga ctg ctt tgt cta mct ttc tsc cga ctt ctc tta ggr acc 397
Arg Arg Arg Leu Leu Cys Leu Xaa Phe Xaa Arg Leu Leu Leu Gly Thr
-15 -10 -5 1
agt ctg ttg aag ttt gtg gkc tcc tgs agy cca ccc ama ccg nat act 445
Ser Leu Leu Lys Phe Val Xaa Ser Xaa Ser Pro Pro Xaa Pro Xaa Thr
5 10 15
ctc acc tct tcc 457
Leu Thr Ser Ser
20

<210> 231
<211> 112
<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 12..110

<221> sig_peptide

<222> 12..83

<223> Von Heijne matrix

score 6.40000009536743

seq LSVLILCVCVCVC/VY

<400> 231

ctgattttkc t atg ytg att ttg tat ctk gca act tta cta aat tta tca 50

Met Leu Ile Leu Tyr Leu Ala Thr Leu Leu Asn Leu Ser

-20

-15

gtt cta ata ctt tgt gtg tgt gtg tgt gtg tgt gtg tat gat tta tat 98

Val Leu Ile Leu Cys Val Cys Val Cys Val Cys Val Tyr Asp Leu Tyr

-10

-5

1

5

ata waa agg gga gt 112

Ile Xaa Arg Gly

<210> 232

<211> 359

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 8..358

<221> sig_peptide

<222> 8..55

<223> Von Heijne matrix

score 6.40000009536743

seq LGTTVLLWSLLRS/SP

<221> misc_feature

<222> 326

<223> n=a, g, c or t

Oligonucleotide

<400> 232

gataatc atg gcg ccc ctc gga aca act gta ttg ctg tgg agc ctc ttg 49

Met Ala Pro Leu Gly Thr Thr Val Leu Leu Trp Ser Leu Leu

-15

-10

-5

agg agt tct ccg ggc gtg gaa ccg gtc tgt ttc ccg gct cga atc cag 97

Arg Ser Ser Pro Gly Val Glu Arg Val Cys Phe Arg Ala Arg Ile Gln

1

5

10

ccc tgg cac ggt ggc ctg ctc caa ccg cta cct tgc tct ttc gag atg 145

Pro Trp His Gly Gly Leu Leu Gln Pro Leu Pro Cys Ser Phe Glu Met

15

20

25

30

ggg ctg cca cgc cgc ccg ttc agc tcc gag gcc gca gaa tct ggt agc 193

Gly Leu Pro Arg Arg Arg Phe Ser Ser Glu Ala Ala Glu Ser Gly Ser

	35	40	45	
cca gag acc aag aaa cct aca ttt atg gat gag gaa gtt caa agc ata				241
Pro Glu Thr Lys Lys Pro Thr Phe Met Asp Glu Glu Val Gln Ser Ile				
	50	55	60	
ctc acg aaa atg aca ggc ttg aac ttg cag aag act ttt aag cca gct				289
Leu Thr Lys Met Thr Gly Leu Asn Leu Gln Lys Thr Phe Lys Pro Ala				
	65	70	75	
ata caa gaa ctg aag cca cca acc tat aag cta atg nct cag gca cag				337
Ile Gln Glu Leu Lys Pro Pro Thr Tyr Lys Leu Met Xaa Gln Ala Gln				
	80	85	90	
ttg gaa gag gct aca aga cag g				359
Leu Glu Glu Ala Thr Arg Gln				
95	100			

<210> 233
 <211> 301
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 4..300

<221> sig_peptide
 <222> 4..105
 <223> Von Heijne matrix
 score 6.40000009536743
 seq LLFVVLLPPPPGS/VX

<221> misc_feature
 <222> 124,129,162
 <223> n=a, g, c or t
 Oligonucleotide

<400> 233	
gcg atg ctc ctc act ttc agc tcc agc tcc cgc cac cgc cgc ctc tat	48
Met Leu Leu Thr Phe Ser Ser Ser Arg His Arg Arg Leu Tyr	
cgc cgc cgc cgc cac cac ctc ctc ttc gtt gtc ctc ctt cct cct ccg	96
Arg Arg Arg Arg His His Leu Leu Phe Val Val Leu Leu Pro Pro Pro	
cct ggc agc gtt gkt ctc tgc agc sgg nrm grn smv raa gtg ctr vbg	144
Pro Gly Ser Val Xaa Leu Cys Ser Xaa Xaa Xaa Xaa Xaa Val Leu Xaa	
kma sga aag ttc cgg gan gga cta cat gga gcc atg ctc cct ggg ctc	192
Xaa Xaa Lys Phe Arg Xaa Gly Leu His Gly Ala Met Leu Pro Gly Leu	
ttc cgc ggg cgc ccg cgc gct gcc ctt cgc ttg aga gtc tca ccg wgt	240
Phe Arg Gly Arg Pro Arg Ala Ala Leu Arg Leu Arg Val Ser Pro Xaa	
tgc cca ggc tgg aaa gtg gcg cga tct cgg ctc aca gca acc tcc gcc	288
Cys Pro Gly Trp Lys Val Ala Arg Ser Arg Leu Thr Ala Thr Ser Ala	
tcm cgg gmc cgg g	301

Ser Arg Xaa Arg
65

<210> 234
<211> 248
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 152..247

<221> sig_peptide
<222> 152..190
<223> Von Heijne matrix
score 6.40000009536743
seq MLLLLQLNLKTLSS

<400> 234
acaagtggg tgctgtcgcc tgcgcatcgg cgggccggga ggctgagcag tactgttgag 60
agcgggtgga ggtgcttggt agcgcgccgt agctgcttcc acgtccttgc ttcacctcag 120
gtaaagagag aagtaatgga aggcctgtct g atg ttg ctt ctt ttg caa cta 172
Met Leu Leu Leu Leu Gln Leu
-10
aac tta aaa aca ctc tca tcc agt acc ata gca ttg aag aag ata agt 220
Asn Leu Lys Thr Leu Ser Ser Ser Thr Ile Ala Leu Lys Lys Ile Ser
-5 1 5 10
ggc gag ttg cta aga aaa cga aag agg g 248
Gly Glu Leu Leu Arg Lys Arg Lys Arg
15

<210> 235
<211> 393
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 339..392

<221> sig_peptide
<222> 339..383
<223> Von Heijne matrix
score 6.40000009536743
seq LFVLLIITQLLYG/GI

<400> 235
gttccaaagt gagctgtctc tggcagcatt catatagaat agaatttgaa tgggtgcaccc 60
agatttgaac aacatggtaa tcatgtgatg gacatggaaa agtgractaa cbtkrgggat 120
cwtggtargg tcaytaagaa taactckaata cawgatgtta aaaggctttc ctttacattc 180
acaaaacaat ttrsttccta gaagtagttt attcttgcct gtggtcattt ttgctccttt 240
ataatactac atctaaatca atttggttaa tatagtagag aaatgaaata aatttcttcc 300
agttaaacca ctgcacttaa agagtagaaa ccctctct atg tca ctc ttt gtt ttg 356
Met Ser Leu Phe Val Leu

-15 -10 393
 ttg atc ata act caa ctg ctg tat ggt ggg ata ctc t
 Leu Ile Ile Thr Gln Leu Leu Tyr Gly Gly Ile Leu
 -5 1

<210> 236
 <211> 222
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 121..222

<221> sig_peptide
 <222> 121..204
 <223> Von Heijne matrix
 score 6.40000009536743
 seq ILFLGVLLSASDL/CV

<400> 236
 ttttgagtta atttttgtat aagttgtaag gattaggtca gggttcttaa gaaaaatatt 60
 gttttggtct atagatgtct cattgcttct gtgctatttg ttggaaaagc tgttcttcca 120
 atg aat tgc ttt tgc aat ttt gtc aaa acc agt gag gca tat atg att 168
 Met Asn Cys Phe Cys Asn Phe Val Lys Thr Ser Glu Ala Tyr Met Ile
 -25 -20 -15
 ctg ttt cta ggt gtt cta ctc tct gca agt gat tta tgt gtc tat ccc 216
 Leu Phe Leu Gly Val Leu Leu Ser Ala Ser Asp Leu Cys Val Tyr Pro
 -10 -5 1
 atc ggg 222
 Ile Gly
 5

<210> 237
 <211> 154
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 54..152

<221> sig_peptide
 <222> 54..95
 <223> Von Heijne matrix
 score 6.40000009536743
 seq SVILALWEAEAGG/SP

<400> 237
 agtcttttgc tcctgtggtt aagattattc tgctaggctg ctcacggtgg ctg atg 56
 Met
 tct gta atc cta gca ctt tgg gag gcc gag gcg ggc gga tcg cct gag 104
 Ser Val Ile Leu Ala Leu Trp Glu Ala Glu Ala Gly Gly Ser Pro Glu
 -10 -5 1

atc ggg agt tcg gga ccg gcc gca cca aca tgg aga agc ccc gtc cag 152
 Ile Gly Ser Ser Gly Pro Ala Ala Pro Thr Trp Arg Ser Pro Val Gln
 5 10 15

gg 154

<210> 238
 <211> 439
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 255..437

<221> sig_peptide
 <222> 255..341
 <223> Von Heijne matrix
 score 6.30000019073486
 seq LGCLLLAVRSSAT/VN

<221> misc_feature
 <222> 359..360,381
 <223> n=a, g, c or t
 Oligonucleotide

<400> 238
 tcaccacaat caatttttaga acatttttcat catcccgaaa ataagccctg ttcccttttag 60
 ctgtcactcc ccactcctac cccccagccc tgtgcaataa tctacttttct gtctttgaag 120
 ctttgcctat tctggacatt ttgtataaaa gggtttggtg aggatgtggt cttttgtgac 180
 tggcttcttg aacttggcat agtgtttttca aggttcaacc atgttgtagc acgtacgttc 240
 ctttttatgg ccaa atg tac gga gag tcc aca ttg ttt atc cat tca tca 290

Met Tyr Gly Glu Ser Thr Leu Phe Ile His Ser Ser
 -25 -20

gtt cat ggg cat ttg ggt tgt ctc ctc ttg gct gtt agg agt agt gct 338
 Val His Gly His Leu Gly Cys Leu Leu Leu Ala Val Arg Ser Ser Ala
 -15 -10 -5

act gtg aac att acg tac chn nkw gtk tgt gtg gac att cak ntt cat 386
 Thr Val Asn Ile Thr Tyr Xaa Xaa Val Cys Val Asp Ile Xaa Xaa His
 1 5 10 15

ttc cat atg ctt atg tct gga att act ggg tca tat ggc aac tct ctt 434
 Phe His Met Leu Met Ser Gly Ile Thr Gly Ser Tyr Gly Asn Ser Leu
 20 25 30

tca ct 439
 Ser

<210> 239
 <211> 229
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 7..228

<221> sig_peptide
 <222> 7..159
 <223> Von Heijne matrix
 score 6.30000019073486
 seq WLYLLEVVAPLSG/IH

<400> 239
 gtcaag atg gcg gcg tct gta tta aac acc gtg ctg agg cgg ctt cct 48
 Met Ala Ala Ser Val Leu Asn Thr Val Leu Arg Arg Leu Pro
 -50 -45 -40
 atg cta tct ctc ttc cga ggt tct cac aga gtt cag gta act ctt cga 96
 Met Leu Ser Leu Phe Arg Gly Ser His Arg Val Gln Val Thr Leu Arg
 -35 -30 -25
 aag aca ttt tgc aca acc tca agt tgg tta tac ctt ctc gag gtt gtc 144
 Lys Thr Phe Cys Thr Thr Ser Ser Trp Leu Tyr Leu Leu Glu Val Val
 -20 -15 -10
 gct cca ctg tca gga atc cac gag tgg aga cct tcc cac gtg tgt ctt 192
 Ala Pro Leu Ser Gly Ile His Glu Trp Arg Pro Ser His Val Cys Leu
 -5 1 5 10
 agc tgt cta ggc agt act tcc tgc aac ccc cct gag g 229
 Ser Cys Leu Gly Ser Thr Ser Cys Asn Pro Pro Glu
 15 20

<210> 240
 <211> 318
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 65..316

<221> sig_peptide
 <222> 65..259
 <223> Von Heijne matrix
 score 6.30000019073486
 seq LMVVAETSQGSWS/AP

<221> misc_feature
 <222> 259
 <223> n=a, g, c or t
 Oligonucleotide

<400> 240
 ctcttcggtt gtccagccct tctcccagcc ctggtccctc agaaggaggg taactccctt 60
 ccag atg tta cgg tcc gcc tgc gtc tct cag cac gcc ggt ggc att tgg 109
 Met Leu Arg Ser Ala Cys Val Ser Gln His Ala Gly Gly Ile Trp
 -65 -60 -55
 gtt gac cgc gga ggc ccc cag tgc cag agg gtg ttc acg ttc tgc cgt 157
 Val Asp Arg Gly Gly Pro Gln Cys Gln Arg Val Phe Thr Phe Cys Arg
 -50 -45 -40 -35
 ggg ctc agc cca aac ttt gga cgc tca gag acc caa cgg gag cgc tgg 205
 Gly Leu Ser Pro Asn Phe Gly Arg Ser Glu Thr Gln Arg Glu Arg Trp
 -30 -25 -20

ata agg cca gga cag ctg atg gtt gtg gca gaa aca tct caa ggt agc 253
 Ile Arg Pro Gly Gln Leu Met Val Val Ala Glu Thr Ser Gln Gly Ser
 -15 -10 -5
 tgg tcn gcc ccc act tcc cca tst acc tct tgt cct ccc ccc aac acc 301
 Trp Ser Ala Pro Thr Ser Pro Xaa Thr Ser Cys Pro Pro Pro Asn Thr
 1 5 10
 asc acc aca ccg gyt cc 318
 Xaa Thr Thr Pro Xaa
 15

<210> 241
 <211> 405
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 123..404

<221> sig_peptide
 <222> 123..257
 <223> Von Heijne matrix
 score 6.30000019073486
 seq GFVSLLVHAADA/WV

<400> 241
 tagctggacc cgtctgggag gtaggtttgt gagcgtgaga gaks gatctg taccgcgggg 60
 atccgaagta tgcttatcca ggtgggctgc ctcaagcctc gatccacccc ccgcgctdvt 120
 ag atg gtg tca agg tcc ttg cgt ggg aga agg act tgg gtg aga tgc 167
 Met Val Ser Arg Ser Leu Arg Gly Arg Arg Thr Trp Val Arg Cys
 -45 -40 -35
 atg cgg aga ttg ccc cca att ccg gcc tgg agc caa ggg aaa ggg atg 215
 Met Arg Arg Leu Pro Pro Ile Pro Ala Trp Ser Gln Gly Lys Gly Met
 -30 -25 -20 -15
 cct gga ttt gtg tct cta ttg gtg gtc cac gct gcg gat gcc tgg gta 263
 Pro Gly Phe Val Ser Leu Leu Val Val His Ala Ala Asp Ala Trp Val
 -10 -5 1
 gcc cag agg ttr tct acg cca tac ttc tca ctg ttt ttg agc ata cct 311
 Ala Gln Arg Leu Ser Thr Pro Tyr Phe Ser Leu Phe Leu Ser Ile Pro
 5 10 15
 aga tgt tcc ttt cct agg cgg agt ata gat cgc acg tgt tct agc stc 359
 Arg Cys Ser Phe Pro Arg Arg Ser Ile Asp Arg Thr Cys Ser Ser Xaa
 20 25 30
 tta gac tca gag ggt tcg agc tct ata asc ccc tcc act ccc ttc a 405
 Leu Asp Ser Glu Gly Ser Ser Ser Ile Xaa Pro Ser Thr Pro Phe
 35 40 45

<210> 242
 <211> 242
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS

<222> 129..242

<221> sig_peptide

<222> 129..191

<223> Von Heijne matrix
score 6.30000019073486
seq SLLPCSLISDCCA/SN

<400> 242

```
cttttgtttt gcaatgccct gccccagag gtggagtcta cagaggcagg caggcctcct    60
tgagctgagg tgggctccac ccagttcgag ctcccagct gctttgttta cctactcaag    120
cctgggca atg gtg ggc gcc ctt ccc cca gcc tcg ctt ctg cct tgc agt    170
      Met Val Gly Ala Leu Pro Pro Ala Ser Leu Leu Pro Cys Ser
            -20                -15                -10
ttg atc tca gac tgc tgt gct agc aat gag cga ggc tcc atg ggc gta    218
Leu Ile Ser Asp Cys Cys Ala Ser Asn Glu Arg Gly Ser Met Gly Val
      -5                1                5
gga ccc tct gag cca cgg cgy ggg    242
Gly Pro Ser Glu Pro Arg Arg Gly
10                15
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<210> 243

<211> 363

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 298..363

<221> sig_peptide

<222> 298..357

<223> Von Heijne matrix
score 6.30000019073486
seq LGSLIASLAPSTG/LG

<400> 243

```
accactctga ggagacgcgt gacagataag aagggctggt gggatcagtc ctggtggtag    60
ctcaggaagc agagcctgga gcatctccac tatggcctgg gctccactac ttctcaccct    120
cctcgctcac tgcacagggt cttgggceaa ctttatgctg actcagccgc actctgtgtc    180
ggagtcgccg gssgaagacg gtaaccatct cctgcacccg cagcagtggc agctttgtca    240
gcaactatgt tcagtgttac cagcggcgcc cggacagtgc cccaccact gtgatct    297
atg agg atg aca aaa gac cct ctg ggg tct ctg atc gct tct ctg gct    345
Met Arg Met Thr Lys Asp Pro Leu Gly Ser Leu Ile Ala Ser Leu Ala
-20                -15                -10                -5
cca tcg aca ggt ctt ggg    363
Pro Ser Thr Gly Leu Gly
1
```

<210> 244

<211> 324

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 153..323

<221> sig_peptide

<222> 153..236

<223> Von Heijne matrix

score 6.30000019073486

seq FFLFLFFXEXXX/XX

<400> 244

aattgatact gcttttagatg tttctgtctc attttacaaa aatgtaagaa aaaagaaaaa 60

tcaaactata ctgttaccta tttcttgtat attcttaaca gaatgttctg tacacataag 120

tgtatgtgtg ttaatcctct tgtttaaatg cc atg aaa ctt cag ttt gcc ttt 173

Met Lys Leu Gln Phe Ala Phe

-25

tgt tat ttt ctt tat tta gat acc ttt ttt ctt ttt ctt ttt ttt ttk 221

Cys Tyr Phe Leu Tyr Leu Asp Thr Phe Phe Leu Phe Leu Phe Phe Xaa

-20

-15

-10

gag ama gyc tkg cyc kgt kgc hta ggm agg agt gca gtg gca maa cct 269

Glu Xaa Xaa Xaa Xaa Xaa Xaa Xaa Gly Arg Ser Ala Val Ala Xaa Pro

-5

1

5

10

cag ctc ayt gca gcc tcc acc ttc kgg tty caa gca att tty ctg ccc 317

Gln Leu Xaa Ala Ala Ser Thr Phe Xaa Phe Gln Ala Ile Phe Leu Pro

15

20

25

cag ckg g 324

Gln Xaa

<210> 245

<211> 280

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 27..278

<221> sig_peptide

<222> 27..233

<223> Von Heijne matrix

score 6.30000019073486

seq GILKVLLFSVSG/LE

<400> 245

gttgcggggc ggggccttcg cagagc atg gcg gcg ggc gag ctt gag ggt ggc 53

Met Ala Ala Gly Glu Leu Glu Gly Gly

-65

aaa ccc ctg agc ggg ctg ctg aat gcg ctg gcc cag gac act ttc cac 101

Lys Pro Leu Ser Gly Leu Leu Asn Ala Leu Ala Gln Asp Thr Phe His

-60

-55

-50

-45

ggg tac ccc ggc atc aca gag gag ctg cta cgg agc cag cta tat cca 149

Gly Tyr Pro Gly Ile Thr Glu Glu Leu Leu Arg Ser Gln Leu Tyr Pro

-40

-35

-30

gag gtg cca ccc gag gag ttc cac ccc ttt ctg gca aag atg agg ggg 197

Glu	Val	Pro	Pro	Glu	Glu	Phe	His	Pro	Phe	Leu	Ala	Lys	Met	Arg	Gly	
			-25					-20					-15			
att	ctt	aag	gta	ctg	ctc	ttt	tct	gta	gtc	tcc	ggc	ttg	gag	cag	aac	245
Ile	Leu	Lys	Val	Leu	Leu	Phe	Ser	Val	Val	Ser	Gly	Leu	Glu	Gln	Asn	
		-10					-5					1				
ccc	ttg	gcc	gct	ggc	ttc	aga	ctc	tcc	cac	ccg	gg					280
Pro	Leu	Ala	Ala	Gly	Phe	Arg	Leu	Ser	His	Pro						
5					10					15						

<210> 246
 <211> 211
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 70..210
 <221> sig_peptide
 <222> 70..162
 <223> Von Heijne matrix
 score 6.30000019073486
 seq SLILSPSPRPVLG/FF

<400>	246																
tttggctggg	gagacccatc	tggtactacca	aggagaagct	atagactact	tctactccac											60	
caggaaggt	atg atg atg	tca aac	gtg atg	ctg atg	cta cag	tta cag	ccc									111	
	Met Met Met	Ser Asn	Val Met	Leu Met	Leu Gln	Leu Gln	Pro										
		-30						-25					-20				
ctg ctg	gcg cas	tct ctg	att ctc	tct ccc	tct ccg	cgt cca	gtg ctg									159	
Leu Leu	Ala Xaa	Ser Leu	Ile Leu	Ser Pro	Ser Pro	Arg Pro	Val Leu										
	-15			-10			-5										
ggc ttt	ttc aga	caa gtg	cat ctc	cta acc	agg tca	cat ttc	agc cgc									207	
Gly Phe	Phe Arg	Gln Val	His Leu	Leu Thr	Arg Ser	His Phe	Ser Arg										
	1		5		10		15										
tg g																211	
Trp																	

<210> 247
 <211> 359
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 249..359
 <221> sig_peptide
 <222> 249..308
 <223> Von Heijne matrix
 score 6.19999980926514
 seq LLFICPPPPPISA/SS

<400> 247


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tttcagaatt ttgtgcagga atatctgagt atttctaatt agattagaat gtcagaatac      60
attcatggac atatgagggg ttttttaaaa ttttttttag atacccttca ccttgaacat      120
ttattatttc tttgtgttgg gaacaatcca aatctctcct agatgttttg aaatgtgcaa      180
tgtattgtta gctgtagtca ccctactgtg ctattgaata ctagagcttg ttccttctgt      240
ctaactgt atg att ata ctc att aac caa ctt ctc ttc atc tgt ccc cca      290
      Met Ile Ile Leu Ile Asn Gln Leu Leu Phe Ile Cys Pro Pro
      -20          -15          -10
cct cca ccc atc tca gcc tct agt aac tac cat ttt act ctc tac ctc      338
Pro Pro Pro Ile Ser Ala Ser Ser Asn Tyr His Phe Thr Leu Tyr Leu
      -5          1          5          10
cat gac att aac ttt ttt agc      359
His Asp Ile Asn Phe Phe Ser
      15

```

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<210> 248
<211> 236
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> 182..235

```

```

<221> sig_peptide
<222> 182..226
<223> Von Heijne matrix
      score 6.19999980926514
      seq DVLLQLLLRVCSP/RT

```

```

<400> 248
attgggttaa tttcactgca ctgactatct ttagatatat attctttgtg ccttcactag      60
aactcctctt acttcatgat atcttaacta taaaatcatc caaccatgaa aacaagcaca      120
caagaaacag aaacaaaaca gtcacaaaaa agcataaaact gttagcattg atccatgatg      180
a atg act gat gta tta ctt caa ttg cta tta aga gtg tgt tct ccc agg      229
      Met Thr Asp Val Leu Leu Gln Leu Leu Arg Val Cys Ser Pro Arg
      -15          -10          -5          1
acc agg g      236
Thr Arg

```

```

<210> 249
<211> 342
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> 266..340

```

```

<221> sig_peptide
<222> 266..304
<223> Von Heijne matrix
      score 6.19999980926514
      seq MGLFLCCSLIFC/LV

```

<400> 249
taggctattt cttaattttc cttctaggat tcttatagtt tgaagtttta catttagatc 60
gtcaatccat cttgagttca tttttgtata tgatgaaaag taggggtctg attttattct 120
tctgcataag accagttatc ccagaaccgt ttgttgaata ggaagttctt ttctcattgc 180
ttgtttgtgg ggactttgtc aaagatcaaa tagttatagg tgtgtggctg tatttcaggg 240
tttctttatt ccatttcact gatct atg ggt ctg ttt ttg tgc tgc tct tta 292
Met Gly Leu Phe Leu Cys Cys Ser Leu
-10 -5
ctg ata ttc tgt ctg gtt gtt cta atc ata act gaa ctg ggc tat ggg 340
Leu Ile Phe Cys Leu Val Val Leu Ile Ile Thr Glu Leu Gly Tyr Gly
1 5 10
gg 342

<210> 250
<211> 382
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 291..380
<221> sig_peptide
<222> 291..332
<223> Von Heijne matrix
score 6.19999980926514
seq GSWALTWLHPAEA/GT

<221> misc_feature
<222> 264..265,279..280
<223> n=a, g, c or t
Oligonucleotide

<400> 250
atacagcggc ctctgacacc agcacagcaa acccgccggg atcaaagtgt accagtcggc 60
agcatgggta aggagagggg tttccaatca cccattgcct gctctgtctg cccctaattt 120
ggaaaggccc tctccagaa aatgctagaa aacctgagtg gggagctggg gagggagtag 180
tggactctgc ttcatgtgcc ccagtctgca caccctcc cccaccacc cactgcattt 240
cccagctcag ccaaactttc tgannaagac gggcagagnn ctgctgggag atg gga 296
Met Gly
tcc tgg gcc ctg act tgg ctc cat cca gca gag gct ggg acc agg gtg 344
Ser Trp Ala Leu Thr Trp Leu His Pro Ala Glu Ala Gly Thr Arg Val
-10 -5 1
cct ttc tgc agc tgg gaa aaa tca gat ggg cgc tct ta 382
Pro Phe Cys Ser Trp Glu Lys Ser Asp Gly Arg Ser
5 10 15

<210> 251
<211> 303
<212> DNA
<213> Homo sapiens

<220>
<221> CDS

<222> 108..302

<221> sig_peptide

<222> 108..233

<223> Von Heijne matrix
score 6.19999980926514
seq LSVLSLVINFSWS/RK

<221> misc_feature

<222> 279

<223> n=a, g, c or t
Oligonucleotide

<400> 251

aaaagctgtg aggttgtaac tcagttcagt agtattttata aatatttggtt ttccactttt 60
gtgcatatta tacaaatgat ggatataaaa tttgtttwga ccatwta atg atg ctt 116
Met Met Leu
-40
rmw wwr rra aga gga tat cct cat aga act gaa cgt tat gat gga ttt 164
Xaa Xaa Xaa Arg Gly Tyr Pro His Arg Thr Glu Arg Tyr Asp Gly Phe
-35 -30 -25
tta aaa tat tct gac cca aat gat att gca ttg tca gta ctg tcc ctg 212
Leu Lys Tyr Ser Asp Pro Asn Asp Ile Ala Leu Ser Val Leu Ser Leu
-20 -15 -10
gtt att aat ttc tcc tgg agt aga aaa tgc ttt gtt cct tac tat atc 260
Val Ile Asn Phe Ser Trp Ser Arg Lys Cys Phe Val Pro Tyr Tyr Ile
-5 1 5
cca ttt aaa cct tac cgv nta cct tac ccc acc gcg gcc cgg g 303
Pro Phe Lys Pro Tyr Arg Xaa Pro Tyr Pro Thr Ala Ala Arg
10 15 20

<210> 252

<211> 259

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 106..258

<221> sig_peptide

<222> 106..222

<223> Von Heijne matrix
score 6.19999980926514
seq CFVCXLFVFLLSG/LN

<221> misc_feature

<222> 134

<223> n=a, g, c or t
Oligonucleotide

<400> 252

attttaaagg attttttaaa ggacctctat agttataagt cagcttaatt aaaaatggat 60
attccatagt catattttata tatatatata cacacatata tatgt atg tat gtg tgt 117

<400> 254
aaacgttttc ttttatctaa tttatatata atttaattaa aataagccag gaggctagt 60
gctaccatgt tagcagcaca gtcctatata ttctttcact tttgttacat ttgttatcaa 120
ttttaactac tattattatt acatacaata caattttaac aataggagat tgctattaga 180
tgaggcttta acagaaaarv attaav atg ara ata tgc tat aac att ttt caa 233

Met Xaa Ile Cys Tyr Asn Ile Phe Gln
-25 -20

aac att ctc ggc ctc ttg ctt att ttc ctg tat ctt tct ttg aat ctt 281
Asn Ile Leu Gly Leu Leu Leu Ile Phe Leu Tyr Leu Ser Leu Asn Leu
-15 -10 -5

ttt tgt att ttc ttt tct gtc cct gcc ctt caa cct aga aga ctg gg 328
Phe Cys Ile Phe Phe Ser Val Pro Ala Leu Gln Pro Arg Arg Leu
1 5 10

<210> 255
<211> 320
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 233..319

<221> sig_peptide
<222> 233..310
<223> Von Heijne matrix
score 6.09999990463257
seq MLTLLGFPSKALT/FI

<221> misc_feature
<222> 129
<223> n=a, g, c or t
Oligonucleotide

<400> 255
caagttgtct cctgcgtagt gtctattagc tcttgaattt cttcaagatc catatactga 60
aacacttcac tctccaactt ttttgccata ttgacaatca ctttcataat ttcacttatt 120
gacyctgynw haaatcmtgt gaagyhatgc agahcatctg gacacagctt tctccagcag 180
ggatyyatdg ttttgggctt gaagggggtt cacggctttt tctataacaa cg atg gca 238

Met Ala
-25

tct tca atg ctg waa tcc ttc cag act ttc atg atg ttg act cta ttg 286
Ser Ser Met Leu Xaa Ser Phe Gln Thr Phe Met Met Leu Thr Leu Leu
-20 -15 -10

ggt ttc cct tcc aaa gct ttg aca ttc att tcc a 320
Gly Phe Pro Ser Lys Ala Leu Thr Phe Ile Ser
-5 1

<210> 256
<211> 305
<212> DNA
<213> Homo sapiens

<220>
 <221> CDS
 <222> 205..303

<221> sig_peptide
 <222> 205..264
 <223> Von Heijne matrix
 score 6.09999990463257
 seq LLSLPGSFIPGNC/RP

<400> 256
 tttgttttat ttggttattt gttttgtttt gtttctctga ggccaatggg tgggaggaag 60
 tataaagaag tgtaaacagg aaagccagct gggcctggag ttccaagtgc ccatatttca 120
 tcagcttcct ctccataact gtggcaggga cacttaaccc ttccctggct gtgagaagtt 180
 attctctgag ggctggtgag caga atg gga aga tct aag agg cag ctc ctt 231
 Met Gly Arg Ser Lys Arg Gln Leu Leu
 -20 -15
 tcc ttg cct ggt tcc ttt atc cct ggg aat tgc agg cca agg att ctg 279
 Ser Leu Pro Gly Ser Phe Ile Pro Gly Asn Cys Arg Pro Arg Ile Leu
 -10 -5 1 5
 agc aat gdw gaa gwc aga agg aag gg 305
 Ser Asn Gly Glu Xaa Arg Arg Lys
 10

<210> 257
 <211> 181
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 37..180

<221> sig_peptide
 <222> 37..111
 <223> Von Heijne matrix
 score 6.09999990463257
 seq CFFLIIFLLPPLPA/MI

<400> 257
 tttctaattgc tattatcctg mtagtgamta agtctc atg aga tct gat ggg ttt 54
 Met Arg Ser Asp Gly Phe
 -25 -20
 atc agg ggt ttc tgc ttc tgc ttc ttc cta att ttt ctc ctg cca ccg 102
 Ile Arg Gly Phe Cys Phe Cys Phe Phe Leu Ile Phe Leu Leu Pro Pro
 -15 -10 -5
 ctt cct gcc atg ata ctg agg cct ctg cag cca tgt gga att ata agt 150
 Leu Pro Ala Met Ile Leu Arg Pro Leu Gln Pro Cys Gly Ile Ile Ser
 1 5 10
 cca att aaa cct ctt ttt cct ttt ttt ttt t 181
 Pro Ile Lys Pro Leu Phe Pro Phe Phe Phe
 15 20

<210> 258

<211> 236
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 119..235

<221> sig_peptide
 <222> 119..166
 <223> Von Heijne matrix
 score 6.09999990463257
 seq LWTASSLPLSTHS/QR

<400> 258
 caaaaaaatc agtctttaag catttgcttg gtaagggttc ttaagattag gtttataata 60
 caaccatctg taatgtatct stcgtttgag ctgtgtggcc atacaattca ttaactag 118
 atg aat aca ttg tgg aca gca tcc tca cta ccc ctc tct act cac tca 166
 Met Asn Thr Leu Trp Thr Ala Ser Ser Leu Pro Leu Ser Thr His Ser
 -15 -10 -5
 caa aga acc atg ata cac tgg aat gtt ttt ctc tgg aat tct ttc tac 214
 Gln Arg Thr Met Ile His Trp Asn Val Phe Leu Trp Asn Ser Phe Tyr
 1 5 10 15
 tct tgt att aaa att ttt ccc c 236
 Ser Cys Ile Lys Ile Phe Pro
 20

<210> 259
 <211> 265
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 128..265

<221> sig_peptide
 <222> 128..220
 <223> Von Heijne matrix
 score 6.09999990463257
 seq CLIGLLVPLLGWG/NQ

<400> 259
 gacttaggat ttgagcatct ttctgttatg ctgttgcccc actcctattg caatactccc 60
 cttcttaaga aagtttttct agactaatgt ctagattaaa cttcttttct ttgacaataa 120
 tgatgcc atg act tgg aca aaa tgc cca ttg cct ctg ggt cct gct ttc 169
 Met Thr Trp Thr Lys Cys Pro Leu Pro Leu Gly Pro Ala Phe
 -30 -25 -20
 ttc acc cag tgc tgc ctt att gga ctc ctt gtg cct ctc ctt ggc tgg 217
 Phe Thr Gln Cys Cys Leu Ile Gly Leu Leu Val Pro Leu Leu Gly Trp
 -15 -10 -5
 gga aat cag aat aca cag tgg tat ccc act tct aag atg cct gat ggg 265
 Gly Asn Gln Asn Thr Gln Trp Tyr Pro Thr Ser Lys Met Pro Asp Gly
 1 5 10 15

<210> 260
 <211> 272
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 162..272

<221> sig_peptide
 <222> 162..257
 <223> Von Heijne matrix
 score 6.09999990463257
 seq IVYFLVLLRVLYT/LQ

<400> 260
 cacaagggttg atttaaaatt cttaaaaaat ttttcaaaat ctttccaaat gaaacaagat 60
 ttattgttaa tctacagaaa tatcctccat tcactttgat atttaaata catcgatcat 120
 tttaggtaga gcatttttat gaccactcat tgcttagtct g atg ggg agg agc aat 176
 Met Gly Arg Ser Asn
 -30
 gat ttt agg ttt gcc ttt cta aca tgc ttt ctt gga tgg gaa ata gta 224
 Asp Phe Arg Phe Ala Phe Leu Thr Cys Phe Leu Gly Trp Glu Ile Val
 -25 -20 -15
 tat ttc ttg gtg ctt ctt cgt gtt tta tac act tta caa tgg ggt ggg 272
 Tyr Phe Leu Val Leu Leu Arg Val Leu Tyr Thr Leu Gln Trp Gly Gly
 -10 -5 1 5

<210> 261
 <211> 98
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 26..97

<221> sig_peptide
 <222> 26..79
 <223> Von Heijne matrix
 score 6.09999990463257
 seq LTSFLTYMPLISS/SC

<400> 261
 tttctaggta tacaatcata ttata atg aaa aca gat aat ttg act tct ttt 52
 Met Lys Thr Asp Asn Leu Thr Ser Phe
 -15 -10
 ctt aca tat atg cct ctt att tct tcc tct tgc tca att gct ccc t 98
 Leu Thr Tyr Met Pro Leu Ile Ser Ser Cys Ser Ile Ala Pro
 -5 1 5

<210> 262
 <211> 419

<212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 28..417

<221> sig_peptide
 <222> 28..264
 <223> Von Heijne matrix
 score 6.09999990463257
 seq ATVAVLSFILSSA/AK

<400> 262
 attcccgggc cctggcttct tggcgcg atg agg ttc cgg ttc tgt ggt gat ctg 54
 Met Arg Phe Arg Phe Cys Gly Asp Leu
 -75
 gac tgt ccc gac tgg gtc ctg gca gaa atc agc acg ctg gcc aag atg 102
 Asp Cys Pro Asp Trp Val Leu Ala Glu Ile Ser Thr Leu Ala Lys Met
 -70 -65 -60 -55
 tcc tct gtg aag ttg cgg ctg ctc tgc agc cag gta cta aag gag ctg 150
 Ser Ser Val Lys Leu Arg Leu Leu Cys Ser Gln Val Leu Lys Glu Leu
 -50 -45 -40
 ctg gga cag ggg att gat tat gag aag atc ctg aag ctc acg gct gac 198
 Leu Gly Gln Gly Ile Asp Tyr Glu Lys Ile Leu Lys Leu Thr Ala Asp
 -35 -30 -25
 gcc aag ttt gag tca ggc gat gtg aag gcc aca gtg gca gtg ctg agt 246
 Ala Lys Phe Glu Ser Gly Asp Val Lys Ala Thr Val Ala Val Leu Ser
 -20 -15 -10
 ttc atc ctc tcc agt gcg gcc aag cac agt gtc gat ggc gaa tcc ttg 294
 Phe Ile Leu Ser Ser Ala Ala Lys His Ser Val Asp Gly Glu Ser Leu
 -5 1 5 10
 tcc agt gaa ctg cag cag ctg ggg ctg ccc aaa gag cac gcg gcc agc 342
 Ser Ser Glu Leu Gln Gln Leu Gly Leu Pro Lys Glu His Ala Ala Ser
 15 20 25
 ctg tgc cgc tgt tat gag gag aag caa agc ccc ttg cag aag cac ttg 390
 Leu Cys Arg Cys Tyr Glu Glu Lys Gln Ser Pro Leu Gln Lys His Leu
 30 35 40
 cgg gtc tgc agc cta cgc atg aat agg tt 419
 Arg Val Cys Ser Leu Arg Met Asn Arg
 45 50

<210> 263
 <211> 371
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 133..369

<221> sig_peptide
 <222> 133..174
 <223> Von Heijne matrix

score 6.09999990463257
seq FLAALFTVAKIWK/QP

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<400> 263
cactatggag aactgtatgg cgggtcctca aaaaactaaa aatagaactc ccatatgac 60
cagcaatccc attgctaggt atataccccc ccaaaaaagg aaatcagtat atgaaagaga 120
tatctgaatc cc atg ttt ctt gca gca ctg ttt aca gta gct aag att tgg 171
          Met Phe Leu Ala Ala Leu Phe Thr Val Ala Lys Ile Trp
                    -10                    -5

aag caa cct aag tgt tca tca aca aac aaa tgg aca aag aaa atg tgg 219
Lys Gln Pro Lys Cys Ser Ser Thr Asn Lys Trp Thr Lys Lys Met Trp
      1              5              10              15

tac ata tac aca atg gag tac tat tca gcc ata aaa aaa gat gat atc 267
Tyr Ile Tyr Thr Met Glu Tyr Tyr Ser Ala Ile Lys Lys Asp Asp Ile
              20              25              30

ctg tca ttt gca aca ata tgg atg gaa ctg gag agc att aca tta agt 315
Leu Ser Phe Ala Thr Ile Trp Met Glu Leu Glu Ser Ile Thr Leu Ser
              35              40              45

gaa ata agt ggg sca cca aaa gac aaa ctt ctc atg ttc tca ctc att 363
Glu Ile Ser Gly Xaa Pro Lys Asp Lys Leu Leu Met Phe Ser Leu Ile
              50              55              60

tgt gga ag 371
Cys Gly
      65
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<210> 264
<211> 283
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 194..283

<221> sig_peptide
<222> 194..274
<223> Von Heijne matrix
score 6.09999990463257
seq LSILQSLVPAAGA/XS

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<400> 264
ctcattccct gtccctcggat cacagtctct tctcactaca gtgtcgccgc ctctgcctgc 60
gtascccggc catggtctctg tagcctcgac cctttgtgc ccccggccg tctccgcgt 120
caccacgcct gcgtctccg ctccacatt ctttcttcag ccgaggccgc cgccgcctct 180
ccttgctgca gcc atg gag tct tcc act ttc gcc ttg gtg cct gtc ttc 229
          Met Glu Ser Ser Thr Phe Ala Leu Val Pro Val Phe
                    -25                    -20

gcc cac ctg agc atc ctc cag agc ctc gtg cca gct gct ggt gca gyc 277
Ala His Leu Ser Ile Leu Gln Ser Leu Val Pro Ala Ala Gly Ala Xaa
      -15              -10              -5              1

tct cct 283
Ser Pro
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<210> 265

<211> 370
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 117..368

<221> sig_peptide
 <222> 117..350
 <223> Von Heijne matrix
 score 6.09999990463257
 seq LLWFLQTFFFGIA/SL

<400> 265
 aaagcgcgct cccggggagg tgttgacagcc atggctacgg cagccggcgc gacctacttt 60
 cagcgaggca gtctgttctg gttcacagtc atcacctca gctttggcta ctacac atg 119
 Met
 ggt tgt ctt ctg gcc tca gag tat ccc tta tca gaa cct tgg gcc cct 167
 Gly Cys Leu Leu Ala Ser Glu Tyr Pro Leu Ser Glu Pro Trp Ala Pro
 -75 -70 -65
 ggg ccc ttc act cag tac ttg gtg gac cac cat cac acc ctc ctg tgc 215
 Gly Pro Phe Thr Gln Tyr Leu Val Asp His His His Thr Leu Leu Cys
 -60 -55 -50
 aat ggg tat tgg ctt gcc tgg ctg att cat gtg gga gag tcc ttg tat 263
 Asn Gly Tyr Trp Leu Ala Trp Leu Ile His Val Gly Glu Ser Leu Tyr
 -45 -40 -35 -30
 gcc ata gta ttg tgc aag cat aaa ggc atc aca agt ggt cgg gct cag 311
 Ala Ile Val Leu Cys Lys His Lys Gly Ile Thr Ser Gly Arg Ala Gln
 -25 -20 -15
 cta ctc tgg ttc cta cag act ttc ttc ttt ggg ata gcg tct ctc asc 359
 Leu Leu Trp Phe Leu Gln Thr Phe Phe Phe Gly Ile Ala Ser Leu Xaa
 -10 -5 1
 atc ttg att gc 370
 Ile Leu Ile
 5

<210> 266
 <211> 274
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 178..273

<221> sig_peptide
 <222> 178..225
 <223> Von Heijne matrix
 score 6.09999990463257
 seq WIWVASILLRIFA/SV

<400> 266
 tatcgtgaaa gaatattgaa ttttatcaaa tctttttttg tatctgttga gatgattaca 60

<222> 62..112
 <223> Von Heijne matrix
 score 6.09999990463257
 seq RLLLLPRPPASTG/AS

<400> 268
 agttgagtgg aaatgggcaa cggcgggacg agcggcctgc agcaggggaa ggggaacgtg 60
 g atg ggg tgg cag cga ctc cta ctg ctg cct cgg cct cct gcc agt aca 109
 Met Gly Trp Gln Arg Leu Leu Leu Leu Pro Arg Pro Pro Ala Ser Thr
 -15 -10 -5
 ggt gca tcg aat gca acc agg rrg cca aag agk ttg tac cga grc tat 157
 Gly Ala Ser Asn Ala Thr Arg Xaa Pro Lys Xaa Leu Tyr Arg Xaa Tyr
 1 5 10 15
 aac cac ggt gtg ctg aag ata acc atc tgt aaa tcc tgc cag aaa cct 205
 Asn His Gly Val Leu Lys Ile Thr Ile Cys Lys Ser Cys Gln Lys Pro
 20 25 30
 gta gac aaa tat atc gag tat gat cct gtt atc atc ttg awk aat gct 253
 Val Asp Lys Tyr Ile Glu Tyr Asp Pro Val Ile Ile Leu Xaa Asn Ala
 35 40 45
 ata ttg tgc aaa gct cad gcc tac agr cat att ctt ttc aat act caa 301
 Ile Leu Cys Lys Ala Xaa Ala Tyr Arg His Ile Leu Phe Asn Thr Gln
 50 55 60
 ata aat aac aaa ctg cct att tta ttg gca ttt tta cct tcc tgt ggv 349
 Ile Asn Asn Lys Leu Pro Ile Leu Leu Ala Phe Leu Pro Ser Cys Gly
 65 70 75
 dga acg gcc cat gac ggc aaa aaa aag ccc aac ttc att ttg ctg ctg 397
 Xaa Thr Ala His Asp Gly Lys Lys Lys Pro Asn Phe Ile Leu Leu Leu
 80 85 90 95
 aaa sat tat tat tat cta gct acg gaa aac 427
 Lys Xaa Tyr Tyr Tyr Leu Ala Thr Glu Asn
 100 105

<210> 269
 <211> 143
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 20..142

<221> sig_peptide
 <222> 20..76
 <223> Von Heijne matrix
 score 6
 seq LLALVVRVILSTA/IL

<400> 269
 ctttctttgc ggaatcacc atg gcg gct ggg gta agt ttg ctg gct ctg gtg 52
 Met Ala Ala Gly Val Ser Leu Leu Ala Leu Val
 -15 -10
 gtt cgg gtc atc cta tcc acc gcc atc ctt tgc ccg agt ggg gcc agt 100
 Val Arg Val Ile Leu Ser Thr Ala Ile Leu Cys Pro Ser Gly Ala Ser
 -5 1 5

cgg cgc cag agg agt tct gag gtt gag tgg gga act gat tcg g 143
 Arg Arg Gln Arg Ser Ser Glu Val Glu Trp Gly Thr Asp Ser
 10 15 20

<210> 270
 <211> 79
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 23..79

<221> sig_peptide
 <222> 23..67
 <223> Von Heijne matrix
 score 6
 seq PLFWLILCSGLLC/NK

<221> misc_feature
 <222> 2..3
 <223> n=a, g, c or t
 Oligonucleotide

<400> 270
 tnnngctaattc ttgcttgtac tt atg aat cct tta ttc tgg ttg att ctc tgc 52
 Met Asn Pro Leu Phe Trp Leu Ile Leu Cys
 -15 -10

tct ggg tta tta tgt aac aag tca ttt 79
 Ser Gly Leu Leu Cys Asn Lys Ser Phe
 -5 1

<210> 271
 <211> 121
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 61..120

<221> sig_peptide
 <222> 61..114
 <223> Von Heijne matrix
 score 6
 seq ISIFLSSLSLS/LS

<400> 271
 cttccttaag aagcggtttc tctccctct tttctctctc tcacctgggt ttgtttgtcc 60
 atg aga ggg gct tgg ata agt ata ttt ctt tct tct cta tct ctc tct 108
 Met Arg Gly Ala Trp Ile Ser Ile Phe Leu Ser Ser Leu Ser Leu Ser
 -15 -10 -5

ctc tct ctt ttt t 121
 Leu Ser Leu Phe

1

<210> 272
<211> 292
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 196..291

<221> sig_peptide
<222> 196..267
<223> Von Heijne matrix
score 6
seq LFVLLPHFFLSFL/SP

<400> 272
ctcatggact gtggctgtct tattttatgt ctctaatacc agattatgaa aatcacagaa 60
aaaaggaaaa aatattatct ccaaagagta agttatgaag ccatgttaga aacccatatg 120
acaatatgaa tttcttttat ctgtcaatct caaggtagaa ttcctcatat ttctgataat 180
gccaaatacc atgaa atg tct caa aaa aga ctt gac ttt ata tac cag ttg 231
Met Ser Gln Lys Arg Leu Asp Phe Ile Tyr Gln Leu
-20 -15
ttt gtc ttg ctg cct cac ttc ttc ctt tct ttt ctt tct ccc ttt tat 279
Phe Val Leu Leu Pro His Phe Phe Leu Ser Phe Leu Ser Pro Phe Tyr
-10 -5 1
ctg cac cca tgg g 292
Leu His Pro Trp
5

<210> 273
<211> 158
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 2..157

<221> sig_peptide
<222> 2..100
<223> Von Heijne matrix
score 6
seq LAHFLIGLTVCFG/EG

<400> 273
c atg tac ctg tac ctg ttg tcc att tgt atg tct tct ttg aag aaa tgt 49
Met Tyr Leu Tyr Leu Leu Ser Ile Cys Met Ser Ser Leu Lys Lys Cys
-30 -25 -20
cta ttc aag ttc tta gcc cac ttt tta atc ggg tta aca gtt tgt ttt 97
Leu Phe Lys Phe Leu Ala His Phe Leu Ile Gly Leu Thr Val Cys Phe
-15 -10 -5
ggg gag ggr wgg cta atg agt tat agg agt tct tat tta tta ctt aaa 145

Gly Glu Gly Xaa Leu Met Ser Tyr Arg Ser Ser Tyr Leu Leu Leu Lys
 1 5 10 15
 gga cca ccg ggg g 158
 Gly Pro Pro Gly

<210> 274
 <211> 113
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 31..111

<221> sig_peptide
 <222> 31..96
 <223> Von Heijne matrix
 score 6
 seq CLLVFLLTETWSS/KL

<400> 274
 ccttttgtct ttgatgatgg tgacatacag atg ggg ttt tgg tgt gaa tgt cct 54
 Met Gly Phe Trp Cys Glu Cys Pro
 -20 -15
 ttc tgt ttg tta gtt ttc ctt cta aca gag tgg acc tct agc aaa ctc 102
 Phe Cys Leu Leu Val Phe Leu Leu Thr Glu Trp Thr Ser Ser Lys Leu
 -10 -5 1
 caa aag acg gg 113
 Gln Lys Thr
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<210> 275
 <211> 254
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 182..253

<221> sig_peptide
 <222> 182..247
 <223> Von Heijne matrix
 score 6
 seq VLHLFPLTPASTG/HW

<400> 275
 cccatctgcc tgctcccact aggggtctga gtagcaggca ccgaagaagt gagccacgcc 60
 ctcttcacac accctttgag gaggacaagg gaacttttcc tgtttcagaa agttgtgttg 120
 agaagaatgg caaggctaac agggcaggtg tccgggcgga ggggcggaac tggctgttgg 180
 c atg tgg tgg ggg aga tgc ttc atc cgg gtc ttg cat ttg ttc cct ctg 229
 Met Trp Trp Gly Arg Cys Phe Ile Arg Val Leu His Leu Phe Pro Leu
 -20 -15 -10
 aca cca gcc tcg aca gga cac tgg g 254

Thr Pro Ala Ser Thr Gly His Trp
 -5 1

<210> 276
 <211> 364
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 189..362

<221> sig_peptide
 <222> 189..275
 <223> Von Heijne matrix
 score 6
 seq LFMALPPVLSSHG/SR

<400> 276
 acttgacatt gcttgttggg gtcagagccc gtccctaaac cagggctcca tatgggctgc 60
 ctgtctgccg caacacagcc tagcggggaa acagtagaaa tgccacttct atgtatttat 120
 catattttatt ttgagataat taacgaagac gttaaataaa gccagactgc actgaccctt 180
 ggggcgcc atg cga gac ccc ctc gcg gac atg gta cac agt tat tta tca 230
 Met Arg Asp Pro Leu Ala Asp Met Val His Ser Tyr Leu Ser
 -25 -20
 tcg tct ttg ttc atg gcc ctt cca cca gtg ctg agc tca cat ggc agc 278
 Ser Ser Leu Phe Met Ala Leu Pro Pro Val Leu Ser Ser His Gly Ser
 -15 -10 -5 1
 agg aac ctg aga atc tgg ggg agt cca ttt ggt gga gcg ctg act aag 326
 Arg Asn Leu Arg Ile Trp Gly Ser Pro Phe Gly Gly Ala Leu Thr Lys
 5 10 15
 ggc aaa gca ccc cca acc cca gca caa cca gcc ctg gg 364
 Gly Lys Ala Pro Pro Thr Pro Ala Gln Pro Ala Leu
 20 25

<210> 277
 <211> 130
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 46..129

<221> sig_peptide
 <222> 46..96
 <223> Von Heijne matrix
 score 6
 seq WLCLPCSLCVSQL/LP

<400> 277
 gtctttgcag gmvgtgttgg gctccaacag ggagctgagt ttgtc atg agc agt gcc 57
 Met Ser Ser Ala
 -15

tgg	ctg	tgt	ctg	cca	tgc	tcc	ctg	tgt	gtg	tcc	cag	ctc	ctt	ccc	tct	105
Trp	Leu	Cys	Leu	Pro	Cys	Ser	Leu	Cys	Val	Ser	Gln	Leu	Leu	Pro	Ser	
			-10					-5					1			
tat	tcc	ctg	ttg	atc	cca	gcc	ccg	g								130
Tyr	Ser	Leu	Leu	Ile	Pro	Ala	Pro									
	5					10										

<210> 278
 <211> 184
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 103..183

<221> sig_peptide
 <222> 103..165
 <223> Von Heijne matrix
 score 5.90000009536743
 seq LSLLGPLXPPMRA/CS

<400> 278																	
cattatgttg	acatttctag	ctacaaggcc	agtattttac	aaaataaggc	cttttcctt											60	
aattaaggtt	gtgacagata	aaagtatatt	cccagctgac	tc atg tca	ccc atg											114	
				Met Ser	Pro Met												
				-20													

tgg	gca	ggc	cta	tta	tcc	cta	ctt	ggc	ccg	ctc	wgt	ccg	cct	atg	agg	162
Trp	Ala	Gly	Leu	Leu	Ser	Leu	Leu	Gly	Pro	Leu	Xaa	Pro	Pro	Met	Arg	
	-15					-10					-5					
gct	tgc	tct	gtg	tgc	gta	ctc	t									184
Ala	Cys	Ser	Val	Cys	Val	Leu										
	1				5											

<210> 279
 <211> 265
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 149..265

<221> sig_peptide
 <222> 149..202
 <223> Von Heijne matrix
 score 5.90000009536743
 seq LSIADLLPSSSFA/NP

<400> 279																	
tgagcatttc	ccaacataatc	tggtgagttt	ttactcttt	ttatgatctt	ttttatttct											60	
aggagttcta	tttggttctt	ttccaagtca	gctatgtcat	gttttaawag	tttccwgtcc											120	
tt dgcrtrwc	twttctawct	tgaggttt	atg tct tta	aac gag tta	agc ata											172	
			Met Ser	Leu Asn	Glu Leu	Ser Ile											

-15

ttc atg tgc tta ttg acc ata tgt ata tct tct ttg gag aaa ctt cca	162
Phe Met Cys Leu Leu Thr Ile Cys Ile Ser Ser Leu Glu Lys Leu Pro	
-10 -5 1 5	
ttc ttt ttt ttt ttt	177
Phe Phe Phe Phe Phe	
10	

<210> 282
 <211> 336
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 42..335

<221> sig_peptide
 <222> 42..113
 <223> Von Heijne matrix
 score 5.90000009536743
 seq ATLVGFTVGSVLG/QI

<400> 282
 ttgcctatta ctcttatatc tacagtgtgg tggacctggg c atg tac cag aaa gtc 56
 Met Tyr Gln Lys Val
 -20

aca agt tac tgt cga agt gcc act ttg gtg ggc ttt aca gtg ggc tct	104
Thr Ser Tyr Cys Arg Ser Ala Thr Leu Val Gly Phe Thr Val Gly Ser	
-15 -10 -5	

gtc cta ggg caa atc ctt gtc tca gtg gca ggc tgg tcg ctg ttc agc	152
Val Leu Gly Gln Ile Leu Val Ser Val Ala Gly Trp Ser Leu Phe Ser	
1 5 10	

ctg aat gtc atc tct ctt acc tgt gtt tca gtg gct ttt gct gtg gcc	200
Leu Asn Val Ile Ser Leu Thr Cys Val Ser Val Ala Phe Ala Val Ala	
15 20 25	

tgg ttt tta cct atg cca cag aag agc ctc ttc ttt cac cac att cct	248
Trp Phe Leu Pro Met Pro Gln Lys Ser Leu Phe Phe His His Ile Pro	
30 35 40 45	

tct acc tgc cag aga gtg aat ggc atc aag gta caa aat ggt ggc att	296
Ser Thr Cys Gln Arg Val Asn Gly Ile Lys Val Gln Asn Gly Gly Ile	
50 55 60	

gtt act gac acc cag ctt cta aca cct tcc tgg ctg gga g	336
Val Thr Asp Thr Gln Leu Leu Thr Pro Ser Trp Leu Gly	
65 70	

<210> 283
 <211> 294
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 238..294

<221> sig_peptide
 <222> 238..288
 <223> Von Heijne matrix
 score 5.90000009536743
 seq ALFFLLRIAWLLG/LF

<221> misc_feature
 <222> 227
 <223> n=a, g, c or t
 Oligonucleotide

<400> 283
 acatacacgt caattaatct gattcatccc ataaacaaaa ctaaagataa aaaccatgtg 60
 attatctcaa tatatgcaga aaaggctttc aataaaattc aaggcctctc catattaaaa 120
 actctaaaaa atctgggtat tgaggaarca tagctcaaaa gtgatgrgct gttttgtac 180
 cagtatcatg ctgttttggt tactgtagcc ctgtagtata gtttgangtt gggtaac 237
 atg atg cct cca gct ttg ttc ttt ttg ctg agg att gct tgg cta tta 285
 Met Met Pro Pro Ala Leu Phe Phe Leu Leu Arg Ile Ala Trp Leu Leu
 -15 -10 -5
 ggg ctc ttt 294
 Gly Leu Phe
 1

<210> 284
 <211> 203
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 90..203

<221> sig_peptide
 <222> 90..152
 <223> Von Heijne matrix
 score 5.90000009536743
 seq ALSLWASVSPSWM/CR

<400> 284
 catctttcgg cctagatgga ggaaccgtgt gctggctggg caggctgctg gcagaggtca 60
 ggagggtctt tccctgagcc ctgccatcc atg aac tgt gta act ttg atc cag 113
 Met Asn Cys Val Thr Leu Ile Gln
 -20 -15
 gcc ttg tcc ctc tgg gcc tca gtt tcc cca agc tgg atg tgt cgt ccc 161
 Ala Leu Ser Leu Trp Ala Ser Val Ser Pro Ser Trp Met Cys Arg Pro
 -10 -5 1
 cct gct tca ttc ata atc acc acc acc acc acc acc tgc ggg 203
 Pro Ala Ser Phe Ile Ile Thr Thr Thr Thr Thr Cys Gly
 5 10 15

<210> 285
 <211> 297
 <212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 240..296

<221> sig_peptide

<222> 240..287

<223> Von Heijne matrix

score 5.90000009536743

seq LLSLMARTDLVFC/SP

<221> misc_feature

<222> 107

<223> n=a, g, c or t

Oligonucleotide

<400> 285

aggcattgtc taggctgctg ggcacatgag ctccgggatg cccatgtcct ctggccaggc 60

agacacagac ctggggcagc accagctttc tgatggcagc ctgctcnttc caacagttcc 120

ctaccagaat cctgcctcac tggagcagag gatgccagca tcagccggga accactcctg 180

tgctaaaacc gccttgggtg cctgtggctt gaggtcttga tgcggatgaa gccggagga 239

atg ttg tct ctc ctc agt ctc atg gca agg act gat ctt gtt ttc tgt 287

Met Leu Ser Leu Leu Ser Leu Met Ala Arg Thr Asp Leu Val Phe Cys

-15 -10 -5

tcc cca cgg g 297

Ser Pro Arg

1

<210> 286

<211> 774

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 8..772

<221> sig_peptide

<222> 8..109

<223> Von Heijne matrix

score 5.90000009536743

seq MAVLAPLIALVYS/VP

<221> misc_feature

<222> 486,565

<223> n=a, g, c or t

Oligonucleotide

<400> 286

agtcgtt atg gtg ggg gag gcg ggg cga gac cta cga cgc cgg cga gca 49

Met Val Gly Glu Ala Gly Arg Asp Leu Arg Arg Arg Ala

-30 -25

gtg gcc gtt acg gcc gaa aag atg gcg gtc ttg gca cct cta att gct 97

Val	Ala	Val	Thr	Ala	Glu	Lys	Met	Ala	Val	Leu	Ala	Pro	Leu	Ile	Ala		
-20					-15					-10					-5		
ctc	gtg	tat	tcg	gtg	ccg	cga	ctt	tca	cga	tgg	ctc	gcc	caa	cct	tac	145	
Leu	Val	Tyr	Ser	Val	Pro	Arg	Leu	Ser	Arg	Trp	Leu	Ala	Gln	Pro	Tyr		
			1				5						10				
tac	ctt	ctg	tcg	gcc	ctg	ctc	tct	gct	gcc	ttc	cta	ctc	gtg	agg	aaa	193	
Tyr	Leu	Leu	Ser	Ala	Leu	Leu	Ser	Ala	Ala	Phe	Leu	Leu	Val	Arg	Lys		
		15					20						25				
ctg	ccg	ccg	ctc	tgc	cac	ggg	ctg	ccc	acc	caa	cgc	gaa	gac	ggg	aac	241	
Leu	Pro	Pro	Leu	Cys	His	Gly	Leu	Pro	Thr	Gln	Arg	Glu	Asp	Gly	Asn		
		30				35					40						
ccg	tgt	gac	ttt	gac	tgg	aga	gaa	gtg	gag	atc	ctg	atg	ttt	ctc	agt	289	
Pro	Cys	Asp	Phe	Asp	Trp	Arg	Glu	Val	Glu	Ile	Leu	Met	Phe	Leu	Ser		
45					50					55					60		
gcc	att	gtg	atg	atg	aag	aac	cgc	aga	tcc	atc	act	gtg	gag	caa	cat	337	
Ala	Ile	Val	Met	Met	Lys	Asn	Arg	Arg	Ser	Ile	Thr	Val	Glu	Gln	His		
				65					70						75		
ata	ggc	aac	att	ttc	atg	ttt	agt	aaa	gtg	gcc	aac	aca	att	ctt	ttc	385	
Ile	Gly	Asn	Ile	Phe	Met	Phe	Ser	Lys	Val	Ala	Asn	Thr	Ile	Leu	Phe		
			80					85							90		
ttc	cgc	ttg	gat	att	cgc	atg	ggc	cta	ctt	tac	atc	aca	ctc	tgc	ata	433	
Phe	Arg	Leu	Asp	Ile	Arg	Met	Gly	Leu	Leu	Tyr	Ile	Thr	Leu	Cys	Ile		
		95					100						105				
gtg	ttc	ctg	atg	acg	tgc	aaa	ccc	ccc	cta	tat	atg	ggc	cct	gag	tat	481	
Val	Phe	Leu	Met	Thr	Cys	Lys	Pro	Pro	Leu	Tyr	Met	Gly	Pro	Glu	Tyr		
		110				115						120					
atc	ang	tac	ttc	aat	gat	aaa	acc	att	gat	gag	gaa	cta	gaa	cgg	gac	529	
Ile	Xaa	Tyr	Phe	Asn	Asp	Lys	Thr	Ile	Asp	Glu	Glu	Leu	Glu	Arg	Asp		
					130					135					140		
aag	agg	gtc	act	tgg	att	gtg	gag	ttc	ttt	gcc	aan	tgg	tct	aat	gac	577	
Lys	Arg	Val	Thr	Trp	Ile	Val	Glu	Phe	Phe	Ala	Xaa	Trp	Ser	Asn	Asp		
				145					150						155		
tgc	caa	tca	ttt	gcc	cct	atc	tat	gct	gac	ctc	tcc	ctt	aaa	tac	aac	625	
Cys	Gln	Ser	Phe	Ala	Pro	Ile	Tyr	Ala	Asp	Leu	Ser	Leu	Lys	Tyr	Asn		
			160					165							170		
tgt	aca	ggg	cta	aat	ttt	ggg	aag	gtg	gat	gtt	gga	cgc	tat	act	gat	673	
Cys	Thr	Gly	Leu	Asn	Phe	Gly	Lys	Val	Asp	Val	Gly	Arg	Tyr	Thr	Asp		
		175					180								185		
gtt	agt	acg	cgg	tac	aaa	gtg	agc	aca	tca	ccc	ctc	acc	aag	caa	ctc	721	
Val	Ser	Thr	Arg	Tyr	Lys	Val	Ser	Thr	Ser	Pro	Leu	Thr	Lys	Gln	Leu		
		190				195									200		
cct	acc	ctg	atc	ctg	ttc	caa	ggg	ggc	aag	gag	gca	atg	cgg	cgg	cca	769	
Pro	Thr	Leu	Ile	Leu	Phe	Gln	Gly	Gly	Lys	Glu	Ala	Met	Arg	Arg	Pro		
					210					215					220		
cag	at															774	
Gln																	

<210> 287
 <211> 614
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS

<222> 155..613

<221> sig_peptide

<222> 155..205

<223> Von Heijne matrix

score 5.80000019073486

seq LWLKLLAFGFAFL/DT

<400> 287

aaaaaccgaa tctgacatca tcacctagca gttcatgcag ctagcaagtg gtttgttctt 60
agggtaacag aggaggaaat tgttcctcgt ctgataagac aacagtggag aaaggacgca 120
tgctgtttct tagggacacg gctgacttcc agat atg acc atg tat ttg tgg ctt 175
Met Thr Met Tyr Leu Trp Leu

-15

aaa ctc ttg gca ttt ggc ttt gcc ttt ctg gac aca gaa gta ttt gtg 223
Lys Leu Leu Ala Phe Gly Phe Ala Phe Leu Asp Thr Glu Val Phe Val
-10 -5 1 5

aca ggg caa agc cca aca cct tcc ccc act gga ttg act aca gca aag 271
Thr Gly Gln Ser Pro Thr Pro Ser Pro Thr Gly Leu Thr Thr Ala Lys
10 15 20

atg ccc agt gtt cca ctt tca agt gac ccc tta cct act cac acc act 319
Met Pro Ser Val Pro Leu Ser Ser Asp Pro Leu Pro Thr His Thr Thr
25 30 35

gca ttc tca ccc gca agc acc ttt gaa aga gaa aat gac ttc tca gag 367
Ala Phe Ser Pro Ala Ser Thr Phe Glu Arg Glu Asn Asp Phe Ser Glu
40 45 50

acc aca act tct ctt agt cca gac aat act tcc acc caa gta tcc ccg 415
Thr Thr Thr Ser Leu Ser Pro Asp Asn Thr Ser Thr Gln Val Ser Pro
55 60 65 70

gac tct ttg gat aat gct agt gct ttt ark acc aca ggt gtt tca tca 463
Asp Ser Leu Asp Asn Ala Ser Ala Phe Xaa Thr Thr Gly Val Ser Ser
75 80 85

gta cag acg cct cas ctt ccc acg cac gca gac tcg cag acg ccc tct 511
Val Gln Thr Pro Xaa Leu Pro Thr His Ala Asp Ser Gln Thr Pro Ser
90 95 100

gct gga act gac acg cag aca ttc agc ggc tcc gcg sca atg caa aac 559
Ala Gly Thr Asp Thr Gln Thr Phe Ser Gly Ser Ala Xaa Met Gln Asn
105 110 115

tca acc cta ccc cag gca gca atg cta tct cag atg tcc cag gag aga 607
Ser Thr Leu Pro Gln Ala Ala Met Leu Ser Gln Met Ser Gln Glu Arg
120 125 130

gga gta c 614
Gly Val
135

<210> 288

<211> 251

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 124..249

<221> sig_peptide
 <222> 124..174
 <223> Von Heijne matrix
 score 5.80000019073486
 seq LWLKLLAFGF AFL/DT

<400> 288
 attttttattt actttttacat ttttgattcg tttttacaga gaaaaacttc tacagagata 60
 acaattattt tgcttttcag aaggacgcat gctgtttcct agggacacgg ctgacttcca 120
 gat atg acc atg tat ttg tgg ctt aaa ctc ttg gca ttt ggc ttt gcc 168
 Met Thr Met Tyr Leu Trp Leu Lys Leu Leu Ala Phe Gly Phe Ala
 -15 -10 -5
 ttt ctg gac aca gaa gta ttt gtg aca ggg caa agc cca aca cct tcc 216
 Phe Leu Asp Thr Glu Val Phe Val Thr Gly Gln Ser Pro Thr Pro Ser
 1 5 10
 ccc act ggt gtt tca tca gta cag acg ccc cag gg 251
 Pro Thr Gly Val Ser Ser Val Gln Thr Pro Gln
 15 20 25

<210> 289
 <211> 416
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 155..415

<221> sig_peptide
 <222> 155..205
 <223> Von Heijne matrix
 score 5.80000019073486
 seq LWLKLLAFGF AFL/DT

<400> 289
 aaaaaccgaa tctgacatca tcacctagca gttcatgcag ctagcaagtg gtttgttctt 60
 agggtaacag aggaggaaat tgttcctcgt ctgataagac aacagtggag aaaggacgca 120
 tgctgtttct tagggacacg gctgacttcc agat atg acc atg tat ttg tgg ctt 175
 Met Thr Met Tyr Leu Trp Leu
 -15
 aaa ctc ttg gca ttt ggc ttt gcc ttt ctg gac aca gaa gta ttt gtg 223
 Lys Leu Leu Ala Phe Gly Phe Ala Phe Leu Asp Thr Glu Val Phe Val
 -10 -5 1 5
 aca ggg caa agc cca aca cct tcc ccc act ggt gtt tca tca gta cag 271
 Thr Gly Gln Ser Pro Thr Pro Ser Pro Thr Gly Val Ser Ser Val Gln
 10 15 20
 acg cct cac ctt ccc acg cac gca gac tcg cag acg ccc tct gct gga 319
 Thr Pro His Leu Pro Thr His Ala Asp Ser Gln Thr Pro Ser Ala Gly
 25 30 35
 act gac acg cag aca ttc agc ggc tcc gcg sca atg caa aac tca acc 367
 Thr Asp Thr Gln Thr Phe Ser Gly Ser Ala Xaa Met Gln Asn Ser Thr
 40 45 50
 cta ccc cag gca gca atg cta tct cag atg tcc cag gag aga gga gta c 416
 Leu Pro Gln Ala Ala Met Leu Ser Gln Met Ser Gln Glu Arg Gly Val

55 60 65 70

<210> 290
<211> 309
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 183..308

<221> sig_peptide
<222> 183..290
<223> Von Heijne matrix
score 5.80000019073486
seq LFLLSGTIWIAIC/KP

<400> 290
gaggcctttt ggtcacttag aagaggtgcc aaagatcaag gagaggaaaag tgggtgggcta 60
caaatgtaaa ttctgtgtgg aagtgcaccc aacgctccga gccatctgca atcacctccg 120
wwagcacgtc cagtatggca atgtcccagc tgtgtcagct gctgtgaagg ggctgcgttc 180
tc atg aga gga gcc acc tgg ccc tgg cca tgt tta ccc gcg agg aca 227
Met Arg Gly Ala Thr Trp Pro Trp Pro Cys Leu Pro Ala Arg Thr
-35 -30 -25
agt aca gct gcc agt att gct cgt ttg ttt ctg ctt tca ggc aca att 275
Ser Thr Ala Ala Ser Ile Ala Arg Leu Phe Leu Leu Ser Gly Thr Ile
-20 -15 -10
tgg atc gcc ata tgc aaa ccc acc acg aac ggg g 309
Trp Ile Ala Ile Cys Lys Pro Thr Thr Asn Gly
-5 1 5

<210> 291
<211> 359
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 142..357

<221> sig_peptide
<222> 142..333
<223> Von Heijne matrix
score 5.80000019073486
seq SALLRSLLLPXLX/QI

<221> misc_feature
<222> 282..283
<223> n=a, g, c or t
Oligonucleotide

<400> 291
caagtccaca gcgctgggtg cagtacctcc ggcttcttca ggagtcctatc tggcctgggtg 60
gagttttgcc taagtttcca cggcccshta aggacccaag agcagaaact ggctgctgag 120

```

aaacaggcctt tgcagagcct g atg gga gtc ctc cca gat ctc gta gta gaa      171
                        Met Gly Val Leu Pro Asp Leu Val Val Glu
                        -60                                -55
att ttt ggg gtg aac aaa tgc cgg ctg agc tgg ggt cta gtc ctg gag      219
Ile Phe Gly Val Asn Lys Cys Arg Leu Ser Trp Gly Leu Val Leu Glu
                        -50                                -40
tca cta caa caa ccc ctc atc aac agg cat ttg att tac tgc ctt ggg      267
Ser Leu Gln Gln Pro Leu Ile Asn Arg His Leu Ile Tyr Cys Leu Gly
                        -35                                -25
gac atc atc ctg grn ntc ttg gat ctc agt gct ctg ttg agg agt ctg      315
Asp Ile Ile Leu Xaa Xaa Leu Asp Leu Ser Ala Leu Leu Arg Ser Leu
                        -20                                -10
ctg cta cca sct ctg sct cag ata ccc cag gca act cta aga gg          359
Leu Leu Pro Xaa Leu Xaa Gln Ile Pro Gln Ala Thr Leu Arg
                        -5                                1                                5

```

```

<210> 292
<211> 254
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> 129..254

```

```

<221> sig_peptide
<222> 129..173
<223> Von Heijne matrix
      score 5.80000019073486
      seq ALGFVLLAPRGWG/SL

```

```

<400> 292
gtttttcagc tgcgccattca cttcgctgtg aagatggcgt cgggcagcgg gacaaaaaac      60
ttggactttc gccgaaagtg ggatgtggga aggtgggcag ggaccagatc aaaggagaca      120
gccaggag atg aca gca ctg ggg ttt gtt ctg tta gct cca cgt ggc tgg      170
      Met Thr Ala Leu Gly Phe Val Leu Leu Ala Pro Arg Gly Trp
      -15                                -10                                -5
ggg agc ctc aca gtc atg gtg gaa ggc aag gaa gag caa gtc acg tct      218
Gly Ser Leu Thr Val Met Val Glu Gly Lys Glu Glu Gln Val Thr Ser
      1                                5                                10                                15
tac acg gat ggc agc agg caa aga gac agc aat ttt          254
Tyr Thr Asp Gly Ser Arg Gln Arg Asp Ser Asn Phe
      20                                25

```

```

<210> 293
<211> 414
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> 221..412

```

```

<221> sig_peptide

```

<222> 221..337

<223> Von Heijne matrix

score 5.80000019073486

seq LISFLHTLQVVCS/VI

<400> 293

gtcagagcac atccggtgtt agaagcgctg gtaggccttg gagaggcggg ttaggaagag 60
tgagagactgc tgcacggact ctggaaccat gaacatatit gatcgaaaga tcaactttga 120
tgcgctttta aaattttctc atataacccc gtcaacgcag cagsrcctga agaagatttc 180
attactgtct tcagaaaact catgatgatc ctggccatga atg aaa agg ata aga 235

Met Lys Arg Ile Arg

-35

aga aag aga aga aat gaa gtg acc atc cag cct ttc cca att aga ctt 283

Arg Lys Arg Arg Asn Glu Val Thr Ile Gln Pro Phe Pro Ile Arg Leu

-30

-25

-20

cct ctc ctt cca ccc ctc att tcc ttt ttg cac aca tta cag gtg gtg 331

Pro Leu Leu Pro Pro Leu Ile Ser Phe Leu His Thr Leu Gln Val Val

-15

-10

-5

tgt tct gtg ata atg aaa agc atc aga aaa gct ttt gta ctt tgt ggt 379

Cys Ser Val Ile Met Lys Ser Ile Arg Lys Ala Phe Val Leu Cys Gly

1

5

10

ttc ctc tat ttt gaa ttt ttt gat caa aaa ctg at 414

Phe Leu Tyr Phe Glu Phe Phe Asp Gln Lys Leu

15

20

25

<210> 294

<211> 334

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 156..332

<221> sig_peptide

<222> 156..221

<223> Von Heijne matrix

score 5.80000019073486

seq XVXLFXXVXVXXA/AL

<400> 294

catgtgtttc tcatctttca accaccaaac ttacataaaa ttcattccacc ttccatttct 60

tcctattata gtacaggaaa ggtccttcct gtcaaaggca aaatcactta tgattgtgtc 120

cccatctctc ttgccttttc aaggactttg agcct atg ctg cca ctg ctt cat 173

Met Leu Pro Leu Leu His

-20

tgt ttt ttt ttk gtt kgt ttg ttt kgt ttk gtt ttk gtt twa ama gca 221

Cys Phe Phe Xaa Val Xaa Leu Phe Xaa Xaa Val Xaa Val Xaa Xaa Ala

-15

-10

-5

gct tta ttg aga tat aat yca agt ata cag kgt ggc cgg gca cag kgg 269

Ala Leu Leu Arg Tyr Asn Xaa Ser Ile Gln Xaa Gly Arg Ala Gln Xaa

1

5

10

15

ctc ama cct gwa atc cca gma ctt tgg gag act aag gma ggc aga tta 317

Leu Xaa Pro Xaa Ile Pro Xaa Leu Trp Glu Thr Lys Xaa Gly Arg Leu

20 25 30 334
 ctt gag cct agg aat tt
 Leu Glu Pro Arg Asn
 35

<210> 295
 <211> 375
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 284..373

<221> sig_peptide
 <222> 284..346
 <223> Von Heijne matrix
 score 5.80000019073486
 seq EMCLSQLFLQVEA/AY

<400> 295
 ataacgctac ctgccgagca agccgagtgg agggaggcaa aggccaggct gaggatcagg 60
 gtggcccggg tggcagcggg gaggcgctgc atgctggagg ctgtgctgag tgcccgggtgc 120
 aggtgagccg gtcttgccga gttgtgccga gtgcctgctg cagtctcatt tccagttcct 180
 ccatgacgtg gcaagtgaag acaggaatga aaggratgta aagcagcttt tctctgaaga 240
 gaagaagaga gagagacaca gccaaagaccg aggctggggcc aag atg gtg tct gtg 295
 Met Val Ser Val
 -20
 ttt cga agc gag gag atg tgt ttg tca caa ctg ttt ctc cag gtg gaa 343
 Phe Arg Ser Glu Glu Met Cys Leu Ser Gln Leu Phe Leu Gln Val Glu
 -15 -10 -5
 gct gca tat tgc tgt gtg gct gag ctc gga ga 375
 Ala Ala Tyr Cys Cys Val Ala Glu Leu Gly
 1 5

<210> 296
 <211> 226
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 104..226

<221> sig_peptide
 <222> 104..187
 <223> Von Heijne matrix
 score 5.80000019073486
 seq WWSVASLLSDVAA/WW

<400> 296
 tggattgaaa taaattccta gctccacggt caggctcagta ggctgccatg atgaaatttg 60
 aagaagagtc tgttatgatg tgtaatacca atttctggag ggc atg gct gct ctc 115
 Met Ala Ala Leu

```

                                -25
cga agt act cta aca tgg aca gaa gtc gtg ggc tgg tgg agt gtt gcg      163
Arg Ser Thr Leu Thr Trp Thr Glu Val Val Gly Trp Trp Ser Val Ala
                                -20          -15          -10
tcg ctg ctt agt gat gtg gca gca tgg tgg cca ccg cac tcc acc tca      211
Ser Leu Leu Ser Asp Val Ala Ala Trp Trp Pro Pro His Ser Thr Ser
                                -5          1          5
aca cgg gga ggg gta      226
Thr Arg Gly Gly Val
10

```

```

<210> 297
<211> 232
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> 90..230

```

```

<221> sig_peptide
<222> 90..221
<223> Von Heijne matrix
      score 5.80000019073486
      seq LVCVFTCSLLAFF/SP

```

```

<400> 297
ctgaactttt tatttttcta tttttataac caggagaaag taaacacata cacacacatg      60
gatggagaga gggacagagg gatggacgg atg aat gca ttr gta gat ggg aaa      113
                                Met Asn Ala Leu Val Asp Gly Lys
                                -40
cgg ctt asa krg tgc ata cgc tat ttc gat tct atc tca cta tat tct      161
Arg Leu Xaa Xaa Cys Ile Arg Tyr Phe Asp Ser Ile Ser Leu Tyr Ser
      -35          -30          -25
aag gca agt tta agt tgt tgt tta gtg tgt gtg ttt act tgt tca ttg      209
Lys Ala Ser Leu Ser Cys Cys Leu Val Cys Val Phe Thr Cys Ser Leu
      -20          -15          -10          -5
cta gct ttc ttc agc cca tgc ac      232
Leu Ala Phe Phe Ser Pro Cys
1

```

```

<210> 298
<211> 258
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> 7..258

```

```

<221> sig_peptide
<222> 7..63
<223> Von Heijne matrix
      score 5.80000019073486

```

seq WVFLVAILKGVQC/EL

```

<400> 298
ccaacc atg gag ttt ggg ctt agc tgg gtt ttc ctt gtt gct att ttg      48
      Met Glu Phe Gly Leu Ser Trp Val Phe Leu Val Ala Ile Leu
            -15                      -10
aaa ggt gtc caa tgt gaa ctg cag gtg gtg gag tct ggg gga ggc ttg      96
Lys Gly Val Gln Cys Glu Leu Gln Val Val Glu Ser Gly Gly Gly Leu
-5              1              5              10
gta cag cca ggg cgg tcc ctc aga ctc tcc tgt cga act tct gga ttc      144
Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Arg Thr Ser Gly Phe
            15              20              25
gcc ttt gat gat tat aat ttg agt tgg gtc cgc cag gct cca ggg aag      192
Ala Phe Asp Asp Tyr Asn Leu Ser Trp Val Arg Gln Ala Pro Gly Lys
            30              35              40
ggg ctg gag tgg gta ggt ttc att aga agc aaa cct tat ggt gag aca      240
Gly Leu Glu Trp Val Gly Phe Ile Arg Ser Lys Pro Tyr Gly Glu Thr
            45              50              55
aca acg tac gcc gcg tgg      258
Thr Thr Tyr Ala Ala Trp
60              65

```

```

<210> 299
<211> 139
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> 83..139

```

```

<221> sig_peptide
<222> 83..124
<223> Von Heijne matrix
      score 5.80000019073486
      seq SLFXLXXLRQSFT/XX

```

```

<400> 299
tttgggagct ccagtgttag gcgcatatat atttyagaat tgtgacaatt tcctgttggt      60
ttagtcctyt tatcattata ta atg tcc ctc ttt gwc ctt yyt yyt ttg aga      112
                        Met Ser Leu Phe Xaa Leu Xaa Xaa Leu Arg
                                -10                      -5
cag agt ttc act cht gwt gcc cag gca      139
Gln Ser Phe Thr Xaa Xaa Ala Gln Ala
            1              5

```

```

<210> 300
<211> 286
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> 196..285

```

<221> sig_peptide
 <222> 196..252
 <223> Von Heijne matrix
 score 5.80000019073486
 seq SFYFLASSSLSTS/AS

<221> misc_feature
 <222> 16,286
 <223> n=a, g, c or t
 Oligonucleotide

<400> 300
 asatcgcgct gggganasgc cacgtcgcta tgagtgtgtt tcagtctacc tggattaaac 60
 gtttgcttct cttcgtctac cttgattaa cgtgcacttc gcagtcctcg gttctccata 120
 cccgtgacct ggggatcgct acggacctta aaataccgcg aacasccttc tcgtscctaag 180
 ctggagagca gtggc atg atc tcg gct cac tgc agc ttc tac ttc ctg gcc 231
 Met Ile Ser Ala His Cys Ser Phe Tyr Phe Leu Ala
 -15 -10
 tca agc agt ctt tcc acc tca gcs tct saa cgc act gga att aca gat 279
 Ser Ser Ser Leu Ser Thr Ser Ala Ser Xaa Arg Thr Gly Ile Thr Asp
 -5 1 5
 gtg agc n 286
 Val Ser
 10

<210> 301
 <211> 242
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 113..241

<221> sig_peptide
 <222> 113..184
 <223> Von Heijne matrix
 score 5.69999980926514
 seq CLFVFLYTPCNC/FG

<400> 301
 tgcaatgggt ggtgttttat aatgctctct tccctaataca tgtaatacag gagattttcc 60
 ttttggaact cctgactgaa agcttcttag tttacacaca tgttcctcca gg atg aac 118
 Met Asn
 gct gaa aat aac ttt ttc ggt ttt gtt tgt ttg ttt gtt ttc ctc tat 166
 Ala Glu Asn Asn Phe Phe Gly Phe Val Cys Leu Phe Val Phe Leu Tyr
 -20 -15 -10
 aca acc cct tgc aat tgc ttt ggt tta gaa cac ctt tgg att cta agt 214
 Thr Thr Pro Cys Asn Cys Phe Gly Leu Glu His Leu Trp Ile Leu Ser
 -5 1 5 10
 ttc atg gtt gtt ctg gga gwy acc agg g 242
 Phe Met Val Val Leu Gly Xaa Thr Arg
 15

<210> 302
 <211> 136
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 42..134

<221> sig_peptide
 <222> 42..110
 <223> Von Heijne matrix
 score 5.69999980926514
 seq LPCCCHLLTCVSS/LR

<400> 302
 agtcacagtg acacagcctt ccaaccaggc cgccccctgg c atg acc atg gct gtg 56
 Met Thr Met Ala Val
 -20
 ggt gca gct gmy cam ctc ccc tgc tgc tgc cat ttr ctc acc tgc gtm 104
 Gly Ala Ala Xaa Xaa Leu Pro Cys Cys Cys His Leu Leu Thr Cys Val
 -15 -10 -5
 tcc agc ctt cgc amt gac att tac cca cat gg 136
 Ser Ser Leu Arg Xaa Asp Ile Tyr Pro His
 1 5

<210> 303
 <211> 175
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 73..174

<221> sig_peptide
 <222> 73..147
 <223> Von Heijne matrix
 score 5.69999980926514
 seq SILLAALSRNISP/GQ

<400> 303
 aagaggaagc ggaakdgcct caggtgggcg gtagtgccaa aagcccaggg cgtccgcgca 60
 aaccgaggcg tc atg cgg aga aaa agg cga gaa aga aaa gag agg aag agc 111
 Met Arg Arg Lys Arg Arg Glu Arg Lys Glu Arg Lys Ser
 -25 -20 -15
 atc ctc ctg gcc gcc ctt tcg agg aac ata agt cct ggt cag aca tac 159
 Ile Leu Leu Ala Ala Leu Ser Arg Asn Ile Ser Pro Gly Gln Thr Tyr
 -10 -5 1
 cga aca tcc ccc gcg g 175
 Arg Thr Ser Pro Ala
 5

<210> 304
 <211> 493
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 402..491

<221> sig_peptide
 <222> 402..470
 <223> Von Heijne matrix
 score 5.69999980926514
 seq LELLTSSDPPSLA/SQ

<400> 304
 ttaggtgttc tgatagttaa gtggtagtat catggtctta atttttcctt gaagtggctt 60
 ttgatttgca ttcccttaat gactaattag gttgagcatc ttttcatgta cttactggcc 120
 ttctttggag aaataccttt tccaaatcca atgggttgtc tttttttatt gttgatctta 180
 agggttctta ggtgttctgg gtaccagttt cttgtgagat gtgtgacttg taaatacttt 240
 cttccattct ccatgttgtc tttttattct cttgatggta ttctttgaaa tacaaaartk 300
 tttatatttg acaaagtcca gtttatttat ttatttattg ccattcgtgc ttttggtttt 360
 gataatccat ttttwtgtt tttatttttta tttacttaga g atg ggg tct ccc tat 416
 Met Gly Ser Pro Tyr
 -20
 gtt gcc cac gtt ggt ctt gaa ctc ttg acc tca agt gat cct ccc tcc 464
 Val Ala His Val Gly Leu Glu Leu Leu Thr Ser Ser Asp Pro Pro Ser
 -15 -10 -5
 ttg gcc tcc caa gtg ctg gga ata cat tm 493
 Leu Ala Ser Gln Val Leu Gly Ile His
 1 5

<210> 305
 <211> 214
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 79..213

<221> sig_peptide
 <222> 79..135
 <223> Von Heijne matrix
 score 5.69999980926514
 seq VCWLTTLTLAHSLS/LT

<400> 305
 cacacacgca ccaaatacac acagasaccc tggccctcac tcacgcacav tctctcacac 60
 tcgtggacac acccccag atg cat ctt tac act cat gta tgc tgg ctc act 111
 Met His Leu Tyr Thr His Val Cys Trp Leu Thr
 -15 -10
 ctc aca ctg gca cac tca cac agc ttg acc cac acg cac aca ctc aca 159
 Leu Thr Leu Ala His Ser His Ser Leu Thr His Thr His Thr Leu Thr

	-5		1		5	
ccc agt cac aca cgt aca cac tca cat acg tgt gct tgc cta cac gca						207
Pro Ser His Thr Arg Thr His Ser His Thr Cys Ala Cys Leu His Ala						
10		15		20		
cac aag g						214
His Lys						
25						

<210> 306
 <211> 458
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 306..458

<221> sig_peptide
 <222> 306..350
 <223> Von Heijne matrix
 score 5.69999980926514
 seq LSLTFYHFPLCWG/HQ

<221> misc_feature
 <222> 286,448
 <223> n=a, g, c or t
 Oligonucleotide

<400> 306	
atcagagagc gccggaagcg gtccgagaat gaagcagtgt gatctacat gcattgtctc	60
agaaagaggc gaatgactcc gatgtccagg tcagttcttg gcagggagtc caggagcaac	120
agaggtgatg gcaaagatgg ctcaagtagct tctgagcccc cagcactgat tgagatgtcc	180
tttcccacat catactcctc atttttcttg cagacatcta aggctggatc aaagtctgta	240
gttctcatta cctgttccca cgtgccagcc tccttttctg ttgtgnmmaa gtcaagtttg	300
gtaaa atg agg ctt tcc tta acc ttt tat cat ttc cca ctg tgt tgg gga	350
Met Arg Leu Ser Leu Thr Phe Tyr His Phe Pro Leu Cys Trp Gly	
-15 -10 -5	
cac cag gct gtg ccc acg tgg tgg saa rgc atc att caa cct tgt cac	398
His Gln Ala Val Pro Thr Trp Trp Xaa Xaa Ile Ile Gln Pro Cys His	
1 5 10 15	
tgt gcc ctc tgc act tct gca gaa ggt gtg caa tca cat atc ata agt	446
Cys Ala Leu Cys Thr Ser Ala Glu Gly Val Gln Ser His Ile Ile Ser	
20 25 30	
gna att tac aga	458
Xaa Ile Tyr Arg	
35	

<210> 307
 <211> 328
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS

<222> 87..326

<221> sig_peptide

<222> 87..128

<223> Von Heijne matrix

score 5.69999980926514

seq NVLIIVFVAFAFG/FL

<400> 307

tatcttctct ccagtctaaa gcctcactga acaaactgtc cttgactgtc agtgctcagg 60

gaactgctct gccacccttc tcctca atg aat gtg tta atc att gtt ttt gtt 113

Met Asn Val Leu Ile Ile Val Phe Val

-10

gca ttt gct ttt ggg ttc ytg gtc atg aag tct ttg ctt aag cca atg 161

Ala Phe Ala Phe Gly Phe Leu Val Met Lys Ser Leu Leu Lys Pro Met

-5 1 5 10

tcg aga agg gtt ttt ctg atg tta tct tct agg att ttt atg gtt tca 209

Ser Arg Arg Val Phe Leu Met Leu Ser Ser Arg Ile Phe Met Val Ser

15

20

25

ggc ctt aga ttt aag tcc ttg atc cat ctt gag ttg att ttt gta tat 257

Gly Leu Arg Phe Lys Ser Leu Ile His Leu Glu Leu Ile Phe Val Tyr

30

35

40

aag ttg aga gat gag gat cca gtt tca ttc ttc tac atg tgg ctt gcc 305

Lys Leu Arg Asp Glu Asp Pro Val Ser Phe Phe Tyr Met Trp Leu Ala

45

50

55

aat tat ccc agc acc att tgt tg 328

Asn Tyr Pro Ser Thr Ile Cys

60 65

<210> 308

<211> 380

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 33..380

<221> sig_peptide

<222> 33..92

<223> Von Heijne matrix

score 5.69999980926514

seq LAWALPSLLRLGA/AQ

<221> misc_feature

<222> 326

<223> n=a, g, c or t

Oligonucleotide

<400> 308

agcggctctcc cggccctgc cgccctgcc a ct atg tcc cgc cgc tct atg ctg 53

Met Ser Arg Arg Ser Met Leu

-20

-15

ctt gcc tgg gct ctc ccc agc ctc ctt cga ctc gga gcg gct cag gag 101

```

Leu Ala Trp Ala Leu Pro Ser Leu Leu Arg Leu Gly Ala Ala Gln Glu
      -10                      -5                      1
aca gaa gac ccg gcc tgc tgc agc ccc ata gtg ccc cgg aac gag tgg      149
Thr Glu Asp Pro Ala Cys Cys Ser Pro Ile Val Pro Arg Asn Glu Trp
      5                      10                      15
aag gcc ctg gca tca gag tgc gcc cag cac ctg agc ctg ccc tta cgc      197
Lys Ala Leu Ala Ser Glu Cys Ala Gln His Leu Ser Leu Pro Leu Arg
      20                      25                      30                      35
tat gtg gtg gta tcg cac acg gcg ggc agc agc tgc aac acc scc gcc      245
Tyr Val Val Val Ser His Thr Ala Gly Ser Ser Cys Asn Thr Xaa Ala
      40                      45                      50
tcg tgc cag cag cag gcc cgg aat gtg cag cac tac cac atg aag aca      293
Ser Cys Gln Gln Gln Ala Arg Asn Val Gln His Tyr His Met Lys Thr
      55                      60                      65
ctg ggc tgg tgc gac gtg ggc tac aac tkc ctn gat tgg aga aga cgg      341
Leu Gly Trp Cys Asp Val Gly Tyr Asn Xaa Leu Asp Trp Arg Arg Arg
      70                      75                      80
gct cgt ata cra ggg ccg tgg mtg gaa ctt cac ggg tsc      380
Ala Arg Ile Xaa Gly Pro Trp Xaa Glu Leu His Gly Xaa
      85                      90                      95

```

```

<210> 309
<211> 284
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> 228..284

```

```

<221> sig_peptide
<222> 228..269
<223> Von Heijne matrix
      score 5.69999980926514
      seq VFLFLMISVFAGC/QI

```

```

<400> 309
aaaagaagaa agctgaatca tactcgatga ttattgatca tttgtatata gctcaagccc      60
tcaagtagcc tgctgtaata ttactagtt acaaagaaaa gattcgtttt gtcacagtta      120
catgaaaggt gcttatattt gcaaatatgg agacaaagtt catcttaaaa gattaaaatg      180
agaatctcct aaatgaagca tttggaatat tgattagtat accagaa atg gtt ttt      236
                                   Met Val Phe
ctt ttt ctt atg atc agc gtt ttt gcc ggt tgt caa atc cct tcc ggg      284
Leu Phe Leu Met Ile Ser Val Phe Ala Gly Cys Gln Ile Pro Ser Gly
      -10                      -5                      1                      5

```

```

<210> 310
<211> 357
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> 243..356

```

<221> sig_peptide
 <222> 243..305
 <223> Von Heijne matrix
 score 5.59999990463257
 seq AGLELLASSNSSA/LP

<400> 310
 ttgagatcac ctgaggcaac atagtgaac cctgtatcta gaataaatta gagaaagaaa 60
 aatagtctgg gcatgatggt gtgcacctat agtctccagc tabtcasgag cctgaggcag 120
 gaggtwcact tgagctkagg agttcaagga tgcagtsacc tgtgattgca ccaactgcatt 180
 ccagcttgga caacagagtg agaccctgtc ttaaaattta aattttktgt yttwtggtag 240
 ag atg ggg tct cgc cct gtt tcc gak gct ggt ctc gaa ctc ctg gcc 287
 Met Gly Ser Arg Pro Val Ser Xaa Ala Gly Leu Glu Leu Leu Ala
 -20 -15 -10
 tcg agc aat tct tct gcc ttg ccc ttc caa tgt tct ggg att aca ggc 335
 Ser Ser Asn Ser Ser Ala Leu Pro Phe Gln Cys Ser Gly Ile Thr Gly
 -5 1 5 10
 atg agc crc cac acc cta gcg g 357
 Met Ser Xaa His Thr Leu Ala
 15

<210> 311
 <211> 470
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 413..469

<221> sig_peptide
 <222> 413..451
 <223> Von Heijne matrix
 score 5.59999990463257
 seq MLCHLSLVFLGXG/QF

<221> misc_feature
 <222> 30
 <223> n=a, g, c or t
 Oligonucleotide

<400> 311
 ccgttaacgg gattctggaa tttgttaggn taattgcttt tcaatatcaa gagatctggc 60
 aatcaaattt aataatatca agcttgcttg gtgagcatgg atttataaga tagaatgggt 120
 tgtgggggrg artatagtkc cgaaaaagrk tattgtttcc cataatgcct ggtattgtat 180
 taagtacttt gcatacagta gggcatttca ttgtcccagt gatcctcctg caaagtaggt 240
 acaattatct tcaatttaca aatgaggaaa ccaagctctc ttcaagctga taagatgctg 300
 aactgagatt tgaaccaagt ccctctgccc ctaagagccc ctacccttag ctgctactat 360
 atgctgtacc catctaagct ttgtgaaata rccttggtcc actgcagaga ag atg ttg 418
 Met Leu
 tgt cac cta tct cta gta ttt ctt ggc ktt ggg cag ttc tgg agt caa 466
 Cys His Leu Ser Leu Val Phe Leu Gly Xaa Gly Gln Phe Trp Ser Gln
 -10 -5 1 5

aat g 470
Asn

<210> 312
<211> 187
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 98..187

<221> sig_peptide
<222> 98..148
<223> Von Heijne matrix
score 5.59999990463257
seq FMCLFAICISSNA/KC

<400> 312
aagtttgttt ttgttggtgg tggatgatgt ttcttatatt ctattccata aagtatgaaa 60
tggaggctcc ttgtgatttt taatttgcac ttctgta atg act aat ctt ttc atg 115
Met Thr Asn Leu Phe Met
-15
tgc ttg ttt gcc atc tgt ata tct tct aat gcg aag tgt ctg ttt agt 163
Cys Leu Phe Ala Ile Cys Ile Ser Ser Asn Ala Lys Cys Leu Phe Ser
-10 -5 1 5
ctt ttt cct ttt ttt att gag ggg 187
Leu Phe Pro Phe Phe Ile Glu Gly
10

<210> 313
<211> 237
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 93..236

<221> sig_peptide
<222> 93..173
<223> Von Heijne matrix
score 5.59999990463257
seq CVLFTLLVSTRSG/RS

<221> misc_feature
<222> 111
<223> n=a, g, c or t
Oligonucleotide

<400> 313
ttgcttagga ttttctaaaa gattacataa aatactgttg aaaagatgat tgcatacaaa 60
acataatctg ttcattgtta aacgtatacg aa atg ttg gga tac atc tgg naa 113
Met Leu Gly Tyr Ile Trp Xaa

-25
 caa gac aaa gtc ttt gct aat tgt gtt cta ttt acg ctc tta gtg tct 161
 Gln Asp Lys Val Phe Ala Asn Cys Val Leu Phe Thr Leu Leu Val Ser
 -20 -15 -10 -5
 aca aga tcc ggg aga tcg cgs gcg ggt tgt gcc tgg agg tgg agg gga 209
 Thr Arg Ser Gly Arg Ser Arg Ala Gly Cys Ala Trp Arg Trp Arg Gly
 1 5 10
 aga tgg tca gta gga cag aag ggc hgg g 237
 Arg Trp Ser Val Gly Gln Lys Gly Xaa
 15 20

<210> 314
 <211> 356
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 272..355
 <221> sig_peptide
 <222> 272..316
 <223> Von Heijne matrix
 score 5.59999990463257
 seq LILSLQVCRPATL/DQ

<221> misc_feature
 <222> 275..276
 <223> n=a, g, c or t
 Oligonucleotide

<400> 314
 ggatttgctt tctttttctc caaaagggga ggaaattgaa actgagtggc ccacgatggg 60
 aagaggggaa agcccagggg tacaggaggc ctctgggtga aggcagaggc taacatgggg 120
 ttcggagcga ccttgccgt tggcctgacc atctttgtgc tgtctgtcgt cactatcatc 180
 atctgcttca cctgctcctg ctgctgcctt tacaagacgt gccgccgacc acgtccggtt 240
 gtcaccacca ccacatccac cactgtggtg c atg nnc ctt atc ctc agc ctc 292
 Met Xaa Leu Ile Leu Ser Leu
 -15 -10
 caa gtg tgc cgc cca gct acc ctg gac caa gct acc agg gct acc aca 340
 Gln Val Cys Arg Pro Ala Thr Leu Asp Gln Ala Thr Arg Ala Thr Thr
 -5 1 5
 cca tgc cgc cta cgg g 356
 Pro Cys Arg Leu Arg
 10

<210> 315
 <211> 162
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 40..162

<221> sig_peptide
 <222> 40..150
 <223> Von Heijne matrix
 score 5.59999990463257
 seq VLMLSLPLPPTPQ/QA

<400> 315
 tacatgtgca gaatgtgcag atttgtcaca taggtgtgt atg tgc cac agg cgt 54
 Met Cys His Arg Arg
 -35
 tgg ctg cac cta tca acc cgt cat cta ggt ttt aag ccc cgc atc cat 102
 Trp Leu His Leu Ser Thr Arg His Leu Gly Phe Lys Pro Arg Ile His
 -30 -25 -20
 tac gta ttt gtc tta atg ctg tcc ctc ccc ttg ccc acc ccc caa 150
 Tyr Val Phe Val Leu Met Leu Ser Leu Pro Leu Pro Pro Thr Pro Gln
 -15 -10 -5
 cag gcc ctc ggg 162
 Gln Ala Leu Gly

1
 <210> 316
 <211> 404
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 297..404

<221> sig_peptide
 <222> 297..353
 <223> Von Heijne matrix
 score 5.59999990463257
 seq FVIFPAALLLCWG/GL

<400> 316
 taagctgaaa aagaatataa aaattaaaga gaaattgaaa atctaagtct tgcagtgaga 60
 atgaccagaa atcgtttccc tctctggggg gttcctgttt aatatgaaag tcctcttaac 120
 aagcgtggac agaggaagtt ttaggtttga ttgaacttc atgtacatga catatttcat 180
 ttttttttct tccctcacia atttcaacct aggccacttg tttgcagaga ctgccaaacc 240
 ttccattgct gcttccaaga tactcctgga atctgagatt accttttatc ctcttg atg 299
 Met
 gac cat gtt gtt att ttt gtc att ttc cct gca gct ctt ctg ctt tgc 347
 Asp His Val Val Ile Phe Val Ile Phe Pro Ala Ala Leu Leu Leu Cys
 -15 -10 -5
 tgg gga gga ctc atc ccc cta tgc atc atc tac ccc ccg ata gct gac 395
 Trp Gly Gly Leu Ile Pro Leu Cys Ile Ile Tyr Pro Pro Ile Ala Asp
 1 5 10
 aca gtt ggg 404
 Thr Val Gly
 15

<210> 317

<211> 450
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 359..448

<221> sig_peptide
 <222> 359..433
 <223> Von Heijne matrix
 score 5.59999990463257
 seq LIIILXFDIYSLA/FI

<221> misc_feature
 <222> 323,410
 <223> n=a, g, c or t
 Oligonucleotide

<400> 317
 tatgtctttt gaatttgtga tgtacatatt aacagtagat taagttgaaa taataaaatc 60
 tgtattgttt atgatttatt agttatatga tgagtagaat atagtctatt gtggscmagt 120
 gtgtatatat aacataaaca atacattaac ccaattttgt gtgaaaatta ttttgggacc 180
 tagtagcttt cttggtcaca acctttcaaa caaacaattt ttttttaaata taattttttc 240
 ccttaataaaa gaaaacaatt cctcaatgtg taatagcaaa taccttttaa caggtcatat 300
 atcatcaatg ctttctttga aancgtactg atgcttataa gatgctttac gagtaaag 358
 atg ctt aca aat ctt ttc ttt caa gta gct cat cct ctg atc att att 406
 Met Leu Thr Asn Leu Phe Phe Gln Val Ala His Pro Leu Ile Ile Ile
 -25 -20 -15 -10
 ctg ntg ttt gat atc tac tcc cta gca ttt atc cat gac gtg gg 450
 Leu Xaa Phe Asp Ile Tyr Ser Leu Ala Phe Ile His Asp Val
 -5 1 5

<210> 318
 <211> 395
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 313..393

<221> sig_peptide
 <222> 313..354
 <223> Von Heijne matrix
 score 5.59999990463257
 seq LFGLRGMLPLTQQ/AP

<400> 318
 aatcgaaaac agcaaatacac acaactgtta aaaatatatt vtgtttacaa agccaagcca 60
 aaattttatg ttttctctcc caaactttga tataaacact aacatttttt agcatgtata 120
 aacatcatta ttaaccagtg tcctattaaa actccttttc tatgatagaa tgtctgttrc 180
 ttttaggtgg ataaggccta gatgattggc ctctaccagc atcctcatct ctgtccctga 240
 tgcccagctt carcctcgct cctgyatgct ggaccgcttc agtghagctc tcagacttgc 300

tctgtgtctc ac atg ctg ttt ggc tta cgt gga atg ctc cca ctc acc cag 351
Met Leu Phe Gly Leu Arg Gly Met Leu Pro Leu Thr Gln
-10 -5
caa gct ccc att cct cat tta aga tgt aaa ttg agt gtc acc tc 395
Gln Ala Pro Ile Pro His Leu Arg Cys Lys Leu Ser Val Thr
1 5 10

<210> 319
<211> 257
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 20..256

<221> sig_peptide
<222> 20..82
<223> Von Heijne matrix
score 5.59999990463257
seq ACVYACVCASVSA/CV

<400> 319
catctgtgtg tgcgtgtgt atg cgt gtg tgt atg cgt ctg tgt gca tgt gtg 52
Met Arg Val Cys Met Arg Leu Cys Ala Cys Val
-20 -15
tat gcg tgt gtg tgc gca tca gtg tct gca tgt gtg tat rtg tgt gta 100
Tyr Ala Cys Val Cys Ala Ser Val Ser Ala Cys Val Tyr Xaa Cys Val
-10 -5 1 5
tgt atg tst gtg cgc gcg cat ctg tgt gtg tgc atg tgt gta tgt atg 148
Cys Met Xaa Val Arg Ala His Leu Cys Val Cys Met Cys Val Cys Met
10 15 20
tgt gtg cat ctc tgt gtg tgc atg tgt gta tgt gtg tgt gca tct gtg 196
Cys Val His Leu Cys Val Cys Met Cys Val Cys Val Cys Ala Ser Val
25 30 35
tgt gtg tgc atg tgt gca tgc gtg tgt atg tgt gtg tgc gtg cgt gca 244
Cys Val Cys Met Cys Ala Cys Val Cys Met Cys Val Cys Val Arg Ala
40 45 50
tct gtg tgt gtg c 257
Ser Val Cys Val
55

<210> 320
<211> 325
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 256..324

<221> sig_peptide
<222> 256..318
<223> Von Heijne matrix

score 5.59999990463257
seq LIANLVLFISIAA/LR

```
<400> 320
accacgcctc ctccaagtcc cagcgaaccc gcgtgcaacc tgtccctaaa aaagccaaag      60
cagtcactct ttacctccca ctttccctcc tcccagcctt tggcaaccac taatctactt      120
tccgtgtata tggatttacc tattcaggac atttcatatg tcctttggtg actggcttct      180
ttcactttgc acaatgtttt taaggttcat tcctgtcata gtgtgtgtca gtacgaaccc      240
ctccttaacc atcta atg gtt atc acc tct aat agt tat ctc ata gcc aat      291
                Met Val Ile Thr Ser Asn Ser Tyr Leu Ile Ala Asn
                  -20                      -15                      -10

ctt gtt tta ttt ata tct atc gcc gcc ctc cg g      325
Leu Val Leu Phe Ile Ser Ile Ala Ala Leu Arg
                  -5                      1
```

```
<210> 321
<211> 201
<212> DNA
<213> Homo sapiens
```

```
<220>
<221> CDS
<222> 31..201
```

```
<221> sig_peptide
<222> 31..183
<223> Von Heijne matrix
      score 5.5
      seq LSLHASLVTKAFS/IN
```

```
<400> 321
catcacaaga acccagagtg gaattctggg atg gaa gag ctg gac aga aag tgg      54
                Met Glu Glu Leu Asp Arg Lys Trp
                  -50                      -45

aga gag aag gtc ctc cca gcg gca aag cta att aaa agg aga aac ctg      102
Arg Glu Lys Val Leu Pro Ala Ala Lys Leu Ile Lys Arg Arg Asn Leu
      -40                      -35                      -30

ttt tcc aca tgc act cct caa tat ggy aca cat gct gct ttc ttg tca      150
Phe Ser Thr Cys Thr Pro Gln Tyr Gly Thr His Ala Ala Phe Leu Ser
      -25                      -20                      -15

tta cat gcc tca ctt gtc acc aaa gca ttt tca atc aat tcc tgg gag      198
Leu His Ala Ser Leu Val Thr Lys Ala Phe Ser Ile Asn Ser Trp Glu
      -10                      -5                      1                      5

tgg      201
Trp
```

```
<210> 322
<211> 159
<212> DNA
<213> Homo sapiens
```

```
<220>
<221> CDS
<222> 77..157
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<221> sig_peptide
 <222> 77..151
 <223> Von Heijne matrix
 score 5.5
 seq PLLLCPLSSGSPC/PR

<400> 322
 aacaaaggga cagaatggtc ccagggttcc ttcttcttcc ttccagttaa gagctcagag 60
 tggaagtggg ctgggg atg gtg tgc ggg gcc caa gct ccc agc tcc caa agg 112
 Met Val Ser Gly Ala Gln Ala Pro Ser Ser Gln Arg
 -25 -20 -15
 ccc ctg ctt cta tgc cct ttg agc tca ggt agc ccc tgc ccc cgg gg 159
 Pro Leu Leu Leu Cys Pro Leu Ser Ser Gly Ser Pro Cys Pro Arg
 -10 -5 1

<210> 323
 <211> 420
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 325..420

<221> sig_peptide
 <222> 325..405
 <223> Von Heijne matrix
 score 5.5
 seq SFLPSLLSSFLLS/LP

<221> misc_feature
 <222> 117
 <223> n=a, g, c or t
 Oligonucleotide

<400> 323
 catgcaggat agtaatacgt tagaatcaaa aataaggtta tacttagaaa atattgattt 60
 gcctttttga ttttgcattg gtataatctg gctctgaaat cagtgcacag aagtganctt 120
 cgaaacaagc ctgagcaata gaagtagatg tggaaataac ttcggtttct caaggcaaat 180
 actttgatag gaacaaacaa ccgttttagat atagaagatg tgatacattc ctttaaaaag 240
 aatttgacct tatgtcattg taggcacacc tcatatttca attattcata tagtttttct 300
 tgagcaattg ctggtttaag aata atg tca tgt ctt ttg cgt gct tat atc 351
 Met Ser Cys Leu Leu Arg Ala Tyr Ile
 -25 -20
 att tgg ata ttt cct tcc ttc ctt cct tcc ctc ctt tct tcc ttc ctt 399
 Ile Trp Ile Phe Pro Ser Phe Leu Pro Ser Leu Leu Ser Ser Phe Leu
 -15 -10 -5
 ctt tcc ctc ccc cct tcc ggg 420
 Leu Ser Leu Pro Pro Ser Gly
 1 5

<210> 324
 <211> 210

<212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 9..209

<221> sig_peptide
 <222> 9..116
 <223> Von Heijne matrix
 score 5.5
 seq LHFVYCFLCCAEA/FL

<400> 324
 ctccttat atg ttt cag tta ctg atc ctt tgt cag atg aat agt ttg aaa 50
 Met Phe Gln Leu Leu Ile Leu Cys Gln Met Asn Ser Leu Lys
 -35 -30 -25
 ata ttt tct ccc att ctt gga tgg tct ctt cat ttt gtt tat tgt ttc 98
 Ile Phe Ser Pro Ile Leu Gly Trp Ser Leu His Phe Val Tyr Cys Phe
 -20 -15 -10
 ctt tgc tgt gca gaa gcc ttt tta ctt gat atg atc cca ttt atg caa 146
 Leu Cys Cys Ala Glu Ala Phe Leu Leu Asp Met Ile Pro Phe Met Gln
 -5 1 5 10
 ttt tac ttt ggt tac ctg tgc ttg tgg ggt att act tta aaa atc ttt 194
 Phe Tyr Phe Gly Tyr Leu Cys Leu Trp Gly Ile Thr Leu Lys Ile Phe
 15 20 25
 gcc cag tcc aat tgg g 210
 Ala Gln Ser Asn Trp
 30

<210> 325
 <211> 192
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 31..192

<221> sig_peptide
 <222> 31..174
 <223> Von Heijne matrix
 score 5.5
 seq VCLRLHVLSAVQT/ER

<400> 325
 aggctgctgc agttggcgma tgaggcgacc atg gcc ttg ctg ggt aag cgc tgt 54
 Met Ala Leu Leu Gly Lys Arg Cys
 -45
 gac gtc ccc acm aac ggc tgc gga ccc gac cgc wgg aam wac ggc gwy 102
 Asp Val Pro Thr Asn Gly Cys Gly Pro Asp Arg Xaa Xaa Xaa Gly Xaa
 -40 -35 -30 -25
 aac ccg caa ara cga gat cat cac cag cmt mgt gtc tgc ctt aga ctc 150
 Asn Pro Gln Xaa Arg Asp His His Gln Xaa Xaa Val Cys Leu Arg Leu

-20 -15 -10
 cat gtg ctc agc gct gtc car act gaa cgc cga ggt gat ggg 192
 His Val Leu Ser Ala Val Gln Thr Glu Arg Arg Gly Asp Gly
 -5 1 5

<210> 326
 <211> 181
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 71..181

<221> sig_peptide
 <222> 71..166
 <223> Von Heijne matrix
 score 5.5
 seq TLALLSSDSVATG/SV

<400> 326
 aatttcgctg cctagtgggg cgtacggggc tcttttgaaa gcctgagtta cgatgtattg 60
 agcgcgtcgt atg cgg cca gca cta agg tcc ttc tgg cac tcc tct ggt 109
 Met Arg Pro Ala Leu Arg Ser Phe Trp His Ser Ser Gly
 -30 -25 -20
 gga ccg ccc cca tcg gcc aca ctt gcc ctg ctc tcc agt gat tct gta 157
 Gly Pro Pro Pro Ser Ala Thr Leu Ala Leu Leu Ser Ser Asp Ser Val
 -15 -10 -5
 gct act ggc tcc gta gtc tcg cgg 181
 Ala Thr Gly Ser Val Val Ser Arg
 1 5

<210> 327
 <211> 185
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 39..185

<221> sig_peptide
 <222> 39..116
 <223> Von Heijne matrix
 score 5.5
 seq LFSGWLWVWGSRS/SQ

<221> misc_feature
 <222> 143,145,175
 <223> n=a, g, c or t
 Oligonucleotide

<400> 327
 caaagacgca ctacttagta cagagaggtt ttgaatac atg ctc tgt gca tgc aag 56

1. The first part of the document is a list of references. The references are listed in a vertical column on the left side of the page. The references are:

- 1. The first part of the document is a list of references. The references are listed in a vertical column on the left side of the page. The references are:

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<220>
<221> CDS
<222> 57..209
```

<400> 328
gacttaggts yaggcgactg cccagacaat gactggtccc gcataccgag cagagc atg 59
Met

```
<210> 329
<211> 318
<212> DNA
<213> Homo sapiens
```

```
<221> sig_peptide
<222> 149..286
<223> Von Heijne matrix
```


score 5.5
seq ILLISTLFYSLLS/GS

```
<400> 329
acacttaacc catctgtttt ctctaatacg cgacagattc ctttcagaca ggacaactgt      60
gatatttcag ttcctgattg taaatacctc ctaagcctga agcttctgtt actagccatt      120
gtgrgcttca gktctttcak yckgcaaaa atg ggc ata ata car kct att ctt      172
                Met Gly Ile Ile Gln Xaa Ile Leu
                -45                -40

gcc aca tca agg gat tgt tat tcc ttt aaa aaa aaa cca ata cca aag      220
Ala Thr Ser Arg Asp Cys Tyr Ser Phe Lys Lys Lys Pro Ile Pro Lys
                -35                -30                -25

aag cct aca atg ttg gcc tta gcc aaa att ctg ttg att tca acg ttg      268
Lys Pro Thr Met Leu Ala Leu Ala Lys Ile Leu Leu Ile Ser Thr Leu
                -20                -15                -10

ttt tat tca ctt cta tcg ggg agc cat gga aaa gra aat caa gac gtg      316
Phe Tyr Ser Leu Leu Ser Gly Ser His Gly Lys Xaa Asn Gln Asp Val
                -5                1                5                10

gg                                                                 318
```

<210> 330
<211> 223
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 135..221

<221> sig_peptide
<222> 135..203
<223> Von Heijne matrix
score 5.5
seq LPFVCLLLRNVS/DL

```
<400> 330
aacagtgtgt gagagttccc tttcctccac atcctcgcca gcatctgtta ttgcctgtct      60
ttttgatacg agccttttta acaggggtaa gatgatattc cattgtagtt ttgatttgca      120
ttctctgatg atca atg atg ttg agc acc ttt tca tat gcc tgt ttg cca      170
                Met Met Leu Ser Thr Phe Ser Tyr Ala Cys Leu Pro
                -20                -15

ttt gta tgt ctt ctt ttg aga aat gtc tat tca gat ctt ttg ccc aat      218
Phe Val Cys Leu Leu Leu Arg Asn Val Tyr Ser Asp Leu Leu Pro Asn
                -10                -5                1                5

cgg gg                                                                 223
Arg
```

<210> 331
<211> 362
<212> DNA
<213> Homo sapiens

<220>
<221> CDS

<222> 272..361

<221> sig_peptide

<222> 272..343

<223> Von Heijne matrix

score 5.5

seq LIVVLCISLVII/DD

<400> 331

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aatggacacc taggttgctt ccatactga gctattgtga ataatgctgc aatgaacatg      60
ggagtggaga catctcctaa gcatactgat ttcagttcct ttgggtatat acccagaagt      120
gggatcatgt ggtaatcttg tttttacttt tttgaggaac ctccatacca ttatccatga      180
tggctatagt aatttacatt cataccagca gtgcacaagg gtctcctttt ctgtatacac      240
ttgccaacac ttgttatctt tcattttttt g atg cta gcc att cta aca ggt      292
                                Met Leu Ala Ile Leu Thr Gly
```

-20

```
ggg agg tgg tat ctc ata gtg gtt tta gtt tgc att tcc ttg gtg att      340
Gly Arg Trp Tyr Leu Ile Val Val Leu Val Cys Ile Ser Leu Val Ile
-15 -10 -5
```

```
att gat gat gat gag cac ggg g      362
Ile Asp Asp Asp Glu His Gly
1 5
```

<210> 332

<211> 89

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 34..87

<221> sig_peptide

<222> 34..75

<223> Von Heijne matrix

score 5.5

seq LLPLGLKVLGLQA/RG

<400> 332

```
cccagaccgg tcttgaactc ctggcctcaa ctg atg ctc ctg cct ctg ggt ctc      54
                                Met Leu Leu Pro Leu Gly Leu
                                -10
```

```
aaa gtg ctg gga tta cag gcg aga ggc acc acg ct      89
Lys Val Leu Gly Leu Gln Ala Arg Gly Thr Thr
-5 1
```

<210> 333

<211> 399

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 255..398

<221> sig_peptide
 <222> 255..338
 <223> Von Heijne matrix
 score 5.5
 seq PTLVMWLSPQMA/SS

<400> 333
 ttcaactgcaa ggcggcgga ggagaggttg tgggtgctagt ttctctaagc catccagtgc 60
 catcctcgtc gctgcagcga cacacgctct cgccgccgcc atgactgagc agatgaccct 120
 tcgtggcacc ctcaagggcc acaacggctg ggtaaccag atcgctacta ccccgagtt 180
 cccggacatg atcctctccg cctctcgagg tacggactaa gataagacca tcatcatgtg 240
 gaaactgacc aggg atg aga cca act atg gaa ttc cac agc gtg ctc tgc 290
 Met Arg Pro Thr Met Glu Phe His Ser Val Leu Cys
 -25 -20
 ggg gtc act ccc act ttg tta gtg atg tgg tta tct cct cag atg gcc 338
 Gly Val Thr Pro Thr Leu Leu Val Met Trp Leu Ser Pro Gln Met Ala
 -15 -10 -5
 agt tcg ccc tct cag gct cct ggg atg gaa ccc tgc gcc tct ggg atc 386
 Ser Ser Pro Ser Gln Ala Pro Gly Met Glu Pro Cys Ala Ser Gly Ile
 1 5 10 15
 tca caa cgg gca a 399
 Ser Gln Arg Ala
 20

<210> 334
 <211> 188
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 33..188

<221> sig_peptide
 <222> 33..131
 <223> Von Heijne matrix
 score 5.5
 seq SLCLLTVAVLVLT/FK

<400> 334
 aatgaagggt actagaacac ctgcccattcc at atg gga aaa aaa aaa atc tgg 53
 Met Gly Lys Lys Lys Ile Trp
 -30
 acc cct agc tca tat ccc atg ccc agt cat aaa cat gta tcc cta tgt 101
 Thr Pro Ser Ser Tyr Pro Met Pro Ser His Lys His Val Ser Leu Cys
 -25 -20 -15
 ctt cta acg gtt gca gtt tta gtt ctt aca ttt aag tct tta att cat 149
 Leu Leu Thr Val Ala Val Leu Val Leu Thr Phe Lys Ser Leu Ile His
 -10 -5 1 5
 ttt gag tda att ttt gca tat gag ata ggg gtc cag ggg 188
 Phe Glu Xaa Ile Phe Ala Tyr Glu Ile Gly Val Gln Gly
 10 15

<210> 335
 <211> 115
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 23..115

<221> sig_peptide
 <222> 23..94
 <223> Von Heijne matrix
 score 5.5
 seq CPSLLSPIPSQA/CP

<400> 335
 ccaatacaca tcactcagtg gc atg agc cct gtc ctc tgc ttc cat cgc tgc 52
 Met Ser Pro Val Leu Cys Phe His Arg Cys
 -20 -15
 tcc tgt ccc tcc ctc ctc agc ccc atc tcc cca tcc cag gcc tgt cct 100
 Ser Cys Pro Ser Leu Leu Ser Pro Ile Ser Pro Ser Gln Ala Cys Pro
 -10 -5 1
 gag ccc ctc ctt ggg 115
 Glu Pro Leu Leu Gly
 5

<210> 336
 <211> 300
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 197..298

<221> sig_peptide
 <222> 197..268
 <223> Von Heijne matrix
 score 5.5
 seq IMFVCMVCVCVC/VY

<400> 336
 catgcttggt gtaacgtgtc aaacaataca gaggtgtagg gaaaatacct agtgccaccc 60
 tccactccaa aaccccatgt cgccagagat aaccatttat tcagacagtg agtatctatt 120
 aagtatctat tgctaggctt tggagatagc ataatgaaca aaatggatgt gctctctgcc 180
 cttgtgattt ggacag atg ctt cag tta tct ttt tct gtg ttt ata ttg att 232
 Met Leu Gln Leu Ser Phe Ser Val Phe Ile Leu Ile
 -20 -15
 atg ttt gta tgt atg tgc gtg tgt gtg tgt gtg tat cga ctg 280
 Met Phe Val Cys Met Cys Val Cys Val Cys Val Tyr Arg Leu
 -10 -5 1
 ttt tct tcc tcc tcc ccg gg 300
 Phe Ser Ser Ser Ser Pro
 5 10

<210> 337
 <211> 307
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 5..307

<221> sig_peptide
 <222> 5..277
 <223> Von Heijne matrix
 score 5.5
 seq RVLLGAGIPPVSS/AP

<400> 337
 caca atg aag tcg act gtt tcg tcg agg gaa gtg gcc acc gtt gat aaa 49
 Met Lys Ser Thr Val Ser Ser Arg Glu Val Ala Thr Val Asp Lys
 -90 -85 -80
 atg aaa aga cgc cat gca gaa tac tgt gca cag ggt ctc cag aga ttt 97
 Met Lys Arg Arg His Ala Glu Tyr Cys Ala Gln Gly Leu Gln Arg Phe
 -75 -70 -65
 aaa gcc caa ctt tct caa gat acc ctt ccc cav cat cca cat ctg gag 145
 Lys Ala Gln Leu Ser Gln Asp Thr Leu Pro Xaa His Pro His Leu Glu
 -60 -55 -50 -45
 awa gag aag ggg ctt gaa ggc ttg gag gaa aat gtg cct cta aag gga 193
 Xaa Glu Lys Gly Leu Glu Gly Leu Glu Glu Asn Val Pro Leu Lys Gly
 -40 -35 -30
 gag aaa cct gga gaa ggg ggt cca gag tct cct aag aag aga aga agg 241
 Glu Lys Pro Gly Glu Gly Gly Pro Glu Ser Pro Lys Lys Arg Arg Arg
 -25 -20 -15
 gtg ctt ctc gga gcg ggc atc cca cca gta agc tca gct ccc agg aga 289
 Val Leu Leu Gly Ala Gly Ile Pro Pro Val Ser Ser Ala Pro Arg Arg
 -10 -5 1
 cag agc cag cag gca aca 307
 Gln Ser Gln Gln Ala Thr
 5 10

<210> 338
 <211> 123
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 16..123

<221> sig_peptide
 <222> 16..75
 <223> Von Heijne matrix
 score 5.5
 seq VHLFFFFFFXETGS/RS

<400> 338
 ttaattaaac tgttg atg cac aac agt tgt aga cct gtg cac ctt ttt ttc 51
 Met His Asn Ser Cys Arg Pro Val His Leu Phe Phe
 -20 -15 -10
 ttt ttt ttt yct gag aca ggt tct cgt tct aat ycc tgg ctg gag tsc 99
 Phe Phe Phe Xaa Glu Thr Gly Ser Arg Ser Asn Xaa Trp Leu Glu Xaa
 -5 1 5
 agt ggt gcg atc ata gct aac tcc 123
 Ser Gly Ala Ile Ile Ala Asn Ser
 10 15

<210> 339
 <211> 451
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 318..449
 <221> sig_peptide
 <222> 318..443
 <223> Von Heijne matrix
 score 5.40000009536743
 seq TFRLYLSLPVSA/GP

<221> misc_feature
 <222> 310..311,394
 <223> n=a, g, c or t
 Oligonucleotide

<400> 339
 gtcacaaaag gagcactaag agcctgcttt actttcttcc tcagttgagt cgtggggaca 60
 gcttgaagga gccaacctca attgcagaga gcagccgtca cccagctac cgctcagagc 120
 ccagcttgga accagagagc ttccgttctc ctacctttgg caaaagtitt cacttcgac 180
 cactatccag tgggtcacgc tcttcagcc tcaagtcagc ccagggcaca ggctttgagc 240
 tgggccaagt gcaatccatt cgttcagagg gcaccacctc cacctcctaa taagagcctg 300
 gccaaccagn nacgcaa atg gaa gcc tat ctt aat gac agc ttg ctc aca 350
 Met Glu Ala Tyr Leu Asn Asp Ser Leu Leu Thr
 -40 -35
 cct tca gac agc cct gat ttt gag tca gtg cag gca ggg cct gna gcc 398
 Pro Ser Asp Ser Pro Asp Phe Glu Ser Val Gln Ala Gly Pro Xaa Ala
 -30 -25 -20
 aga ccc acc ttt agg cta tac ctc tcc ctt cct gtc agc cag gct ggc 446
 Arg Pro Thr Phe Arg Leu Tyr Leu Ser Leu Pro Val Ser Gln Ala Gly
 -15 -10 -5 1
 cca gc 451
 Pro

<210> 340
 <211> 304
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 94..303

<221> sig_peptide
 <222> 94..135
 <223> Von Heijne matrix
 score 5.40000009536743
 seq PALGPALLQGSIX/RV

<221> misc_feature
 <222> 244..245
 <223> n=a, g, c or t
 Oligonucleotide

<400> 340
 gcgcagggga gaaacaaggc gccttggagt tcaggtgact cccacacggg tcatgctgtt 60
 gtctcctgat ccagccggcc ctgccaggtg acc atg cct gct ctg ggc cca gct 114
 Met Pro Ala Leu Gly Pro Ala
 -10
 ctt ctc cag ggc tct ctg kgc cgv gtg ggt cct cac cct cca gcs cct 162
 Leu Leu Gln Gly Ser Leu Xaa Arg Val Gly Pro His Pro Pro Ala Pro
 -5 1 5
 tcc acc aac tgc att cac tcc caa tgg cac gta tct gca gca csk ggc 210
 Ser Thr Asn Cys Ile His Ser Gln Trp His Val Ser Ala Ala Xaa Gly
 10 15 20 25
 aag gga ccc cac ctc agg cac cct ctr sct ggg nns tac caa ctt cct 258
 Lys Gly Pro His Leu Arg His Pro Leu Xaa Gly Xaa Tyr Gln Leu Pro
 30 35 40
 gtt cca gct gag ccc tgg gct gca gct gga ggc cac agt gtc cac c 304
 Val Pro Ala Glu Pro Trp Ala Ala Ala Gly Gly His Ser Val His
 45 50 55

<210> 341
 <211> 379
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 315..377

<221> sig_peptide
 <222> 315..371
 <223> Von Heijne matrix
 score 5.40000009536743
 seq LCCSGCVPSLCCS/SY

<400> 341
 gtagccgccc ccgaaacttc cgccgcccgcg tccgcccgcct ccggaactaa acgggggtgag 60
 gtcacattcg gttatctcta acgttggaaa acgatggagc taacacccat tatggagatt 120
 aamcvacttt tcatcaggtt tttaacttaa gtcgtgagga atacaacggt gaacacaaga 180
 ttcattttat tttcatcacc atgggacgta tcctgttggt gagttctctg ggtcagacct 240
 ctgaagactt ctcatagga tcctagtctc wrrgcttgcc ctgaaattac tcgctgctca 300

gggagagagt tgaa atg gtt ggc atc ctc cca ctc tgt tgc tcc ggc tgt 350
Met Val Gly Ile Leu Pro Leu Cys Cys Ser Gly Cys
-15 -10

gtc ccc tcg ctc tgt tgt tcc agc tat gt 379
Val Pro Ser Leu Cys Cys Ser Ser Tyr
-5 1

<210> 342
<211> 289
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 223..288

<221> sig_peptide
<222> 223..264
<223> Von Heijne matrix
score 5.40000009536743
seq AHSILLLASQAGC/LR

<400> 342
gggacccttt tagctatgaa atattttgga ttgcgtaggg tcttgccgag cgcgaaaagt 60
agcgtgggcc aggacagcgg gaggtaagtc gccaaagaaa gggttgggaa ragctcagaa 120
tcggacggct aggaagaaat gaccaaagg agcctgatag cccctattc tgcacgctgt 180
tcctggaaac cgcctttgca aagacagtga gagaaatcta ac atg gct cac tcc 234
Met Ala His Ser

atc ttg ctt cta gcc tcg cag gcc ggc tgt ctt cgc tca ttc ctg ggc 282
Ile Leu Leu Leu Ala Ser Gln Ala Gly Cys Leu Arg Ser Phe Leu Gly
-10 -5 1 5
aat tgg g 289
Asn Trp

<210> 343
<211> 169
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 78..167

<221> sig_peptide
<222> 78..137
<223> Von Heijne matrix
score 5.40000009536743
seq WVFLVAIFKGVHC/EG

<400> 343
agctctggga gaggagcccc cgccctggga ttcccagggtg ttttcatttg gtgatcagca 60
ctgaacacag aagagtc atg acg gag ttt ggg ctg agc tgg gtt ttc ctt 110
Met Thr Glu Phe Gly Leu Ser Trp Val Phe Leu
-20 -15 -10

gtt gct att ttt aaa ggt gtc cac tgt gaa ggt cma att ggt gga gtc 158
Val Ala Ile Phe Lys Gly Val His Cys Glu Gly Xaa Ile Gly Gly Val
-5 1 5

ggg ggg gcg gg 169
Gly Gly Ala
10

<210> 344
<211> 112
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 63..110
<221> sig_peptide
<222> 63..104
<223> Von Heijne matrix
score 5.40000009536743
seq NTVFLLLFPGCFF/FE

<400> 344
tgtgttttct ctgtcccaaa tttaatgcat tggggaagtt tataattaca ggaattccac 60
gc atg aac act gtt ttt ttg ttg ttg ttt ttt ggt tgt ttt ttt ttt 107
Met Asn Thr Val Phe Leu Leu Leu Phe Phe Gly Cys Phe Phe Phe
-10 -5 1
gag ac 112
Glu

<210> 345
<211> 349
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 207..347
<221> sig_peptide
<222> 207..278
<223> Von Heijne matrix
score 5.40000009536743
seq SCCCLSSSSFIAG/RR

<400> 345
tcatcgtcta cgtggacggc agctggagcc cgtggagcaa gtggtcggcc tgtgggctgg 60
actgcacca ctggcggacc gtgagtgtc tgaccagca ccccgcaacg gaggggagga 120
gtgccagggc actgacctg acaccgcaa ctgtaccagt gacctctgtg tacacactgc 180
ttctggccct gaggacgtgg ccctct atg tgg gcc tca tgc ccg tgg ccg tct 233
Met Trp Ala Ser Ser Pro Trp Pro Ser
-20
gcb tgg tcc tgc tgc tgc ttg tcc tca tcc tgc ttt att gcc gga aga 281
Ala Trp Ser Cys Cys Cys Leu Ser Ser Ser Ser Phe Ile Ala Gly Arg


```

aaactctctg gggcccgccc cactcggaag gattactgaa atgagtcatt tccgggacgc 120
cttttttact gttgaatgaa agg atg cta aca cat ggg gct tcc ctg tct tta 173
                        Met Leu Thr His Gly Ala Ser Leu Ser Leu
                        -20                        -15
gtc ata ttt ctg tta aca gtg aag cat tgc ttt aga tac aga gta tac 221
Val Ile Phe Leu Leu Thr Val Lys His Cys Phe Arg Tyr Arg Val Tyr
-10                        -5                        1                        5
aag act tt 229
Lys Thr

```

```

<210> 348
<211> 210
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> 106..210
<221> sig_peptide
<222> 106..171
<223> Von Heijne matrix
      score 5.40000009536743
      seq FWTSIPILPLSSG/RQ

```

```

<400> 348
aaagaatcca gttgagccta tcgggacttt tgacctacag aactgtgaga taaaaaatgg 60
gtgtcgtttt agataacca tggcagcatt ccctcctctg ctgga atg tcg tca gtg 117
                        Met Ser Ser Val
                        -20
gag act gac tgg gga ttc tgg act tcc atc ccc atc ctc cca ctc agc 165
Glu Thr Asp Trp Gly Phe Trp Thr Ser Ile Pro Ile Leu Pro Leu Ser
-15                        -10                        -5
agt ggt agg cag ctc ccc ctc ccc act aga gaa tgg gga atg tgg 210
Ser Gly Arg Gln Leu Pro Leu Pro Thr Arg Glu Trp Gly Met Trp
      1                        5                        10

```

```

<210> 349
<211> 431
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> 184..429
<221> sig_peptide
<222> 184..282
<223> Von Heijne matrix
      score 5.40000009536743
      seq LSAILSMLSLSFS/TT

```

```

<221> misc_feature
<222> 214

```

<223> n=a, g, c or t
Oligonucleotide

<400> 349

```

aggacatcct ctccaatcca ccacacacca cttaccctct ctgctggcaa gaggggacct      60
gattcatcct cagcgtaaac actcattcta cccaactgat tgagacagaa cagaagataa      120
ctgaaacttc tctgccttcc cgctgcaaga agtgaatgag cgatccctct caactgactk      180
raa atg ttt gcc tca ccc agg aga tgg agc tct ncg aag gcc ttc tct      228
    Met Phe Ala Ser Pro Arg Arg Trp Ser Ser Xaa Lys Ala Phe Ser
          -30                      -25                      -20

ggc cag cgg aca ctc cta tct gcc atc ctc agc atg cta tca ctc agc      276
Gly Gln Arg Thr Leu Leu Ser Ala Ile Leu Ser Met Leu Ser Leu Ser
          -15                      -10                      -5

ttc tcc aca aca tcc ctg ctc agc aac tac tgg ttt gtg ggc aca cag      324
Phe Ser Thr Thr Ser Leu Leu Ser Asn Tyr Trp Phe Val Gly Thr Gln
          1                      5                      10

aag gtg ccc aag ccc ctg tgc gag aaa ggt ctg gca gcc aag tgc ttt      372
Lys Val Pro Lys Pro Leu Cys Glu Lys Gly Leu Ala Ala Lys Cys Phe
          15                      20                      25                      30

gac atg cca gtg tcc ctg gat gga gat acc aac aca tcc acc cag gag      420
Asp Met Pro Val Ser Leu Asp Gly Asp Thr Asn Thr Ser Thr Gln Glu
          35                      40                      45

gtg gta mma ta      431
Val Val Xaa

```

<210> 350

<211> 386

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 197..385

<221> sig_peptide

<222> 197..244

<223> Von Heijne matrix

score 5.40000009536743

seq HSVFLCAPALVFP/RP

<400> 350

```

aaagtaaagc ggaggcagcg ggggaagatg gcggcggccg ttccacagcg ggcgtggacc      60
gtggagcagc tgcgcagtga gcagctgccc aagaaggaca ttatcaagtt tctgcaggaa      120
cacggttcag attcgggtacc agaggcgtag gggcggccgg gctgggtgcgg ctgagggacg      180
cctcaccccc ctggag atg ccc ata cat tcc gta ttc ctc tgt gcc ccc gcc      232
    Met Pro Ile His Ser Val Phe Leu Cys Ala Pro Ala
          -15                      -10                      -5

ctc gtc ttc ccg cgg ccg gtg gcc tgg aag gcg gag agg ccc agc ttg      280
Leu Val Phe Pro Arg Pro Val Ala Trp Lys Ala Glu Arg Pro Ser Leu
          1                      5                      10

tgc ttt ggt gcc tcg ctc ccg cct ctc ggg cgt tct cta ctg ggg cag      328
Cys Phe Gly Ala Ser Leu Pro Leu Gly Arg Ser Leu Leu Gly Gln
          15                      20                      25

ggg agc agc ttt att tct tgg ggc aca cag gct gca att gta gag tta      376

```

Gly Ser Ser Phe Ile Ser Trp Gly Thr Gln Ala Ala Ile Val Glu Leu
 30 35 40

kaa cct cat t
 Xaa Pro His
 45

386

<210> 351
 <211> 307
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 68..307

<221> sig_peptide
 <222> 68..253
 <223> Von Heijne matrix
 score 5.30000019073486
 seq LACVFFLSHPLFX/XP

<221> misc_feature
 <222> 279
 <223> n=a, g, c or t
 Oligonucleotide

<400> 351
 ttttactctg taattgttac taattgattt ttgmataggg agcacattcc catggttcaa 60
 aattcaa atg gta tac gat gaa aaa tct ctc tcc tgt tcc cat acc cca 109
 Met Val Tyr Asp Glu Lys Ser Leu Ser Cys Ser His Thr Pro
 -60 -55 -50
 gcc acc cag ttc ctc tcc tgg gat gca tcc agt gtt tac agt ttc tta 157
 Ala Thr Gln Phe Leu Ser Trp Asp Ala Ser Ser Val Tyr Ser Phe Leu
 -45 -40 -35
 tat atc ctc tca gca aga gtt aat gta gac gta dgc agm tac att cgt 205
 Tyr Ile Leu Ser Ala Arg Val Asn Val Asp Val Xaa Xaa Tyr Ile Arg
 -30 -25 -20
 gtg tac ata ctt gcc tgt gtg ttt ttc ctc tca cac ccc ctt ttt aad 253
 Val Tyr Ile Leu Ala Cys Val Phe Phe Leu Ser His Pro Leu Phe Xaa
 -15 -10 -5
 sra cca aat ggt agt gta tat tgt cnm cgt cat tct ccc cct tac ctt 301
 Xaa Pro Asn Gly Ser Val Tyr Cys Xaa Arg His Ser Pro Pro Tyr Leu
 1 5 10 15
 ttt tgc 307
 Phe Cys

<210> 352
 <211> 170
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 56..169

<221> sig_peptide
 <222> 56..163
 <223> Von Heijne matrix
 score 5.30000019073486
 seq VCLLIISLVLISG/LG

<400> 352
 gttctttggt gatacaaaca ctgtattttg agtaatcttt tccctatatt tcgaa atg 58
 Met
 ctg cct tta tca cct act aaa ttc cta aat gtg ttc ttg ggc ctg ttc 106
 Leu Pro Leu Ser Pro Thr Lys Phe Leu Asn Val Phe Leu Gly Leu Phe
 -35 -30 -25 -20
 ctc tat tat ctt caa ttg gta tgt ctg ctt att att tct ttg gtt ttg 154
 Leu Tyr Tyr Leu Gln Leu Val Cys Leu Leu Ile Ile Ser Leu Val Leu
 -15 -10 -5
 ata tct ggg tta ggg g 170
 Ile Ser Gly Leu Gly
 1

<210> 353
 <211> 293
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 149..292

<221> sig_peptide
 <222> 149..235
 <223> Von Heijne matrix
 score 5.30000019073486
 seq LNQTLMLLREVLA/SH

<400> 353
 tttctaattct sbtcaaattt tatcaccata caatcagtggt taktgttgga aatagtgcaa 60
 ctgcattatt gactaccatt gaagaaatgc atttgctaag caaaaaaata ttcttcaatt 120
 agcttgaagt cttcatgcaa gttaaatta atg gac aag gtt gaa ctc cca cca 172
 Met Asp Lys Val Glu Leu Pro Pro
 -25
 cct gat ctt gga cca agt tct gca cta aat cag aca ctc atg ttg ctg 220
 Pro Asp Leu Gly Pro Ser Ser Ala Leu Asn Gln Thr Leu Met Leu Leu
 -20 -15 -10
 cgt gaa gtt tta gca tct cac gat tct tca gtk gta cca tta gat gct 268
 Arg Glu Val Leu Ala Ser His Asp Ser Ser Val Val Pro Leu Asp Ala
 -5 1 5 10
 cgt caa gct gat ttt gtg cag ggg g 293
 Arg Gln Ala Asp Phe Val Gln Gly
 15

<210> 354
 <211> 331
 <212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 148..330

<221> sig_peptide

<222> 148..243

<223> Von Heijne matrix
score 5.30000019073486
seq LVWLWFVVPQTIT/MI

<221> misc_feature

<222> 124

<223> n=a, g, c or t
Oligonucleotide

<400> 354

catttctagc	ttttgdktta	aagtgcacaga	cttgccactc	ttcttttccc	ttgaacactt	60
acaggctgtg	ggagggttat	tagttggctc	aatttcaata	mtgttccttt	cyccagggaa	120
ttgnraggcc	caaggagagg	gagagag	atg ggg gga	aca gct ggt	tgg agc agt	174
			Met Gly Gly Thr Ala Gly Trp Ser Ser			
			-30		-25	
cag aac aca	cac aac att	kga gta	cac cat ctt	gtg tgg	ctg tgg ttc	222
Gln Asn Thr	His Asn Ile	Xaa Val	His His Leu	Val Trp Leu	Trp Phe	
	-20		-15		-10	
gtg gtc ccc	caa aca att	aca atg	ata aca cca	aag atc	act gaa cac	270
Val Val Pro	Gln Thr Ile	Thr Met	Ile Thr Pro	Lys Ile	Thr Glu His	
	-5		1		5	
aga cca sta	ata aca gat	atr dtr	ata atg	aya aca	ttt gaa awa	318
Arg Pro Xaa	Ile Thr Asp	Xaa Xaa	Ile Met	Xaa Thr	Phe Glu Xaa	Leu
10		15		20		25
gga gaa tta	ccc a					331
Gly Glu Leu	Pro					

<210> 355

<211> 93

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 2..91

<221> sig_peptide

<222> 2..55

<223> Von Heijne matrix
score 5.30000019073486
seq ALYLCVCVCVCLI/AR

<400> 355

t atg tgt	ctv agt	gta gct	ttg tat	tta tgt	gtg tgt	gtg tgt	gta tgt	49
Met Cys Leu	Ser Val	Ala Leu	Tyr Leu	Cys Val	Cys Val	Cys Val	Cys	
	-15		-10				-5	

ctg att gca cgg gtg tac ttt tgt att tat gtg tgt gtg tgg tt 93
 Leu Ile Ala Arg Val Tyr Phe Cys Ile Tyr Val Cys Val Trp
 1 5 10

<210> 356
 <211> 178
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 92..178

<221> sig_peptide
 <222> 92..133
 <223> Von Heijne matrix
 score 5.30000019073486
 seq LHLLFGLFPVLWM/FL

<400> 356
 tgacccttgt ccagtcctttt ccaggaaaaa catgccctca agatgttttt ctatcttgag 60
 gaaatgatgg aaatgagata gttccaaggg t atg ctt cac ctt ctt ttt ggc 112
 Met Leu His Leu Leu Phe Gly
 -10
 tta ttt cct gtt ctt tgg atg ttt cta gtg tat ttc ttt ctt tct tct 160
 Leu Phe Pro Val Leu Trp Met Phe Leu Val Tyr Phe Phe Leu Ser Ser
 -5 1 5
 ttt ttt ttt ttt ttt ttt 178
 Phe Phe Phe Phe Phe Phe
 10 15

<210> 357
 <211> 107
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 40..105

<221> sig_peptide
 <222> 40..93
 <223> Von Heijne matrix
 score 5.30000019073486
 seq CVYLFACMCVCA/FF

<221> misc_feature
 <222> 54
 <223> n=a, g, c or t
 Oligonucleotide

<400> 357
 tatatttata taaatatata taaatacaca catatatat atg tat gtg tgt atn 54
 Met Tyr Val Cys Xaa


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agcatttgcm ttcggagggc cagargggca ggcagagctt aattccttgg gcaaggctgg      60
ggctgttgga atgggggtctg gagggcagga gccaccctgt ctgggccaga aaggggcctk    120
ggtgcagggc aggc atg tgg ccc aag arg ggg cta ctg gga ttg ggg ctc      170
                Met Trp Pro Lys Xaa Gly Leu Leu Gly Leu Gly Leu
                -20                -15                -10
cca ctg ctg ccc cct aac cat ccc tcg gta gcc caa ggg aca ctc gtt      218
Pro Leu Leu Pro Pro Asn His Pro Ser Val Ala Gln Gly Thr Leu Val
                -5                1                5
tcc tcc cac tct ggt tct ggc tct gag ggt agg gtg gcg ctc agg agt      266
Ser Ser His Ser Gly Ser Gly Ser Glu Gly Arg Val Ala Leu Arg Ser
                10                15                20
gat gtc cac agc ccc aag aca acc csc caa cg      298
Asp Val His Ser Pro Lys Thr Thr Xaa Gln
25                30

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<210> 360
<211> 460
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> 54..458

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<221> sig_peptide
<222> 54..179
<223> Von Heijne matrix
      score 5.30000019073486
      seq AMAXLFLSAPPQA/EV

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<221> misc_feature
<222> 150,285,328
<223> n=a, g, c or t
      Oligonucleotide

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<400> 360
gaggttgggc tgccgtgctg ctcggcggcg ctgaggccaa atagttgcat cac atg      56
                Met
tat cta atc cga gag tct cat gct tct ggt agc tcc tca gtg acc agc      104
Tyr Leu Ile Arg Glu Ser His Ala Ser Gly Ser Ser Ser Val Thr Ser
-40                -35                -30
tcc tgc tca ctg mcc tca gra agc ccc aac cct cag gca atg gck ncc      152
Ser Cys Ser Leu Xaa Ser Xaa Ser Pro Asn Pro Gln Ala Met Ala Xaa
-25                -20                -15                -10
ttg ttc ctg tct gcc cca ccc cag gcc gag gtg acc ttc gag gac gtg      200
Leu Phe Leu Ser Ala Pro Pro Gln Ala Glu Val Thr Phe Glu Asp Val
                -5                1                5
gct gtg tac ctc tcc cgg gag gaa tgg ggc cgc ctg ggc cct gct cag      248
Ala Val Tyr Leu Ser Arg Glu Glu Trp Gly Arg Leu Gly Pro Ala Gln
                10                15                20
agg ggc bkc tac agg gac gtg atg ctg gag acc tac ngg aac bta gtc      296
Arg Gly Xaa Tyr Arg Asp Val Met Leu Glu Thr Tyr Xaa Asn Xaa Val
                25                30                35
tca ctg gga gta gga cct gca ggc ccc aag cnt gga gtg atc tcg cag      344

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Ser	Leu	Gly	Val	Gly	Pro	Ala	Gly	Pro	Lys	Xaa	Gly	Val	Ile	Ser	Gln	
40					45					50					55	
ttg	gag	cga	ggg	gat	gag	ccc	tgg	gtc	ctg	gat	gtt	cag	ggc	acc	tct	392
Leu	Glu	Arg	Gly	Asp	Glu	Pro	Trp	Val	Leu	Asp	Val	Gln	Gly	Thr	Ser	
			60						65					70		
ggg	aaa	gag	cac	ctg	aag	aag	tca	aca	gcc	cag	ctc	ttg	gga	cca	gaa	440
Gly	Lys	Glu	His	Leu	Lys	Lys	Ser	Thr	Ala	Gln	Leu	Leu	Gly	Pro	Glu	
			75					80					85			
ctg	aag	tac	aag	gag	ttg	ay										460
Leu	Lys	Tyr	Lys	Glu	Leu											
			90													

<210> 361
 <211> 318
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 153..317

<221> sig_peptide
 <222> 153..263
 <223> Von Heijne matrix
 score 5.30000019073486
 seq ALSSLCVSWGTSSTV

<400> 361																
ctcttttccg	gttaacgcgg	cgtagagaagc	catgagcagc	aaagtctctc	gcgacaccct											60
gtacgaggcg	gtgcgggaag	tcctgcacgg	gaaccagcgc	aasgccgcaa	gttcctggag											120
acggtggagt	tgcaggatca	gcttgaagaa	ct atg atc	ccc aga agg	aca agc											173
			Met Ile	Pro Arg Arg	Thr Ser											
			-35													
gct tct cgg	gca ccg tca	gtc ccc caa	aac gca	ggc tta	agt cca	ctc										221
Ala Ser Arg	Ala Pro Ser	Val Pro Gln	Asn Ala	Gly Leu	Ser Pro	Leu										
-30	-25	-20	-15													
ccc gcc cta	agt tct ctg	tgt gtg tcc	tgg ggg acc	agc agc act	gtg											269
Pro Ala Leu	Ser Ser Leu	Cys Val Ser	Trp Gly Thr	Ser Ser Thr	Val											
	-10	-5	1													
acg agg cta	agg ccg tgg	ata tcc ccc	aca tgg aca	tcg agg gcg	cg g											318
Thr Arg Leu	Arg Pro Trp	Ile Ser Pro	Thr Trp Thr	Ser Arg Ala	Arg											
5	10	15														

<210> 362
 <211> 360
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 192..359

<221> sig_peptide
 <222> 192..233

<223> Von Heijne matrix
 score 5.30000019073486
 seq VCIFCFLTSKAFP/NP

<221> misc_feature
 <222> 277
 <223> n=a, g, c or t
 Oligonucleotide

<400> 362
 tattgggttg ttttcttatt atcaaattgt gaaagttctt tacatattct gggtagaact 60
 cctttatcag atacatgttt tgcaaattgt ttctaccatt ctctgtctdh tctttctctt 120
 aatactttca cagtttttca tagcagaaat ttataaatta atgaagccca ctttatactt 180
 ttatttcttt t atg gtt tgc atc ttt tgt ttc tta act tcg aaa gct ttt 230
 Met Val Cys Ile Phe Cys Phe Leu Thr Ser Lys Ala Phe
 -10 -5
 cct aac cct aga tca cag gat ttt ctc tta gat ttc tct agg cat tnt 278
 Pro Asn Pro Arg Ser Gln Asp Phe Leu Leu Asp Phe Ser Arg His Xaa
 1 5 10 15
 ata ggt tta ggt ttc aca ttt agg tcc gca atg cat ttt gaa aac ttc 326
 Ile Gly Leu Gly Phe Thr Phe Arg Ser Ala Met His Phe Glu Asn Phe
 20 25 30
 cgt ctg waa ggt ttg ggt caa gat tcc ctt tgt c 360
 Arg Leu Xaa Gly Leu Gly Gln Asp Ser Leu Cys
 35 40

<210> 363
 <211> 212
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 138..212

<221> sig_peptide
 <222> 138..197
 <223> Von Heijne matrix
 score 5.30000019073486
 seq GFCSVTSSPLASA/GR

<221> misc_feature
 <222> 152
 <223> n=a, g, c or t
 Oligonucleotide

<400> 363
 cacaaaatca aaaackkagt tgacgtatgc cactttccag ttactattga gatatatatg 60
 cgtgtgtgta tatattacat atatatgtta tatatcatat tkatatattt akaaawttat 120
 atmgavcata catatat atg taw atr tat ktn kkt ava ggg ttt tgc tct 170
 Met Xaa Xaa Tyr Xaa Xaa Gly Phe Cys Ser
 -20 -15 -10
 gtc aca agc agt cct ctt gcc tca gca ggt agg act aca cgc 212
 Val Thr Ser Ser Pro Leu Ala Ser Ala Gly Arg Thr Thr Arg

```

-5          1          5

<210> 364
<211> 242
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 127..240

<221> sig_peptide
<222> 127..195
<223> Von Heijne matrix
      score 5.30000019073486
      seq LVPCPLLISVALS/VK

<221> misc_feature
<222> 71,73
<223> n=a, g, c or t
      Oligonucleotide

<400> 364
actttaactt cctggagctc taatttctcc ttctcaggta gaagaatgcc attcactccc      60
aagtggtag nmncagcag ccagtggtag gaagggtcat caagtcagtt gtcagaaacc      120
tcactk atg tca ctg twt ahg cta tgt gac cct gac cta gtt cct tgc      168
      Met Ser Leu Xaa Xaa Leu Cys Asp Pro Asp Leu Val Pro Cys
              -20              -15              -10
cct ctc ttg atc tca gtt gct tta tct gta aaa ttt cac att tkt cag      216
Pro Leu Leu Ile Ser Val Ala Leu Ser Val Lys Phe His Ile Xaa Gln
              -5              1              5
caa gtc aac ctt cca tgt tcc tct ca      242
Gln Val Asn Leu Pro Cys Ser Ser
      10              15

<210> 365
<211> 248
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 7..246

<221> sig_peptide
<222> 7..123
<223> Von Heijne matrix
      score 5.30000019073486
      seq LXPCLTSFSCXGA/SF

<400> 365
tgtaca atg atg atc ctt atc cta att ctt gag cat atc gtc acc kcc      48
      Met Met Ile Leu Ile Leu Ile Leu Glu His Ile Val Thr Xaa
              -35              -30

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aaa aga aac ccc aaa cct gtt aca gtc cct gct ttt ctg csc cct tgc      96
Lys Arg Asn Pro Lys Pro Val Thr Val Pro Ala Phe Leu Xaa Pro Cys
-25                -20                -15                -10
ttg act tct ttc tct tgt kct gga gca tct ttc tct ctk ttw ggt gdg      144
Leu Thr Ser Phe Ser Cys Xaa Gly Ala Ser Phe Ser Leu Xaa Gly Xaa
                -5                1                5
aga agg ggt tgg caa cat ggc agc tgc tgc tcc acc att ccc tta ttt      192
Arg Arg Gly Trp Gln His Gly Ser Cys Cys Ser Thr Ile Pro Leu Phe
                10                15                20
csa act cta aat tcc ctt ggg cag gga ctc att ggc cca gcc tac ata      240
Xaa Thr Leu Asn Ser Leu Gly Gln Gly Leu Ile Gly Pro Ala Tyr Ile
                25                30                35
ggt gcd gg
Gly Ala
40

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<210> 366
<211> 351
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 293..349

<221> sig_peptide
<222> 293..340
<223> Von Heijne matrix
      score 5.30000019073486
      seq HAISILLCIGASS/QG

<221> misc_feature
<222> 36
<223> n=a, g, c or t
      Oligonucleotide

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<400> 366
aaaacatata tccacacaaa aacttgcaca cataknttca tagcagcatt attcatccaa      60
aaagtagagg tactcaaatg actttcaact gataaacaca gatgaacaaa atgtatgtcc      120
aaacagtaga atattattca gctataaaaa agaacagagt acacttagca aactaagaat      180
agaaggaact tcctcaatct gataaaggac atccatgaaa aaccaccac taatgtcata      240
cttaatcatg aaaaaccgaa tgcttttctc ctaagatagg aaaaagacaa gt atg tct      298
                                     Met Ser
                                     -15
act cat gcc atc tct att cta ctt tgt att ggt gct tct agc cag ggc      346
Thr His Ala Ile Ser Ile Leu Leu Cys Ile Gly Ala Ser Ser Gln Gly
                -10                -5                1
agg gg
Arg

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<210> 367
<211> 208
<212> DNA
<213> Homo sapiens

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<220>
 <221> CDS
 <222> 7..207

<221> sig_peptide
 <222> 7..99
 <223> Von Heijne matrix
 score 5.19999980926514
 seq ATVNAASLPPCFG/VK

<400> 367
 gtctcg atg gag gag caa gaa acg gaa gag gtc ggg ggg aga agc agc 48
 Met Glu Glu Gln Glu Thr Glu Glu Val Gly Gly Arg Ser Ser
 -30 -25 -20
 cgg aaa aat gca gcc acc gtc aac gcc gcc tcc ctg cca ccg tgc ttc 96
 Arg Lys Asn Ala Ala Thr Val Asn Ala Ala Ser Leu Pro Pro Cys Phe
 -15 -10 -5
 ggg gta aaa agc tgc cgt tgc cgt cgg tgc agt tgc cgt cgc tgc ctc 144
 Gly Val Lys Ser Cys Arg Cys Arg Arg Cys Ser Cys Arg Arg Cys Leu
 1 5 10 15
 cta tac ttc tct tgg cct cgg gga agg att tcc cca ccg gtg gga caa 192
 Leu Tyr Phe Ser Trp Pro Arg Gly Arg Ile Ser Pro Pro Val Gly Gln
 20 25 30
 tgt gcg ggg agg gga t 208
 Cys Ala Gly Arg Gly
 35

<210> 368
 <211> 446
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 11..445

<221> sig_peptide
 <222> 11..109
 <223> Von Heijne matrix
 score 5.19999980926514
 seq CCCHAGASSGATA/WE

<400> 368
 agaatccaag atg cgc ggg atc car gca aar ggg tct ccg ggc cag agt 49
 Met Arg Gly Ile Gln Ala Lys Gly Ser Pro Gly Gln Ser
 -30 -25
 tcg gcc gst gtt ctg wcg cct tgc tgc tgt cac gcg ggc gct tcg tcc 97
 Ser Ala Xaa Val Leu Xaa Pro Cys Cys Cys His Ala Gly Ala Ser Ser
 -20 -15 -10 -5
 ggg gcg acg gcg tgg gag gag acc ccg cgg tcg cgt tgc cac atc gcc 145
 Gly Ala Thr Ala Trp Glu Glu Thr Pro Arg Ser Arg Cys His Ile Ala
 1 5 10
 gtt kcg agt aca aat aca gct tca agg ggc cgc acc tgg tgc aga gcg 193

<222> 39..131

<221> sig_peptide

<222> 39..77

<223> Von Heijne matrix

score 5.19999980926514

seq MLLAVSLSLVSNC/NF

<400> 370

atcttagagg aaagtctttc agtttttccc cattcagt atg tta tta gct gtg agc 56
Met Leu Leu Ala Val Ser

-10

ctg tcc ctt gtc tct aat tgt aac ttt gta ctc act gac caa ctt ttc 104

Leu Ser Leu Val Ser Asn Cys Asn Phe Val Leu Thr Asp Gln Leu Phe

-5

1

5

cct gcc cct gcs tcc ctc atc ccc gaa g 132

Pro Ala Pro Ala Ser Leu Ile Pro Glu

10

15

<210> 371

<211> 127

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 4..126

<221> sig_peptide

<222> 4..90

<223> Von Heijne matrix

score 5.19999980926514

seq TGVFLFSIIGSFG/FP

<400> 371

tga atg aac caa gat ttc aac cca gaa att gag gct tca cca caa gtg 48

Met Asn Gln Asp Phe Asn Pro Glu Ile Glu Ala Ser Pro Gln Val

-25

-20

-15

aag act ggg gtt ttc ttg ttt tca att att ggg agt ttt gga ttt cca 96

Lys Thr Gly Val Phe Leu Phe Ser Ile Ile Gly Ser Phe Gly Phe Pro

-10

-5

1

gga atg tgc aat tgt aaa aac cca gcc cgg g 127

Gly Met Cys Asn Cys Lys Asn Pro Ala Arg

5

10

<210> 372

<211> 196

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 125..196

<221> sig_peptide
 <222> 125..184
 <223> Von Heijne matrix
 score 5.19999980926514
 seq IVSSLFSWLLSLT/SV

<221> misc_feature
 <222> 119
 <223> n=a, g, c or t
 Oligonucleotide

<400> 372
 taaaaatctt ttatgttcta cccactcctt cctcggtccc tctccccact cctccctccc 60
 cccatcttaa gcccatggca acccctgata tttttactgt ctccatcggt ttgccttbnc 120
 caga atg cca tgt agt tgg agt cat ata gta agt agc ctt ttc agt tgg 169
 Met Pro Cys Ser Trp Ser His Ile Val Ser Ser Leu Phe Ser Trp
 -20 -15 -10
 ctt ctt tca ctt acc agt gtg ccc ggg 196
 Leu Leu Ser Leu Thr Ser Val Pro Gly
 -5 1

<210> 373
 <211> 148
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 56..148

<221> sig_peptide
 <222> 56..139
 <223> Von Heijne matrix
 score 5.19999980926514
 seq PVLSCCLTAGRA/RL

<400> 373
 actttcttca caccaggac gcagggtgcc gctgccggcc acagaaaccc caaga atg 58
 Met
 ttt ttc ttt ggc tat tca gag gac atc tat tgt gtg tca ggc cct gtg 106
 Phe Phe Phe Gly Tyr Ser Glu Asp Ile Tyr Cys Val Ser Gly Pro Val
 -25 -20 -15
 ctg agc tgt tgt tgc ctg aca gca gga aga gcg cgg ctc tgg 148
 Leu Ser Cys Cys Cys Leu Thr Ala Gly Arg Ala Arg Leu Trp
 -10 -5 1

<210> 374
 <211> 200
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 26..199

<221> sig_peptide
 <222> 26..73
 <223> Von Heijne matrix
 score 5.19999980926514
 seq AALICPWSSQVPS/SP

<400> 374
 ctaggaggga ctcaatgctc tttgt atg cct tat gca gcg ctg atc tgt ccc 52
 Met Pro Tyr Ala Ala Leu Ile Cys Pro
 -15 -10
 tgg agt tcc cag gtt ccc agc tcc ccc cct gca agc ctt gaa gcc tcc 100
 Trp Ser Ser Gln Val Pro Ser Ser Pro Pro Ala Ser Leu Glu Ala Ser
 -5 1 5
 agc aac gtc tat ctc cag gag agc agg gca gcc tat gca agt gtt ccg 148
 Ser Asn Val Tyr Leu Gln Glu Ser Arg Ala Ala Tyr Ala Ser Val Pro
 10 15 20 25
 gca gga cca gaa gtg gcc act caa cac acg tcc tca cca gtc acc cct 196
 Ala Gly Pro Glu Val Ala Thr Gln His Thr Ser Ser Pro Val Thr Pro
 30 35 40
 atg g 200
 Met

<210> 375
 <211> 112
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 52..111

<221> sig_peptide
 <222> 52..105
 <223> Von Heijne matrix
 score 5.19999980926514
 seq LTYSLAFLLFKA/GT

<400> 375
 aataaccctt tcacagcact tgcctgtttt taatgaatct aattattcac a atg caa 57
 Met Gln
 ctt tta tat tta aca tac tct tta gct ttc ctg cta ttt atc aag gct 105
 Leu Leu Tyr Leu Thr Tyr Ser Leu Ala Phe Leu Leu Phe Ile Lys Ala
 -15 -10 -5
 ggc acc g 112
 Gly Thr
 1

<210> 376
 <211> 146
 <212> DNA
 <213> Homo sapiens

<220>

<221> CDS
<222> 74..145

<221> sig_peptide
<222> 74..133
<223> Von Heijne matrix
score 5.19999980926514
seq AAAVTSSAAPSRA/RQ

<400> 376
ggctggagcg cgcgcctcct agcggascgg ggcaattgga aggccgcgcc tcaggaaaac 60
agggatgtag tga atg gca ccg agc cgc ccc agg gct gcc gcc gtc acc 109
Met Ala Pro Ser Arg Pro Arg Ala Ala Ala Val Thr
-20 -15 -10
tcc tcg gcg gct ccg agt cgt gcg agg cag ggg gcc c 146
Ser Ser Ala Ala Pro Ser Arg Ala Arg Gln Gly Ala
-5 1

<210> 377
<211> 389
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 218..388

<221> sig_peptide
<222> 218..343
<223> Von Heijne matrix
score 5.19999980926514
seq QHLLSWAXQXGRX/QV

<221> misc_feature
<222> 139
<223> n=a, g, c or t
Oligonucleotide

<400> 377
cattttgtcg gtagaggcag aaggwgaagg tcgggttgta gaagctgggg tggccggcag 60
ctcgcctcatc ggtgttcgtg ggctttgtcg gtccgtgcct cgtctctccc tggaaaggga 120
gggaggcttc gacgtcgrnr aggragmmgc tgccgcgtta gttccgagct tgaagtcact 180
aggacttctc tcaaacttgt gtgctgagga gactcag atg ttg gcc tca gct cct 235
Met Leu Ala Ser Ala Pro
-40
agg ctg aac tca gca gat cgg ccc atg aaa act tct gta ttg aga caa 283
Arg Leu Asn Ser Ala Asp Arg Pro Met Lys Thr Ser Val Leu Arg Gln
-35 -30 -25
agg aag gga tct gtc aga aag caa cac ttg tta tct tgg gct tdg cag 331
Arg Lys Gly Ser Val Arg Lys Gln His Leu Leu Ser Trp Ala Xaa Gln
-20 -15 -10 -5
yaa ggh aga kga cag gta gtg gag atc ctg caa tct gaa aag cag act 379
Xaa Gly Arg Xaa Gln Val Val Glu Ile Leu Gln Ser Glu Lys Gln Thr
1 5 10

daa rgt gac g 389
 Xaa Xaa Asp
 15

<210> 378
 <211> 143
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 2..142

<221> sig_peptide
 <222> 2..115
 <223> Von Heijne matrix
 score 5.19999980926514
 seq LHGSLDAVSQAQG/RP

<400> 378
 a atg tac ccc cta ggc agg gga gag cag ggc cct gct gca ccc aag tcc 49
 Met Tyr Pro Leu Gly Arg Gly Glu Gln Gly Pro Ala Ala Pro Lys Ser
 -35 -30 -25
 tgg ttg ctc ctc ccc acc aca ctg gcc ctc cat gga agc ctt gat gca 97
 Trp Leu Leu Leu Pro Thr Thr Leu Ala Leu His Gly Ser Leu Asp Ala
 -20 -15 -10
 gtg agc cag gcc caa gga cgc ccc ggc cac cct gac gca ccc ccc a 143
 Val Ser Gln Ala Gln Gly Arg Pro Gly His Pro Asp Ala Pro Pro
 -5 1 5

<210> 379
 <211> 261
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 198..260

<221> sig_peptide
 <222> 198..245
 <223> Von Heijne matrix
 score 5.19999980926514
 seq FIAALFTIAETWN/QP

<400> 379
 cagatggtgg tgagggttgta gagaaaaagg aacgcttata cactgttggt gcgagtgtaa 60
 attagtttaa ccattgtgga agatgatatg gcaattccac aaagacctaa agtcagraat 120
 tmcattcaa cccagtaatc ccattactgg gtatatactc aaaggaatat aaattgttgt 180
 gttacaaaga cacatgc atg cgt gtg ttc att gca gca ctg ttc aca ata 230
 Met Arg Val Phe Ile Ala Ala Leu Phe Thr Ile
 -15 -10
 gca gag aca tgg aat caa ccc aaa tgc cca g 261
 Ala Glu Thr Trp Asn Gln Pro Lys Cys Pro

-5

1

5

<210> 380
<211> 228
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 63..227

<221> sig_peptide
<222> 63..152
<223> Von Heijne matrix
score 5.19999980926514
seq LCFLSVHFRLRWG/DS

<400> 380
gggacgtggg aaaatgacta cgcgtcactc gtgatgtcgc gcatccgata ggcccttttc 60
ag atg gca aaa ggc ctg agg gtg aat ctg ggc gag ctg gtt gag tcc 107
Met Ala Lys Gly Leu Arg Val Asn Leu Gly Glu Leu Val Glu Ser
-30 -25 -20
atg cgt ttg tgc ttc ctc tca gtc cac ttt cgc tta cga tgg ggc gac 155
Met Arg Leu Cys Phe Leu Ser Val His Phe Arg Leu Arg Trp Gly Asp
-15 -10 -5 1
tct tgt cca tcg tca cct cac cgg gaa act ttt cct gcc ggg cca gtt 203
Ser Cys Pro Ser Ser Pro His Arg Glu Thr Phe Pro Ala Gly Pro Val
5 10 15
aat ggt ccc ctg tac cac ccc cgg g 228
Asn Gly Pro Leu Tyr His Pro Arg
20 25

<210> 381
<211> 300
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 39..299

<221> sig_peptide
<222> 39..89
<223> Von Heijne matrix
score 5.09999990463257
seq QLLVLFGSQTGTA/QD

<400> 381
agtttttagt ctcagaccag accaccgggc gcgccccg atg ccg agc ccg cag ctt 56
Met Pro Ser Pro Gln Leu
-15
ctg gtg ctc ttc ggc agc cag aca ggc acg gct cag gat gtg tcg gag 104
Leu Val Leu Phe Gly Ser Gln Thr Gly Thr Ala Gln Asp Val Ser Glu
-10 -5 1 5

aga ctg ggt cgc gag gcc cgg ggc cgg cgg ctt ggc tgc cgg gtg cag	152
Arg Leu Gly Arg Glu Ala Arg Gly Arg Arg Leu Gly Cys Arg Val Gln	
10 15 20	
gcc ctg gac tcc tac ccg gtg gtg aat ctg att aac gag ccc ctg gtg	200
Ala Leu Asp Ser Tyr Pro Val Val Asn Leu Ile Asn Glu Pro Leu Val	
25 30 35	
ata ttt gtt tgt gca act ayw ggc caa gga gac ccc cct gac aac atg	248
Ile Phe Val Cys Ala Thr Xaa Gly Gln Gly Asp Pro Pro Asp Asn Met	
40 45 50	
aag aac ttc tgg agg ttt ata ttc cgg aag aac ctg ccc tcc acc gcc	296
Lys Asn Phe Trp Arg Phe Ile Phe Arg Lys Asn Leu Pro Ser Thr Ala	
55 60 65	
cgg g	300
Arg	
70	

<210> 382
 <211> 151
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 8..151

<221> sig_peptide
 <222> 8..130
 <223> Von Heijne matrix
 score 5.09999990463257
 seq SFLFLACIFQXS/XX

<400> 382	
atacata atg tct tcc att ttg ggt gtc tca tcc tca tgg tgg tat tta	49
Met Ser Ser Ile Leu Gly Val Ser Ser Ser Trp Trp Tyr Leu	
-40 -35 -30	
tat tat ggc tat tgt ata ttt gtt aaa aag tgc tct ttt tgc agt ttc	97
Tyr Tyr Gly Tyr Cys Ile Phe Val Lys Lys Cys Ser Phe Cys Ser Phe	
-25 -20 -15	
ctg ttc ctt gcc tgt att ttt caa ggc tkt tck ckt kat wca aac aca	145
Leu Phe Leu Ala Cys Ile Phe Gln Gly Xaa Ser Xaa Xaa Xaa Asn Thr	
-10 -5 1 5	
caa agc	151
Gln Ser	

<210> 383
 <211> 255
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 101..253

<221> sig_peptide

<222> 101..184

<223> Von Heijne matrix
score 5.09999990463257
seq CLCGSAPCLLCRC/CP

<400> 383

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gcgtccggaa gtgtctcgca gatagtaa atctctcgaa aggcgagaaa gaagctgtct 60
ccatcttgtc tgtatccgct gcwcttgtga cgttgtggag atg ggg agc gtc ctg 115
                                         Met Gly Ser Val Leu
                                         -25
ggg ctg tgc tcc atg gcg agc tgg ata cca tgt ttg tgt gga agt gcc 163
Gly Leu Cys Ser Met Ala Ser Trp Ile Pro Cys Leu Cys Gly Ser Ala
-20 -15 -10
ccg tgt ttg cta tgc cga tgc tgt cct agt gga aac aac tcc act gta 211
Pro Cys Leu Leu Cys Arg Cys Cys Pro Ser Gly Asn Asn Ser Thr Val
-5 1 5
act aga ttg atc tat gca ctt ttc ttg ctt gtt gga gta tgg gg 255
Thr Arg Leu Ile Tyr Ala Leu Phe Leu Leu Val Gly Val Trp
10 15 20
```

<210> 384

<211> 456

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 128..454

<221> sig_peptide

<222> 128..265

<223> Von Heijne matrix
score 5.09999990463257
seq IGSCSVMSSGALC/VP

<400> 384

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tacaactttg aaaagccctt cctctggctt gctagacagc tcattggaga ccgtaacttg 60
gaatttggtg ccatgcctgc tcttgccctca ccagagattg tcatggaccc aaatttgcca 120
gtgtagt atg agc wkr wtt agm agg ttg stt aga caa ctg ctc tcc cag 169
      Met Ser Xaa Xaa Xaa Arg Leu Xaa Arg Gln Leu Leu Ser Gln
      -45 -40 -35
rtg agg rwg atg acc tgt gag aat gaa gct gga gcc cag tgt car aag 217
Xaa Arg Xaa Met Thr Cys Glu Asn Glu Ala Gly Ala Gln Cys Gln Lys
-30 -25 -20
tct agt ttt ata ggc agc tgt tct gtg atg tca agt ggt gca ctg tgt 265
Ser Ser Phe Ile Gly Ser Cys Ser Val Met Ser Ser Gly Ala Leu Cys
-15 -10 -5
gtg cca ctt tat tat cta gct aag ggc aac atg tgc tcc atc tgt ggg 313
Val Pro Leu Tyr Tyr Leu Ala Lys Gly Asn Met Cys Ser Ile Cys Gly
1 5 10 15
atg ctg aag gag atg aat ggg ctt tgg agt gaa tgt gac agt tta aaa 361
Met Leu Lys Glu Met Asn Gly Leu Trp Ser Glu Cys Asp Ser Leu Lys
20 25 30
aat acc ttc att gtt tgg rcc tgc ata ttt agc tgt ttg gga atg caa 409
```


Asn	Thr	Phe	Ile	Val	Trp	Xaa	Cys	Ile	Phe	Ser	Cys	Leu	Gly	Met	Gln	
		35					40					45				
ttg	awt	tct	tct	kgr	gtt	tca	aat	gta	aga	ctg	cta	ctg	tca	cat	ca	456
Leu	Xaa	Ser	Ser	Xaa	Val	Ser	Asn	Val	Arg	Leu	Leu	Leu	Ser	His		
	50					55					60					

<210> 385
 <211> 193
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 1..192

<221> sig_peptide
 <222> 1..78
 <223> Von Heijne matrix
 score 5.09999990463257
 seq AFPFVCLTFCVGG/GP

<400>	385																
atg	cct	cat	cca	ctg	gct	acc	tct	gcg	ttt	ctg	cgt	tcc	gcc	ttt	cct		48
Met	Pro	His	Pro	Leu	Ala	Thr	Ser	Ala	Phe	Leu	Arg	Ser	Ala	Phe	Pro		
	-25					-20					-15						
ttt	gtt	tgt	ctc	acg	ttt	tgc	gtg	gga	ggc	ggg	ccc	ggg	att	tca	ggg		96
Phe	Val	Cys	Leu	Thr	Phe	Cys	Val	Gly	Gly	Gly	Pro	Gly	Ile	Ser	Gly		
	-10				-5				1				5				
gtc	tac	cgg	ctc	ctt	atg	gcg	aat	gca	acc	cga	aga	gag	agt	gag	gta		144
Val	Tyr	Arg	Leu	Leu	Met	Ala	Asn	Ala	Thr	Arg	Arg	Glu	Ser	Glu	Val		
			10				15				20						
agc	ctc	cgc	ggg	ttg	ggc	agg	gac	gga	gag	ggg	gcc	cgc	gcg	act	cca	g	193
Ser	Leu	Arg	Gly	Leu	Gly	Arg	Asp	Gly	Glu	Gly	Ala	Arg	Ala	Thr	Pro		
	25					30					35						

<210> 386
 <211> 281
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 199..279

<221> sig_peptide
 <222> 199..267
 <223> Von Heijne matrix
 score 5.09999990463257
 seq SLMVFLNLFFLNC/DP

<400>	386																
tg	ttt	at	agg	ttt	ta	act	ct	tat	gg	tt	aga	at	gg	tt	gt	g	60
ct	g	ta	att	tt	c	agg	aca	cat	t	cc	c	aga	ag	t	ga	aa	120
ac	tt	aga						at	t	g	t	cc	ag	tt	g		180

```

ggttttctgcc agcagtat atg aca gtt ggg ctc cat att tta aga gat tca      231
                        Met Thr Val Gly Leu His Ile Leu Arg Asp Ser
                        -20                                -15
cta atg gtg ttt ctc aac ctt ttt ttt tta aac tgt gac cca cac agg      279
Leu Met Val Phe Leu Asn Leu Phe Phe Leu Asn Cys Asp Pro His Arg
                        -10                                -5                                1
gg                                                                 281

```

```

<210> 387
<211> 111
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> 5..109

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```

<221> sig_peptide
<222> 5..67
<223> Von Heijne matrix
      score 5.09999990463257
      seq MFCVSLLLHHAYP/LP

```

```

<400> 387
cacc atg gta aga tgg gga cat ccc cct atg ttc tgt gtc tct ctc ctg      49
      Met Val Arg Trp Gly His Pro Pro Met Phe Cys Val Ser Leu Leu
      -20                                -15                                -10
ctc cac cat gct tat cct ttg cct tcc acc atg att gta agt ttc cca      97
Leu His His Ala Tyr Pro Leu Pro Ser Thr Met Ile Val Ser Phe Pro
      -5                                1                                5                                10
agg cct ccc ctg gg                                                                 111
Arg Pro Pro Leu

```

```

<210> 388
<211> 374
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> 96..374

```

```

<221> sig_peptide
<222> 96..173
<223> Von Heijne matrix
      score 5.09999990463257
      seq AMVCFGCPGGASS/RC

```

```

<221> misc_feature
<222> 344
<223> n=a, g, c or t
      Oligonucleotide

```

```

<400> 388

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ttttggccgc catgttttcg tcgcagtaac tgccttggtg tcagtagtca ttgccagttt 60
 cgggcgttct ggacaattgg gatgctgcag agttc atg gct ggg gct gct cgt 113
 Met Ala Gly Ala Ala Arg

-25
 tgg gtg gga caa kaa tcc tct gca atg gtt tgt ttt ggc tgc cca gga 161
 Trp Val Gly Gln Xaa Ser Ser Ala Met Val Cys Phe Gly Cys Pro Gly
 -20 -15 -10 -5

ggg ggc tca agt cgc tgc cgc tcc cct cgt ggg cgt cag gcc tca aga 209
 Gly Ala Ser Ser Arg Cys Arg Ser Pro Arg Gly Arg Gln Ala Ser Arg
 1 5 10

gtt ccc cgc cta gaa aat gga gct cag cga gtc gtg cgt acc atg gtg 257
 Val Pro Arg Leu Glu Asn Gly Ala Gln Arg Val Val Arg Thr Met Val
 15 20 25

cac ctg gtt ttg cag cct aag cgg gtc act tta gtg cat cct cct cgc 305
 His Leu Val Leu Gln Pro Lys Arg Val Thr Leu Val His Pro Pro Arg
 30 35 40

gga ttg gag cct gtt tgc acc cct ata gcm vga atg arn ccc aag tca 353
 Gly Leu Glu Pro Val Cys Thr Pro Ile Ala Xaa Met Xaa Pro Lys Ser
 45 50 55 60

cac ggg ctc aga agt tct ttg 374
 His Gly Leu Arg Ser Ser Leu
 65

<210> 389
 <211> 192
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 52..192

<221> sig_peptide
 <222> 52..153
 <223> Von Heijne matrix
 score 5.09999990463257
 seq PXLLSXLHGLLYG/SP

<400> 389
 ggcagacttc aaccaggctg tgggaggaga gctcagtggg gcacagagaa g atg ggt 57
 Met Gly

gtt gtc agt ggg ggt gtt ggt gac ttg acc aca aaa acc caa gag aat 105
 Val Val Ser Gly Gly Val Gly Asp Leu Thr Thr Lys Thr Gln Glu Asn
 -30 -25 -20

ggg ctc tta cca gvc cty ctc tcc wkc ctk cac gga ctg ctc tat ggc 153
 Gly Leu Leu Pro Xaa Leu Leu Ser Xaa Leu His Gly Leu Leu Tyr Gly
 -15 -10 -5

agc cct gat gca gar ctc acg ggc ccg gat ccc tgg gat 192
 Ser Pro Asp Ala Glu Leu Thr Gly Pro Asp Pro Trp Asp
 1 5 10

<210> 390
 <211> 371
 <212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 321..371

<221> sig_peptide

<222> 321..365

<223> Von Heijne matrix

score 5.09999990463257

seq FLSXTCVLSCXRS/LS

<400> 390

tctgttcagg	ttttgtattt	gttcatagta	taatcttggt	ttgtagggtg	tgtgtatctg	60
ggaagaaact	ttacaatctc	taacaggcct	ggaaggtcta	atctataaaa	gtatttcatt	120
gaccttgaag	aaggtcaatt	atttatataa	gaaaataaac	tcaacatttt	atccataaaa	180
aatgtaattc	cggaatttat	gtagtaaaaa	ttataacact	gataacataa	aaagtgtctat	240
taatccttaa	gaaagagtta	ccttttcttt	tctatcttca	tcacagctag	cccagtccta	300
gtctatttca	ttagcttcct	atg ggc ttc ctc tca	ckt aca tgc gtg ctc tct			353
		Met Gly Phe Leu Ser Xaa Thr Cys Val Leu Ser				
		-15	-10	-5		
tgc dtg cgc tgc ctc tct						371
Cys Xaa Arg Ser Leu Ser						
1						

<210> 391

<211> 328

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 184..327

<221> sig_peptide

<222> 184..300

<223> Von Heijne matrix

score 5

seq LVCFFNSVSFLFG/VS

<400> 391

ccgttatgtg	ttcagctcaa	ttagattaat	taccttcctc	accaggagtc	acaatgcttt	60
gcagtttatc	tgcggttaact	aaatgttagt	tttgtaagta	aaaggtactg	ttattgacct	120
cgaaagggct	atagttcctt	tgaacttaca	gagaagagtt	ccaaacaact	atttctaacc	180
aag atg gaa tat ggg tca gca aaa ttg tct tca ggt aga gtt ttc tac						228
Met Glu Tyr Gly Ser Ala Lys Leu Ser Ser Gly Arg Val Phe Tyr						
	-35		-30		-25	
ttg cca aga gac ttt ggc att gag agg aga gtt ctt gtt tgt ttt ttt						276
Leu Pro Arg Asp Phe Gly Ile Glu Arg Arg Val Leu Val Cys Phe Phe						
	-20		-15		-10	
aac tct gta tca ttt ctg ttt ggt gtc tct ara aaa aaa tcc gra caa						324
Asn Ser Val Ser Phe Leu Phe Gly Val Ser Xaa Lys Lys Ser Xaa Gln						
	-5	1		5		
tgg g						328

Trp

<210> 392
<211> 303
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 252..302

<221> sig_peptide
<222> 252..290
<223> Von Heijne matrix
score 5
seq MLSGLVLNSWALA/YQ

<400> 392
tgacctgta gcagttatct ttgttaaact ccttcatttc ttattttaaa taattaatta 60
attaatttag agacaggggc tcactatgtc acccaggctg tagtgcagtg gtgcaatcat 120
ggctcactgt agccttgacc tcccaggctc aagcaatctt cctacctcag cctctcaggc 180
agctgggact acagaccac agcactacgc ctgacttatg attttatttt ttgtggagac 240
agggtcttac t atg ttg tct ggg ctt gtc tta aac tct tgg gcc tta gcc 290
Met Leu Ser Gly Leu Val Leu Asn Ser Trp Ala Leu Ala
-10 -5
tac caa cta gct g 303
Tyr Gln Leu Ala
1

<210> 393
<211> 366
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 298..366

<221> sig_peptide
<222> 298..345
<223> Von Heijne matrix
score 5
seq VFFXGXSIIILVLG/ST

<221> misc_feature
<222> 265
<223> n=a, g, c or t
Oligonucleotide

<400> 393
tttttccccg cccctgagac cctgcagcac catctgtcat ggcggtctggg ctgtttggtt 60
tgagcgctcg ccgtcttttg gcggcagcgg cgacgcgagg gctcccggcc gccgcgctcc 120
gctgggaatc tagcttctcc argamytgtg gtcgccccgt ccgctgtggc gggaaagcgg 180
tccccagaac cgaccacacc gtggcaagag gaccacagaac ccgaggacga aaacttgat 240

gagaagaasc cagactccca tggknatgac aaggaccccg ttttggacgt ctggaac 297
atg cga ctt gtc ttc ttc ktw ggc gks tcc atc atc ctg gtc ctt ggc 345
Met Arg Leu Val Phe Phe Xaa Gly Xaa Ser Ile Ile Leu Val Leu Gly
-15 -10 -5
agc acc ttt gkg gcc tat ctg 366
Ser Thr Phe Xaa Ala Tyr Leu
1 5

<210> 394
<211> 126
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 21..125

<221> sig_peptide
<222> 21..68
<223> Von Heijne matrix
score 5
seq SDFLLFVSLSL/PF

<400> 394
agcttggcat ataggctcaa atg tta tca tca gat ttt ttt ctc ctc ttt gtc 53
Met Leu Ser Ser Asp Phe Phe Leu Leu Phe Val
-15 -10
tct tta tct tta tct cca ttt cct ttt ttt ctt ttt cct ccc ctc ttt 101
Ser Leu Ser Leu Ser Pro Phe Pro Phe Phe Leu Phe Pro Pro Leu Phe
-5 1 5 10
tcc tgc ttt ctc tta ccc acc cgg g 126
Ser Cys Phe Leu Leu Pro Thr Arg
15

<210> 395
<211> 329
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 154..327

<221> sig_peptide
<222> 154..195
<223> Von Heijne matrix
score 5
seq FIAALFTVAKIWN/QP

<400> 395
tgaaaatgta aattagtga gttattatgg magtcagtat ggaacttcct caaaaaacta 60
acaataaaac tcccatatga tccagcaatc ctaccactgr atatitatcc aaaggaaagg 120
aagtcggtat atttaacagg catctgcacc ccc atg ttt att gca gca cta ttc 174
Met Phe Ile Ala Ala Leu Phe

score 5
seq LSLFVFFWLVGFS/FF

<221> misc_feature
<222> 284..285
<223> n=a, g, c or t
Oligonucleotide

<400> 397
ttgtgaactc ttctattatt attaagtgtt gtcaattgtc agcatccata ttctattccg 60
atgatgaata gaagcattat atttcagcat caaaatgcag ttggggtcgt aatgagcatc 120
attagggacc tta atg gga gtc aga act gta tgt cat ttt att cag gtt 169
Met Gly Val Arg Thr Val Cys His Phe Ile Gln Val
-25 -20 -15
ttt cta agt tta ttt gtg ttt ttt tgg tta gtt ggt ttt tct ttt ttc 217
Phe Leu Ser Leu Phe Val Phe Phe Trp Leu Val Gly Phe Ser Phe Phe
-10 -5 1
ttt ttt tta cdb ttt tct acc aag cag gtg aga gtw gaa cag cat tgt 265
Phe Phe Leu Xaa Phe Ser Thr Lys Gln Val Arg Val Glu Gln His Cys
5 10 15
gat ttt aaa agt aca cca nnd gta gag tct tcc agt acc gtt ggc cat 313
Asp Phe Lys Ser Thr Pro Xaa Val Glu Ser Ser Ser Thr Val Gly His
20 25 30
gcc 316
Ala
35

<210> 398
<211> 251
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 63..251

<221> sig_peptide
<222> 63..143
<223> Von Heijne matrix
score 5
seq LSCFYLLAIVSNA/VM

<400> 398
atgttgtagc ttctgtcata atttccttcc cttttaaggc tgaataattt tccattgtgt 60
at atg tac cat att ttg ttc atc cat tca ttc att gat aga tac ttg 107
Met Tyr His Ile Leu Phe Ile His Ser Phe Ile Asp Arg Tyr Leu
-25 -20 -15
agt tgc ttc tac ctt ttg gca att gtg agt aat gct gtt atg aac atg 155
Ser Cys Phe Tyr Leu Leu Ala Ile Val Ser Asn Ala Val Met Asn Met
-10 -5 1
ggg gta caa atg tct gtt ttg agt cct tgt ttt gct ttc gtg cat tct 203
Gly Val Gln Met Ser Val Leu Ser Pro Cys Phe Ala Phe Val His Ser
5 10 15 20
att aaa aat gtt aag gtt ctt tgc ttt tta ctt ttt ttt ctc ttt ggg 251

Ile Lys Asn Val Lys Val Leu Cys Phe Leu Leu Phe Phe Leu Phe Gly
 25 30 35

<210> 399
 <211> 120
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 10..120

<221> sig_peptide
 <222> 10..75
 <223> Von Heijne matrix
 score 5
 seq VQWLLVYSPSCAA/TI

<400> 399
 tcattttacc atg cag ttc acc gtt tta atg tgt cca gtt cag tgg ttg tta 51
 Met Gln Phe Thr Val Leu Met Cys Pro Val Gln Trp Leu Leu
 -20 -15 -10
 gtg tat tca ccc agt tgt gca gcc acc atc aca gtc aat ttt aaa aca 99
 Val Tyr Ser Pro Ser Cys Ala Ala Thr Ile Thr Val Asn Phe Lys Thr
 -5 1 5
 ttt tca tca ccc caa acc ggg 120
 Phe Ser Ser Pro Gln Thr Gly
 10 15

<210> 400
 <211> 463
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 342..461

<221> sig_peptide
 <222> 342..452
 <223> Von Heijne matrix
 score 5
 seq VSCLSAGLRVCCS/QR

<221> misc_feature
 <222> 246,260
 <223> n=a, g, c or t
 Oligonucleotide

<400> 400
 ctctgtcccc gcggctgggt ctctgtctgct ccggttcctg ggctcctaata tcttgggtcca 60
 gcttcttcca ggcacatcct ctctctgccc ctccgtccat tttggagccg gagatgggtgg 120
 gctkggggcc gcccagtag tgagacagtg gaagtaaacc ccatctgccg tccccgtgcg 180
 tagagaaaaa cggtgaccgc gaggtctggg aggagagttg cctctgagga agaagggcac 240

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agaganccaa aattagtttn gaaagcatcc tgatttgggtg cccgaggcct ggaaagaaat 300
ggcggctggg gtgcggcgga ggtaggggag gaaaacgttg g atg aga agg gcc tgg 356
                                   Met Arg Arg Ala Trp
                                   -35
act cag gaa agg gaa ccg cgt ccg tgt gag ccc gct gag cgc gca gac 404
Thr Gln Glu Arg Glu Pro Arg Pro Cys Glu Pro Ala Glu Arg Ala Asp
-30 -25 -20
cct gcc cct gtc tcc tgt ctg tct gca ggt ctg cgc gtc tgt tgt tcc 452
Pro Ala Pro Val Ser Cys Leu Ser Ala Gly Leu Arg Val Cys Cys Ser
-15 -10 -5
cag cgc tct gc 463
Gln Arg Ser
1

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<210> 401
 <211> 206
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 94..204

<221> sig_peptide
 <222> 94..168
 <223> Von Heijne matrix
 score 4.90000009536743
 seq DFFICLLAICVSS/FE

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<400> 401
tactgtttat tgattctttg attatggcca ttcttacagg agtaagggtg tatcacactg 60
tggttttgat ttgcatttcc ctgatcatta gtg atg ttg cat ttg att tgc att 114
                                   Met Leu His Leu Ile Cys Ile
                                   -25 -20
tcc ctg atc gtt aat gat ttt ttc ata tgt ttg ttg gcc att tgc gta 162
Ser Leu Ile Val Asn Asp Phe Phe Ile Cys Leu Leu Ala Ile Cys Val
-15 -10 -5
tct tct ttt gag aat tgt cta ttt atg tcc tta gcc cac agt gg 206
Ser Ser Phe Glu Asn Cys Leu Phe Met Ser Leu Ala His Ser
1 5 10

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<210> 402
 <211> 330
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 42..329

<221> sig_peptide
 <222> 42..230
 <223> Von Heijne matrix
 score 4.90000009536743

seq VTSLANLIPPVKA/XP

<400> 402

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acagggctcc actgcagtta ggagccggtg agtccgggtg g atg agg tca gag cgc      56
                               Met Arg Ser Glu Arg
                               -60
ccc atg gtg tgg tgc tgc ctc ttt gtc cgt tcg cag cga aaa cgg aaa      104
Pro Met Val Trp Cys Cys Leu Phe Val Arg Ser Gln Arg Lys Arg Lys
                               -55                               -50                               -45
cag agc acc caa gat gaa gat gct gtt agc ctt tgc agt ctc gac ata      152
Gln Ser Thr Gln Asp Glu Asp Ala Val Ser Leu Cys Ser Leu Asp Ile
                               -40                               -35                               -30
agt gag cct agt aat aaa cgg gtc aaa ccc ctt tcc cga gtc acg tcg      200
Ser Glu Pro Ser Asn Lys Arg Val Lys Pro Leu Ser Arg Val Thr Ser
                               -25                               -20                               -15
cta gca aac ctc atc ccg ccc gtg aag gcc ayg cca tta aag cgc ttc      248
Leu Ala Asn Leu Ile Pro Pro Val Lys Ala Xaa Pro Leu Lys Arg Phe
                               -10                               -5                               1                               5
agt caa acc ctg cag cgc tcc att agc ttc cgc agt gag agt cgc cct      296
Ser Gln Thr Leu Gln Arg Ser Ile Ser Phe Arg Ser Glu Ser Arg Pro
                               10                               15                               20
gac atc ctc gcc ccc cga ccc tgg tcc aga aat g      330
Asp Ile Leu Ala Pro Arg Pro Trp Ser Arg Asn
                               25                               30
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<210> 403

<211> 311

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 168..311

<221> sig_peptide

<222> 168..227

<223> Von Heijne matrix

score 4.90000009536743

seq CILISTAFPSLLT/QI

<400> 403

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tgagcagatg gtgccaggat ttaaacctat gtttatcaga tgcagatgac ccaaacagtg      60
gcttatctgt tggtaat ttt tat ttagatc aagttaaaca taaatgactt tgcattactc      120
tttggtcact ttttcctagt catttcaa at agtctgtctt atttctc atg gtt ttt      176
                               Met Val Phe
                               -20
tgg aca aaa ttt tgt att tta att agt aca gca ttt cct tct tta ttg      224
Trp Thr Lys Phe Cys Ile Leu Ile Ser Thr Ala Phe Pro Ser Leu Leu
                               -15                               -10                               -5
aca cag att att ttc cct aaa tct att aca ttt gct ttc cag ttt ttc      272
Thr Gln Ile Ile Phe Pro Lys Ser Ile Thr Phe Ala Phe Gln Phe Phe
                               1                               5                               10                               15
tgg aac agg gaa aaa caa aaa aca aaa aca cca act ggg      311
Trp Asn Arg Glu Lys Gln Lys Thr Lys Thr Pro Thr Gly
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20

25

<210> 404
 <211> 274
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 80..274

<221> sig_peptide
 <222> 80..190
 <223> Von Heijne matrix
 score 4.90000009536743
 seq MLIMLGIFNVHS/AV

<400> 404
 ccctgcgagg gcatcctggg ctttctccca ccgctttccg agcccgcttg cacctcggcg 60
 atccccgact cccttcttt atg gcg tcg ctc ctg tgc tgt ggg ccg aag ctg 112
 Met Ala Ser Leu Leu Cys Cys Gly Pro Lys Leu
 -35 -30
 gcc gcc tgc ggc atc gtc ctc agc gcc tgg gga gtg atc atg ttg ata 160
 Ala Ala Cys Gly Ile Val Leu Ser Ala Trp Gly Val Ile Met Leu Ile
 -25 -20 -15
 atg ctc gga ata ttt ttc aat gtc cat tcc gct gtg ttg att gag gac 208
 Met Leu Gly Ile Phe Phe Asn Val His Ser Ala Val Leu Ile Glu Asp
 -10 -5 1 5
 gtt ccc ttc acg gag aaa gat ttt gag aat ggc ccc cag aac ata tac 256
 Val Pro Phe Thr Glu Lys Asp Phe Glu Asn Gly Pro Gln Asn Ile Tyr
 10 15 20
 aac ctt tac gag cat ggg 274
 Asn Leu Tyr Glu His Gly
 25

<210> 405
 <211> 153
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 69..152

<221> sig_peptide
 <222> 69..116
 <223> Von Heijne matrix
 score 4.90000009536743
 seq SALLLEXLQXAIP/RX

<400> 405
 tttcccctgc cctgtcctct cattccccctt cttctggagc atttcatcca cagaccctt 60
 gcccaaga atg tct gtc tca gct ctg ctt cta gag mtc ctc caa gmt gcc 110
 Met Ser Val Ser Ala Leu Leu Leu Glu Xaa Leu Gln Xaa Ala

	-15		-10		-5	
atc	cct	cg	g	mam	acc	tca
Ile	Pro	Arg	Xaa	Thr	Ser	Gly
	1				5	
						10

<210> 406
 <211> 206
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 57..206

<221> sig_peptide
 <222> 57..173
 <223> Von Heijne matrix
 score 4.90000009536743
 seq VIAIVSFTTLCSS/LY

<400> 406	
aaataaaaaa	tattaaaaaa
taatctcatc	tttgatttta
gatttagggg	gtgtgc atg
	Met
cag gct tgt tat atg ggt atg tgg tat act gcc gag gct tgg ggt acg	107
Gln Ala Cys Tyr Met Gly Met Trp Tyr Thr Ala Glu Ala Trp Gly Thr	
	-35 -30 -25
att gag tcc ctc acc cag gta gtg agc gta atc gca ata gtt agt ttt	155
Ile Glu Ser Leu Thr Gln Val Val Ser Val Ile Ala Ile Val Ser Phe	
	-20 -15 -10
aca acc ctg tgc tcc tct ctg tat tcc ccc caa gta gtc ccc agt gtt	203
Thr Thr Leu Cys Ser Ser Leu Tyr Ser Pro Gln Val Val Pro Ser Val	
	-5 1 5 10
ggg	206
Gly	

<210> 407
 <211> 479
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 277..477

<221> sig_peptide
 <222> 277..462
 <223> Von Heijne matrix
 score 4.90000009536743
 seq PLAACPLLLPIFS/HA

<221> misc_feature
 <222> 22
 <223> n=a, g, c or t
 Oligonucleotide

<400> 407
aatggattga gatggggaag anaaaaagcc ccaaattcat gaaatgtagc tgckacagtc 60
cccacctcct tagctgtccc caaaacctaa gcaggtaatc ataacttcca ttctgtgctc 120
accttacctc tgctggcacc tttttggaca gggttctcta cttggcgagg tgacccaaat 180
cttcattcct gcagggtctg agtcctmrgc cgctgcgata gtttgaacat tgtttgtccc 240
cacmraaact catcttgagg cttgggtcccc actgta atg atg ttg aga ggt ggc 294
Met Met Leu Arg Gly Gly

-60
ggg aca ttt aag grg tgt ttg agt cat gag gga tcc agc ttc acg aag 342
Gly Thr Phe Lys Xaa Cys Leu Ser His Glu Gly Ser Ser Phe Thr Lys
-55 -50 -45

gga tta gcg cag gag tgc gtg agt rct tct tgt ggg act cga ttg att 390
Gly Leu Ala Gln Glu Cys Val Ser Xaa Ser Cys Gly Thr Arg Leu Ile
-40 -35 -30 -25

act gca gtw gcc agt kgt tac aaa gca agg ctg cct ctg gcc gcg tgc 438
Thr Ala Val Ala Ser Xaa Tyr Lys Ala Arg Leu Pro Leu Ala Ala Cys
-20 -15 -10

ccd ctt ctg ctt cct att ttc tcc cat gct aga agc agc ac 479
Pro Leu Leu Leu Pro Ile Phe Ser His Ala Arg Ser Ser
-5 1 5

<210> 408
<211> 289
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 84..287

<221> sig_peptide
<222> 84..203
<223> Von Heijne matrix
score 4.90000009536743
seq SLKICGLVFGILA/LT

<400> 408
agccgactca cttgcaactc cacctcagca gtggtctctc agtcctctca aagcaaggaa 60
agagtactgt gtgctgagag acc atg gca aag aat cct cca gag aat tgt gaa 113
Met Ala Lys Asn Pro Pro Glu Asn Cys Glu
-40 -35

gac tgt cac att cta aat gca gaa gct ttt aaa tcc aag aaa ata tgt 161
Asp Cys His Ile Leu Asn Ala Glu Ala Phe Lys Ser Lys Lys Ile Cys
-30 -25 -20 -15

aaa tca ctt aag att tgt gga ctg gtg ttt ggt atc ctg gcc cta act 209
Lys Ser Leu Lys Ile Cys Gly Leu Val Phe Gly Ile Leu Ala Leu Thr
-10 -5 1

cta att gtc ctg ttt tgg ggg agc aag cac ttc tgg ccg gag gta ccc 257
Leu Ile Val Leu Phe Trp Gly Ser Lys His Phe Trp Pro Glu Val Pro
5 10 15

aaa aaa gcc tat gac atg gag cac act acg gg 289
Lys Lys Ala Tyr Asp Met Glu His Thr Thr
20 25

<210> 409
 <211> 341
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 94..339

<221> sig_peptide
 <222> 94..216
 <223> Von Heijne matrix
 score 4.90000009536743
 seq LSLVSHAPGEALA/RA

<400> 409
 gtgttgacaga aatccggcaa tcgacctgag gacttgcgag ccgctcagct cccgggacgt 60
 ttggagctgc tgctaaataa tttctgctca gcc atg tcg ccg gct cca gat gca 114
 Met Ser Pro Ala Pro Asp Ala
 -40 -35
 gcc ccg gct cct gcg tcg atc tcc ctg ttt gac ctc agc gcg gat gct 162
 Ala Pro Ala Pro Ala Ser Ile Ser Leu Phe Asp Leu Ser Ala Asp Ala
 -30 -25 -20
 ccg gtc ttt cag ggc ctg agc ctg gtg agc cac gcg cct ggg gag gct 210
 Pro Val Phe Gln Gly Leu Ser Leu Val Ser His Ala Pro Gly Glu Ala
 -15 -10 -5
 ctg gcc ccg gct ccg cgt act tcc tgt tca ggc tca ggg gag aga gaa 258
 Leu Ala Arg Ala Pro Arg Thr Ser Cys Ser Gly Ser Gly Glu Arg Glu
 1 5 10
 agc cca gaa aga aag cta ctc cag ggt cct atg gat att tca gag aag 306
 Ser Pro Glu Arg Lys Leu Leu Gln Gly Pro Met Asp Ile Ser Glu Lys
 15 20 25 30
 tta ttt tgt tca act tgt gac cag acc ttc cag aa 341
 Leu Phe Cys Ser Thr Cys Asp Gln Thr Phe Gln
 35 40

<210> 410
 <211> 321
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 153..320

<221> sig_peptide
 <222> 153..257
 <223> Von Heijne matrix
 score 4.90000009536743
 seq LFIFIGSLQPVP/RF

<400> 410
 cacacacaaa ctctcaagtgcgctaattcc ctctcaccaa accaatcaca atacagataa 60

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aagagaataa cttgtgttca tttttgtaca aacaaaaaag atataaattg tgaatgrtgc 120
atgrttttta awtwmccaag taaactgggc aa atg ctt ctg cat tat tta aag 173
                               Met Leu Leu His Tyr Leu Lys
                               -35                               -30
cta aaa ggt gat cag tgg aaa ctt tcc tct gtt agt act cta ata ctt 221
Leu Lys Gly Asp Gln Trp Lys Leu Ser Ser Val Ser Thr Leu Ile Leu
                               -25                               -20                               -15
ttt ata ttt atc ggc tca cta caa cct gtg cct acc agg ttc aag cga 269
Phe Ile Phe Ile Gly Ser Leu Gln Pro Val Pro Thr Arg Phe Lys Arg
                               -10                               -5                               1
ttc tcc tgt ctc gdc cac ctg agt agc cga gac cac agg caa gca cta 317
Phe Ser Cys Leu Xaa His Leu Ser Ser Arg Asp His Arg Gln Ala Leu
5                               10                               15                               20
cgg g 321
Arg

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<210> 411
<211> 635
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> 84..635

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<221> sig_peptide
<222> 84..542
<223> Von Heijne matrix
      score 4.90000009536743
      seq MIVSLAAVAWVGQ/QV

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<400> 411
gggttggtggt tgggtgtgcgg gtttcggttg gaggactcgt tggggaggtg gcctgcgctt 60
gtagagactg catccccgag acg atg gcg gag gga gat aat cgc agc acc aac 113
                               Met Ala Glu Gly Asp Asn Arg Ser Thr Asn
                               -150                               -145
ctg ctg gct gca gag act gca agt ctg gaa gaa cag ctg caa gga tgg 161
Leu Leu Ala Ala Glu Thr Ala Ser Leu Glu Glu Gln Leu Gln Gly Trp
                               -140                               -135                               -130
gga gaa gtg atg ctg atg gct gat aaa gtc ctc cga tgg gaa aga gcc 209
Gly Glu Val Met Leu Met Ala Asp Lys Val Leu Arg Trp Glu Arg Ala
                               -125                               -120                               -115
tgg ttt cca cct gcc atc atg ggt gtg gtt tct ttg gtg ttt ctg att 257
Trp Phe Pro Pro Ala Ile Met Gly Val Val Ser Leu Val Phe Leu Ile
                               -110                               -105                               -100
atc tac tat cta gat cca tct gtt ctg tcc ggc gtt tcc tgt ttt gtt 305
Ile Tyr Tyr Leu Asp Pro Ser Val Leu Ser Gly Val Ser Cys Phe Val
                               -95                               -90                               -85                               -80
atg ttt ttg tgc ttg gct gac tac ctt gtt ccc att cta gcg cct aga 353
Met Phe Leu Cys Leu Ala Asp Tyr Leu Val Pro Ile Leu Ala Pro Arg
                               -75                               -70                               -65
att ttt ggc tcc aat aaa tgg acc act gaa caa cag caa aga ttc cat 401
Ile Phe Gly Ser Asn Lys Trp Thr Thr Glu Gln Gln Gln Arg Phe His
                               -60                               -55                               -50

```


gaa att tgc agc aat cta gta aaa act cga cgc aga gct gtg ggt tgg	449
Glu Ile Cys Ser Asn Leu Val Lys Thr Arg Arg Arg Ala Val Gly Trp	
-45 -40 -35	
tgg aaa cgc ctc ttc aca cta aag gaa gaa aaa cct aag atg tac ttc	497
Trp Lys Arg Leu Phe Thr Leu Lys Glu Glu Lys Pro Lys Met Tyr Phe	
-30 -25 -20	
atg acc atg atc gtt tcc ctt gct gcg gtt gct tgg gtg gga caa caa	545
Met Thr Met Ile Val Ser Leu Ala Ala Val Ala Trp Val Gly Gln Gln	
-15 -10 -5 1	
gtc cac aac ctg ctt ctc acc tac ctg ata gtg act tcc tta cta ttg	593
Val His Asn Leu Leu Leu Thr Tyr Leu Ile Val Thr Ser Leu Leu Leu	
5 10 15	
ctt cct gga cta aac caa cat gga atc att ttg aag tac att	635
Leu Pro Gly Leu Asn Gln His Gly Ile Ile Leu Lys Tyr Ile	
20 25 30	

<210> 412
 <211> 335
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 33..335

<221> sig_peptide
 <222> 33..110
 <223> Von Heijne matrix
 score 4.90000009536743
 seq LLRGLLAGPAATS/WS

<400> 412	
aatggacgag aggtcagggg aggtttttga ag atg gcg gcc ctc aag gct ctg	53
Met Ala Ala Leu Lys Ala Leu	
-25 -20	
gtg tcc ggc tgt ggg cgg ctt ctc cgt ggg cta cta gcg ggc ccg gca	101
Val Ser Gly Cys Gly Arg Leu Leu Arg Gly Leu Leu Ala Gly Pro Ala	
-15 -10 -5	
gcg acc agc tgg tct cgg ctt cca gct gcg ggg ttc agg gaa gtg gtg	149
Ala Thr Ser Trp Ser Arg Leu Pro Ala Arg Gly Phe Arg Glu Val Val	
1 5 10	
gag acc caa gaa ggg aag aca act ata att gaa ggc cgt atc aca gcg	197
Glu Thr Gln Glu Gly Lys Thr Thr Ile Ile Glu Gly Arg Ile Thr Ala	
15 20 25	
act ccc aag gag agt cca aat cct cct aac ccc tct ggc cag tgc ccc	245
Thr Pro Lys Glu Ser Pro Asn Pro Pro Asn Pro Ser Gly Gln Cys Pro	
30 35 40 45	
atc tgc cgt tgg aac ctg aag cac aag tat aac tat gac gat gtt ctg	293
Ile Cys Arg Trp Asn Leu Lys His Lys Tyr Asn Tyr Asp Asp Val Leu	
50 55 60	
ctg ctt agc cag ttc atc cgg cct cat gga ggc atg ctg ccc	335
Leu Leu Ser Gln Phe Ile Arg Pro His Gly Gly Met Leu Pro	
65 70 75	

<210> 413
 <211> 158
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 25..156

<221> sig_peptide
 <222> 25..93
 <223> Von Heijne matrix
 score 4.90000009536743
 seq LVGFKQVVAWTFA/SD

<221> misc_feature
 <222> 17
 <223> n=a, g, c or t
 Oligonucleotide

<400> 413
 agaaactgac atttgbntgt tttta atg ggg tcc ctg ctg ttc atc agg cag 51
 Met Gly Ser Leu Leu Phe Ile Arg Gln
 -20 -15
 aca ctt gtg ggc ttt aaa cag gtc gtt gct tgg acc ttt gct tct gat 99
 Thr Leu Val Gly Phe Lys Gln Val Val Ala Trp Thr Phe Ala Ser Asp
 -10 -5 1
 tca cat tgt gsa aaw gtg gww atg gtd wtc tws agt cag ttg arw aat 147
 Ser His Cys Xaa Xaa Val Xaa Met Val Xaa Xaa Ser Gln Leu Xaa Asn
 5 10 15
 ccc cca ctg gg 158
 Pro Pro Leu
 20

<210> 414
 <211> 202
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 59..202

<221> sig_peptide
 <222> 59..130
 <223> Von Heijne matrix
 score 4.90000009536743
 seq LLLRGSLLASXRA/XX

<221> misc_feature
 <222> 160
 <223> n=a, g, c or t
 Oligonucleotide

<400> 414
ctgggagcga ccgctccgct cgtctcgttg gttccggagg tcgctgcggc ggtgggaa 58
atg ctg gcg cgc gcg gcg gag grc act ggg gcc ctt ttg ctg agg ggc 106
Met Leu Ala Arg Ala Ala Glu Xaa Thr Gly Ala Leu Leu Leu Arg Gly
-20 -15 -10
tct cta ctg gct tct grc cgc gck ycg sys vcg cct cct ctg gga ttg 154
Ser Leu Leu Ala Ser Xaa Arg Ala Xaa Xaa Xaa Pro Pro Leu Gly Leu
-5 1 5
scc cgn aac acc gwt ggt act gtt cgt gcc gca gca gga ggc ctg ggt 202
Xaa Arg Asn Thr Xaa Gly Thr Val Arg Ala Ala Ala Gly Gly Leu Gly
10 15 20

<210> 415
<211> 229
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 146..229
<221> sig_peptide
<222> 146..196
<223> Von Heijne matrix
score 4.90000009536743
seq LLSFCLCSDFISQ/DA

<400> 415
gtmaaaactcc cgcagacttc tctgtagatc gctgagcgat actttcggca gcacctcctt 60
gattctcagt tttgctggag gccgcaacca ggccctactc aaccctcctt cccaggaggc 120
ccaggccccc aagctcagat cacc atg aat gcc tcc ctc ttg tct ttc tgc 172
Met Asn Ala Ser Leu Leu Ser Phe Cys
-15 -10
ctt tgt tca gat ttc atc tct caa gat gcc ctc ctt ctc act gtc ata 220
Leu Cys Ser Asp Phe Ile Ser Gln Asp Ala Leu Leu Thr Val Ile
-5 1 5
ttt cct ccc 229
Phe Pro Pro
10

<210> 416
<211> 265
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 27..263
<221> sig_peptide
<222> 27..206
<223> Von Heijne matrix
score 4.90000009536743
seq LVGVIVHSGQAHA/GH

```

<400> 416
atgatgaaca aataagggttt ccctgg atg cta aac atg gag cct tac aca gtt      53
                        Met Leu Asn Met Glu Pro Tyr Thr Val
                        -60                        -55
tca gga atg gct cgc caa gat tct tct tct gaa gtt ggg gaa aat ggg      101
Ser Gly Met Ala Arg Gln Asp Ser Ser Ser Glu Val Gly Glu Asn Gly
-50                        -45                        -40
cga agt gtg gat cag ggc ggt gga gga tcc cca cga aaa aag gtt gcc      149
Arg Ser Val Asp Gln Gly Gly Gly Gly Ser Pro Arg Lys Lys Val Ala
-35                        -30                        -25                        -20
ctc aca gaa aac tat gaa ctt gtc ggt gtc atc gta cac agt ggg cag      197
Leu Thr Glu Asn Tyr Glu Leu Val Gly Val Ile Val His Ser Gly Gln
                        -15                        -10                        -5
gca cac gca ggc cac tac tat tcc ttc att aag gac agg cga ggg tgt      245
Ala His Ala Gly His Tyr Tyr Ser Phe Ile Lys Asp Arg Arg Gly Cys
                        1                        5                        10
gga aaa gga aag tgg ctg gg      265
Gly Lys Gly Lys Trp Leu
15

```

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<210> 417
<211> 228
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> 160..228

<221> sig_peptide
<222> 160..219
<223> Von Heijne matrix
      score 4.90000009536743
      seq LHLXSSRXPPILA/SP

```

```

<221> misc_feature
<222> 166..167,190
<223> n=a, g, c or t
      Oligonucleotide

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<400> 417
ttgtctgtct taggcctgga cactgttggt gacttatttc cagattttaa tttctctttg      60
gttgaagact gccaaactgtc tcatagagtg tttgatttat ttattttatty athtwgacat      120
gaggwykctc tctgcmaacc caggctggak tgcagtgac atg atv nng gct cac      174
                        Met Xaa Xaa Ala His
                        -20
ttc agc ctc cac ctc nkg agc tca agg art cck ccc atc tta gcc tcc      222
Phe Ser Leu His Leu Xaa Ser Ser Arg Xaa Pro Pro Ile Leu Ala Ser
-15                        -10                        -5                        1
cca gta
Pro Val
228

```

```

<210> 418

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<211> 225
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 125..223

<221> sig_peptide
 <222> 125..175
 <223> Von Heijne matrix
 score 4.90000009536743
 seq VCELSIFFTYVLA/IY

<400> 418
 aaaagtttgt aataagttgc actttcatca agactgtatt agggagtcca gtctccccac 60
 atccttgatca gcacgggatg acatcagttt tttaaatttt accaacttat tgggaaaaaa 120
 aaaa atg ata cgt cct gtt tgt gaa ttg agc att ttt ttc acc tat gta 169
 Met Ile Arg Pro Val Cys Glu Leu Ser Ile Phe Phe Thr Tyr Val
 -15 -10 -5
 cta gcc att tac ata tct cct tct gtg aat tgt ctg ttt ata tcc ttt 217
 Leu Ala Ile Tyr Ile Ser Pro Ser Val Asn Cys Leu Phe Ile Ser Phe
 1 5 10
 cct gcg gg 225
 Pro Ala
 15

<210> 419
 <211> 293
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 42..293

<221> sig_peptide
 <222> 42..128
 <223> Von Heijne matrix
 score 4.80000019073486
 seq LLSARLLSQEKRA/AE

<400> 419
 gtgctctatg gagctattgc ggccgtgggt ggtcgcgggc r atg cgg ggc tgc cag 56
 Met Arg Gly Cys Gln
 -25
 ctc ctc ggg ctt cgt agc tct tgg ccc ggg gac cta cta agt gct cgg 104
 Leu Leu Gly Leu Arg Ser Ser Trp Pro Gly Asp Leu Leu Ser Ala Arg
 -20 -15 -10
 ctc ttg tcc caa gag aag cgg gca gcg gaa acg cac ttt ggg ttt gag 152
 Leu Leu Ser Gln Glu Lys Arg Ala Ala Glu Thr His Phe Gly Phe Glu
 -5 1 5
 act gtg tcg gaa gag gag aag agg ggg gac tta aca tca gtt gta agt 200
 Thr Val Ser Glu Glu Glu Lys Arg Gly Asp Leu Thr Ser Val Val Ser

10	15	20	
cta gag tac cct gaa gtg caa tta cag ggt caa agg gtc tat gcm ttc	248		
Leu Glu Tyr Pro Glu Val Gln Leu Gln Gly Gln Arg Val Tyr Ala Phe			
25 30 35 40			
ctg tca ccc att tgt acc tat ggc tct gag gga tgc agc ctc aag	293		
Leu Ser Pro Ile Cys Thr Tyr Gly Ser Glu Gly Cys Ser Leu Lys			
45 50 55			

<210> 420
 <211> 194
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 30..194

<221> sig_peptide
 <222> 30..134
 <223> Von Heijne matrix
 score 4.80000019073486
 seq PWVLDIFLTLVFA/LG

<400> 420	
agttgctaga aagcaatgcg cctattcac atg gag aat ctt ccc ttt cct cta	53
Met Glu Asn Leu Pro Phe Pro Leu	
-35 -30	
aaa tta ctt agt gcc tca tca cta aac acc ccc agc tcc aca cca tgg	101
Lys Leu Leu Ser Ala Ser Ser Leu Asn Thr Pro Ser Ser Thr Pro Trp	
-25 -20 -15	
gtg ttg gat atc ttc ctc acc ttg gtg ttt gcc ctg ggg ttc ttc ttc	149
Val Leu Asp Ile Phe Leu Thr Leu Val Phe Ala Leu Gly Phe Phe Phe	
-10 -5 1 5	
cta tta ctc ccc tac ttc tct tac ctc cgt tgt gac aac cca cca	194
Leu Leu Leu Pro Tyr Phe Ser Tyr Leu Arg Cys Asp Asn Pro Pro	
10 15 20	

<210> 421
 <211> 90
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 29..88

<221> sig_peptide
 <222> 29..67
 <223> Von Heijne matrix
 score 4.80000019073486
 seq MCVCVFAIFGVRC/CV

<221> misc_feature
 <222> 61

<223> n=a, g, c or t
Oligonucleotide

<400> 421
tatttgggat ttgttgctct gtgtgtat atg tgc gtg tgt gtg ttt gct ata 52
Met Cys Val Cys Val Phe Ala Ile
-10
ttt ggg gtn cgt tgc tgt gtg tgt gtc cgc tgt att tg 90
Phe Gly Val Arg Cys Cys Val Cys Val Arg Cys Ile
-5 1 5

<210> 422
<211> 161
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 22..159

<221> sig_peptide
<222> 22..153
<223> Von Heijne matrix
score 4.80000019073486
seq XPCPLLFPGACFP/CP

<400> 422
tcatttgggt ttttatttaa t atg att tgc ata ttt tac tct aag att tcc 51
Met Ile Cys Ile Phe Tyr Ser Lys Ile Ser
-40 -35
atc tct gtc ggc tgt ggg agg aca gca gcc gag caa gtt gga tgt aaa 99
Ile Ser Val Gly Cys Gly Arg Thr Ala Ala Glu Gln Val Gly Cys Lys
-30 -25 -20
cag agg tca ttt cac ckc ccy tgc cct ctg ctg ttt cct ggt gcd tgc 147
Gln Arg Ser Phe His Xaa Pro Cys Pro Leu Leu Phe Pro Gly Ala Cys
-15 -10 -5
ttt ccc tgc cca ac 161
Phe Pro Cys Pro
1

<210> 423
<211> 420
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 333..419

<221> sig_peptide
<222> 333..380
<223> Von Heijne matrix
score 4.80000019073486
seq ICVSLMASDGASS/PV

<221> misc_feature
 <222> 323..324,328
 <223> n=a, g, c or t
 Oligonucleotide

<400> 423
 ctgccgcygg acacgggttc ttccagcttt tggctattgt gaataacgct gctatggaca 60
 tgaatgtaca aacatccctt cagatcctcc tttcagttct tgtgggtaca taccgccagt 120
 ggaactgtgg catcatatgg taactctgtg ttttaacattt tgaggaacca ccctactgct 180
 tcccacagag gctgtaccag tttacttccc accaacagtg caaggattcc aatttctcca 240
 catccgtgcc aacactatth tctttttgtc gctgtttgtca ttgtttgtct ggaaaatagc 300
 catgctgagg ggtgagaggt grnnghanrg tt atg aat ttg att tgc gtt tcc 353

Met Asn Leu Ile Cys Val Ser
 -15 -10
 ctg atg gcc agt gat ggg gca tct tcc cct gtg ctt ggt ggc tct tca 401
 Leu Met Ala Ser Asp Gly Ala Ser Ser Pro Val Leu Gly Gly Ser Ser
 -5 1 5
 cac tct tcc tcc cwt rgg g 420
 His Ser Ser Ser Xaa Xaa
 10

<210> 424
 <211> 432
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 256..432

<221> sig_peptide
 <222> 256..396
 <223> Von Heijne matrix
 score 4.80000019073486
 seq LVSALPQASFSSS/SE

<400> 424
 agtgaggagt carggaggtg tgtgtgagag agagagagaa aagagagaga cagagacggg 60
 gagagagaga gggagagaga agagagggag gagggaagaa gaaaagacgg agggaggtga 120
 ggaggaaggg agggggagag acagagacct agaggggctg aagaccaga cagagctggc 180
 agagctactg agaagaggac tggagcgctc tgagagcctc tcaagatctt ttgggggagc 240
 ccaataaatg tgaac atg gga tct gtc acr gga gct gtc ctc aag acg cta 291
 Met Gly Ser Val Thr Gly Ala Val Leu Lys Thr Leu
 -45 -40

ctt ctg tta tct act caa aat tgg aac aga gtc gaa gct ggg aat tcc 339
 Leu Leu Leu Ser Thr Gln Asn Trp Asn Arg Val Glu Ala Gly Asn Ser
 -35 -30 -25 -20
 tat gac tgt gat gat cct ctt gtg tct gcc ttg cct cag gca tcc ttc 387
 Tyr Asp Cys Asp Asp Pro Leu Val Ser Ala Leu Pro Gln Ala Ser Phe
 -15 -10 -5

agc agt tct tcc gag ctc tcc agc agt cat agt cct gga ttt gca 432
 Ser Ser Ser Ser Glu Leu Ser Ser Ser His Ser Pro Gly Phe Ala
 1 5 10

<210> 425
 <211> 419
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 278..418

<221> sig_peptide
 <222> 278..370
 <223> Von Heijne matrix
 score 4.80000019073486
 seq FLLFLFSSCDVP/VP

<400> 425
 ccgaattatt ttagtggttac ttatctttga ataaaaatgta tttttcttgg atcaattagt 60
 tgcagcacgt tcttaggaat ggaatagaga agcatcctaa gccagaagga tttttttttt 120
 tctagatcac agtgaagctt taatatggkk ggatatttgt cccagcccaa atcccatgct 180
 gaattgaaac ccctagtgc t ggaggtggg cctgggtggaa ggtgtttgga tcatgaggac 240
 acatctctga tgaatggcct agctcatcct cttagtg atg atg agt gag tyc tca 295
 Met Met Ser Glu Xaa Ser
 -30
 caa gat ctg gtt gta aag tgt gcc cca cca csg cca ttc ttt ctc ttg 343
 Gln Asp Leu Val Val Lys Cys Ala Pro Pro Xaa Pro Phe Phe Leu Leu
 -25 -20 -15 -10
 ttc ctg ttt tct tca tgt gat gtg cct gtt ccc ctt cac ctt ctg caa 391
 Phe Leu Phe Ser Ser Cys Asp Val Pro Val Pro Leu His Leu Leu Gln
 -5 1 5
 tgg ctg caa agc ttc ctg agg cct agg g 419
 Trp Leu Gln Ser Phe Leu Arg Pro Arg
 10 15

<210> 426
 <211> 232
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 54..230

<221> sig_peptide
 <222> 54..134
 <223> Von Heijne matrix
 score 4.80000019073486
 seq VLLTSGVKPQTFA/VS

<400> 426
 gcagtgagtg ttacagttct taaagatggg gtgtccggag tttgttcctt cca atg 56
 Met
 ttc aga tgt gtc cgg ttt ctt cct tct ggc ggg ttc gtg gtc ttg ctg 104
 Phe Arg Cys Val Arg Phe Leu Pro Ser Gly Gly Phe Val Val Leu Leu

-25		-20		-15		
act tca gga gtg aag cca caa acc ttc gca gtg agt gtt aca gct ctt	152					
Thr Ser Gly Val Lys Pro Gln Thr Phe Ala Val Ser Val Thr Ala Leu						
-10	-5	1	5			
aaa ggt ggc atg ccc gga gtt gtt cat tcc tcc ggt ggg ttc gtg gtt	200					
Lys Gly Gly Met Pro Gly Val Val His Ser Ser Gly Gly Phe Val Val						
10	15	20				
ttg cta act tca gga gcg aas tgc aga cct tc	232					
Leu Leu Thr Ser Gly Ala Xaa Cys Arg Pro						
25	30					

<210> 427
 <211> 383
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 226..381
 <221> sig_peptide
 <222> 226..315
 <223> Von Heijne matrix
 score 4.80000019073486
 seq CLFLNARLAGTLC/QL

<400> 427			
acagacatca gctcgggtca accgcggggc tcgagcccga gtggctgagg gctgttacct	60		
tcaaaccctt gaatcccacg ttttcccctt gacttcctgt caccgttaga gaaaagtgga	120		
cagcgtctcg gtcacagagt tggagaaata gtgcaggac tcttcaggga gagcgttttc	180		
ctcatcaaag caaactgcaa aatcgcttct gccggcgtgg acctg atg aga gtc ggt	237		
Met Arg Val Gly			
-30			
cgt cgt gag gga cac cct ctg ttc cct aac gtc ccc cgc tgc tta ttt	285		
Arg Arg Glu Gly His Pro Leu Phe Pro Asn Val Pro Arg Cys Leu Phe			
-25	-20	-15	
tta aac gct cgg ttg gcg gga acc ctg tgc cag ctg aaa ctc ctt cag	333		
Leu Asn Ala Arg Leu Ala Gly Thr Leu Cys Gln Leu Lys Leu Leu Gln			
-10	-5	1	5
ttt ggc cgc cta gga aac acc gag agt cac cta cat ggg ctg gct ggg	381		
Phe Gly Arg Leu Gly Asn Thr Glu Ser His Leu His Gly Leu Ala Gly			
10	15	20	
gg	383		

<210> 428
 <211> 132
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 32..130
 <221> sig_peptide

<222> 32..124
 <223> Von Heijne matrix
 score 4.80000019073486
 seq LLCPLTCPHHSLS/TV

<400> 428
 ttcaacaaat gagtcacatgt gttttcgtat t atg tat ttt gat atc cag att 52
 Met Tyr Phe Asp Ile Gln Ile
 -30 -25
 gtc tca gat gtg gtc agc ggg att ccc ttc aaa ctt ctg tgc cct tta 100
 Val Ser Asp Val Val Ser Gly Ile Pro Phe Lys Leu Leu Cys Pro Leu
 -20 -15 -10
 aca tgt ccc cat cat tct ctg agc acc gtg gg 132
 Thr Cys Pro His His Ser Leu Ser Thr Val
 -5 1

<210> 429
 <211> 165
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 25..165
 <221> sig_peptide
 <222> 25..117
 <223> Von Heijne matrix
 score 4.80000019073486
 seq FSPFLPSLPLLEA/ER

<400> 429
 caaactgttg aaaagttaac tctt atg tta ttt ata ttt tca gac ata gat 51
 Met Leu Phe Ile Phe Ser Asp Ile Asp
 -30 -25
 tgg aag atg gac tta tgc ttt ttc tct ttc tct cct ttc ctt ccc tcc 99
 Trp Lys Met Asp Leu Cys Phe Phe Ser Phe Ser Pro Phe Leu Pro Ser
 -20 -15 -10
 ctt cct ttg ttg gag gct gaa aga atg agg gtc agt gat caa ctt cag 147
 Leu Pro Leu Leu Glu Ala Glu Arg Met Arg Val Ser Asp Gln Leu Gln
 -5 1 5 10
 tat acc act gga kac ggg 165
 Tyr Thr Thr Gly Xaa Gly
 15

<210> 430
 <211> 236
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 52..234

<221> sig_peptide
 <222> 52..159
 <223> Von Heijne matrix
 score 4.80000019073486
 seq VLLAIGMFFTAWF/FV

<400> 430
 gccgacgtgt tcttccggtg gcggasggcg gattagcctt cgcggggcaa a atg gag 57
 Met Glu
 -35
 ctc gag gcc atg agc aga tat acc agc cca gtg aac cca gct gtc ttc 105
 Leu Glu Ala Met Ser Arg Tyr Thr Ser Pro Val Asn Pro Ala Val Phe
 -30 -25 -20
 ccc cat ctg acc gtg gtg ctt ttg gcc att ggc atg ttc ttc acc gcc 153
 Pro His Leu Thr Val Val Leu Leu Ala Ile Gly Met Phe Phe Thr Ala
 -15 -10 -5
 tgg ttc ttc gtt tac gag gtc acc tct acc aag tac act cgt gat atc 201
 Trp Phe Phe Val Tyr Glu Val Thr Ser Thr Lys Tyr Thr Arg Asp Ile
 1 5 10
 tat aaa gag ctc ctc atc tcc tta gtg gcc cga gg 236
 Tyr Lys Glu Leu Leu Ile Ser Leu Val Ala Arg
 15 20 25

<210> 431
 <211> 354
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 239..352

<221> sig_peptide
 <222> 239..289
 <223> Von Heijne matrix
 score 4.80000019073486
 seq LKLISTNFSLCQS/VQ

<221> misc_feature
 <222> 345
 <223> n=a, g, c or t
 Oligonucleotide

<400> 431
 aggccttctg agtgcagctg gcaccatggg tgtgctccag agcaacttct gcttgctctg 60
 agccccctgc cctgcctccc ctttcacccat gtttcctctg acaagatttt aagtacagca 120
 attcaagaag atttctcctc ctaaacgaca tttatctgaa gtctattgcc tcttgattgc 180
 tggaaaagad tcttaaaatc atttcaaaag taacttataa acaaacttat taaaagtg 238
 atg aaa gga gca ttg aaa tta att agc act aat ttt tca ctg tgc caa 286
 Met Lys Gly Ala Leu Lys Leu Ile Ser Thr Asn Phe Ser Leu Cys Gln
 -15 -10 -5
 agt gtg cag tgt cct tca gag gaa aca ata aca gat ctg gtg agt gtg 334
 Ser Val Gln Cys Pro Ser Glu Glu Thr Ile Thr Asp Leu Val Ser Val
 1 5 10 15

cca tgc cag tng gga ctg gg
 Pro Cys Gln Xaa Gly Leu
 20

354

<210> 432
 <211> 431
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 153..431

<221> sig_peptide
 <222> 153..359
 <223> Von Heijne matrix
 score 4.80000019073486
 seq MMVLSLGIILASA/SF

<400> 432
 gtaaaaaaac actggaataa ggaagggctg atgactttca gaagatgaag gtaagtagaa 60
 accgttgatg ggactgagaa accagagtta aaacctcttt ggagcttctg aggactcagc 120
 tggaaccaac gggcacagtt ggcaacacca tc atg aca tca caa cct gtt ccc 173
 Met Thr Ser Gln Pro Val Pro
 -65
 aat gag acc atc ata gtg ctc cca tca aat gtc atc aac ttc tcc caa 221
 Asn Glu Thr Ile Ile Val Leu Pro Ser Asn Val Ile Asn Phe Ser Gln
 -60 -55 -50
 gca gag aaa ccc gaa ccc acc aac cag ggg cag gat agc ctg aag aaa 269
 Ala Glu Lys Pro Glu Pro Thr Asn Gln Gly Gln Asp Ser Leu Lys Lys
 -45 -40 -35
 cat cta cac gca gaa atc aaa gtt att ggg act atc cag atc ttg tgt 317
 His Leu His Ala Glu Ile Lys Val Ile Gly Thr Ile Gln Ile Leu Cys
 -30 -25 -20 -15
 ggc atg atg gta ttg agc ttg ggg atc att ttg gca tct gct tcc ttc 365
 Gly Met Met Val Leu Ser Leu Gly Ile Ile Leu Ala Ser Ala Ser Phe
 -10 -5 1
 tct cca aat ttt acc caa gtg act tct aca ctg ttg aac tct gct tac 413
 Ser Pro Asn Phe Thr Gln Val Thr Ser Thr Leu Leu Asn Ser Ala Tyr
 5 10 15
 cca ttc ata gga ccc ggg 431
 Pro Phe Ile Gly Pro Gly
 20

<210> 433
 <211> 201
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 37..201

<221> sig_peptide

<222> 37..156

<223> Von Heijne matrix
score 4.80000019073486
seq IVSAACKCGSSQA/AI

<400> 433

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aatatttatg aagcagtttg gaaccaaagg ggtagt atg gta gac gag tgt ctt      54
                                     Met Val Asp Glu Cys Leu
                                     -40                               -35
aca gag cct gtg tgg gga agc aaa agg caa ggg tgt agt tca cag gca      102
Thr Glu Pro Val Trp Gly Ser Lys Arg Gln Gly Cys Ser Ser Gln Ala
                                     -30                               -25                               -20
gaa gcg agc tgt gac att gtc agt gca gcg tgt aag tgt ggc tcc tca      150
Glu Ala Ser Cys Asp Ile Val Ser Ala Ala Cys Lys Cys Gly Ser Ser
                                     -15                               -10                               -5
cag gcg gcc att gat tgt gag acc tca tct tgc tct gaa gat ttc ccg      198
Gln Ala Ala Ile Asp Cys Glu Thr Ser Ser Cys Ser Glu Asp Phe Pro
          1                      5                      10
gtg
Val
15
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<210> 434

<211> 334

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 242..334

<221> sig_peptide

<222> 242..283

<223> Von Heijne matrix
score 4.80000019073486
seq AWWFSGTFPLTHP/CS

<400> 434

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aagctgtact ctttcagcac atttcctttc atctccccct tcttccctct tctgtgctct      60
caagactttc cccctcttgc tgccacagat gcagtgaagc ctgcatata taaggtaaa      120
tgtgtggcaa ctctgcaggt ggggtctatg caagctacag acccctctga gtgtggtcag      180
tgccttagcc tggcctggat gcctaccagg cccaccaaac acctagctgc tggatattat      240
a atg gca tgg tgg ttt tct gga acc ttc cca cta act cac ccc tgc agc      289
  Met Ala Trp Trp Phe Ser Gly Thr Phe Pro Leu Thr His Pro Cys Ser
          -10                      -5                      1
gga tac ggc tct ctg atg gct cct tct agc cct acc cct tct ggg      334
Gly Tyr Gly Ser Leu Met Ala Pro Ser Ser Pro Thr Pro Ser Gly
          5                      10                      15
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<210> 435

<211> 386

<212> DNA

<213> Homo sapiens

<220>
 <221> CDS
 <222> 152..385

<221> sig_peptide
 <222> 152..322
 <223> Von Heijne matrix
 score 4.80000019073486
 seq VTSLANLIPPVKA/TP

<400> 435
 agtcgagtc tgcgggcta gaagccggct gtcgggtctc gtgtcgccgc cgccgcccgg 60
 catcgtggag ctggggcccc cttttgcctg ggagttttgt agtcgcctag ggtcagcggg 120
 gacatcccaa agggcaggcc cggcagccgc c atg gtg gcc aag gat tac ccc 172
 Met Val Ala Lys Asp Tyr Pro
 -55
 ttc tac ctc acg gtc aag aga gcg aac tgc agc ctg gag cta cct ccg 220
 Phe Tyr Leu Thr Val Lys Arg Ala Asn Cys Ser Leu Glu Leu Pro Pro
 -50 -45 -40 -35
 gcc agc ggt ccg gcc aag gac gct gag gag cct agt aat aaa cgg gtc 268
 Ala Ser Gly Pro Ala Lys Asp Ala Glu Glu Pro Ser Asn Lys Arg Val
 -30 -25 -20
 aaa ccc ctt tcc cga gtc acg tcg cta gca aac ctc atc ccg ccc gtg 316
 Lys Pro Leu Ser Arg Val Thr Ser Leu Ala Asn Leu Ile Pro Pro Val
 -15 -10 -5
 aag gcc acg cca tta aag cgc ttc agt caa acc ctg cag cgc tcc att 364
 Lys Ala Thr Pro Leu Lys Arg Phe Ser Gln Thr Leu Gln Arg Ser Ile
 1 5 10
 agc ttc cgc agt gag agc gcc t 386
 Ser Phe Arg Ser Glu Ser Ala
 15 20

<210> 436
 <211> 472
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 191..472

<221> sig_peptide
 <222> 191..274
 <223> Von Heijne matrix
 score 4.80000019073486
 seq GVLLEPFVHQVGG/HS

<400> 436
 tttttttggt gcgagagaaa caataggacg gaaacgccga ggaacccggc tgaggcggca 60
 gcgagcatcc tggccagaac aagccaagga gccaaagacga gagggacaca cggacaaaaca 120
 acagacagaa gacgtactgg ccgctggact ccgctgcctc ccccatctcc ccgcatctg 180
 cgcccggagg atg agc cca gcc ttc agg gcc atg gat gtg gag ccc cgc 229
 Met Ser Pro Ala Phe Arg Ala Met Asp Val Glu Pro Arg
 -25 -20

gcc aaa ggc gtc ctt ctg gag ccc ttt gtc cac cag gtc ggg ggg cac	277
Ala Lys Gly Val Leu Leu Glu Pro Phe Val His Gln Val Gly Gly His	
-15 -10 -5 1	
tca tgc gtg ctc cgc ttc aat gag aca acc ctg tgc aag ccc ctg gtc	325
Ser Cys Val Leu Arg Phe Asn Glu Thr Thr Leu Cys Lys Pro Leu Val	
5 10 15	
cca agg gaa cat cag ttc tac gag acc ctc cct gct gag atg cgc aaa	373
Pro Arg Glu His Gln Phe Tyr Glu Thr Leu Pro Ala Glu Met Arg Lys	
20 25 30	
ttc act ccc cag tac aaa gga caa agc caa agg ccc ctt gtt agc tgg	421
Phe Thr Pro Gln Tyr Lys Gly Gln Ser Gln Arg Pro Leu Val Ser Trp	
35 40 45	
cca tcc ctg ccc cat ttt ttc ccc tgg tcc ttt ccc ctg tgg cca cag	469
Pro Ser Leu Pro His Phe Phe Pro Trp Ser Phe Pro Leu Trp Pro Gln	
50 55 60 65	
gga	472
Gly	

<210> 437
 <211> 469
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 213..467

<221> sig_peptide
 <222> 213..314
 <223> Von Heijne matrix
 score 4.80000019073486
 seq ILAFLQSPRAILP/GN

<221> misc_feature
 <222> 432..433
 <223> n=a, g, c or t
 Oligonucleotide

<400> 437	
ggattcccgcc cccgagggttt ctaaattccag acattcccgt ttggctgagc actctaggcc	60
tacatccatg aagctaggag agcgacactc aaagactgca ctattgagag aagctaactg	120
taaaggcagt gaatatattc gggagtccag ctccggaacc cgaggagctct tttagtggga	180
ggggcggcgc tgatggcgct tctggcctcc ga atg cta ggg ggc gct gtg atc	233
Met Leu Gly Gly Ala Val Ile	
-30	
gcc ggg cgg cct ctt ggg cgc tgg gag tcc acc gcg caa ssc atc ctg	281
Ala Gly Arg Pro Leu Gly Arg Trp Glu Ser Thr Ala Gln Xaa Ile Leu	
-25 -20 -15	
gcc ttt ctt cag tcc cca cgt gcg atc ctt ccc ggc aac ttt ttc gag	329
Ala Phe Leu Gln Ser Pro Arg Ala Ile Leu Pro Gly Asn Phe Phe Glu	
-10 -5 1 5	
aaa aat gcc caa att caa ggc ggc ccg tgg ggt ggg ggg tca gga aaa	377
Lys Asn Ala Gln Ile Gln Gly Gly Pro Trp Gly Gly Gly Ser Gly Lys	
10 15 20	

aca tgc gcc cct ggc cga tsa gat cct ggc tgg gaa tgc ggt gcg ggc	425
Thr Cys Ala Pro Gly Arg Xaa Asp Pro Gly Trp Glu Cys Gly Ala Gly	
25 30 35	
ggg ggt nng gga gaa gcg gcg ggg tcg cgg gam agg ara agc gg	469
Gly Gly Xaa Gly Glu Ala Ala Gly Ser Arg Xaa Arg Xaa Ser	
40 45 50	

<210> 438
 <211> 169
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 77..169

<221> sig_peptide
 <222> 77..124
 <223> Von Heijne matrix
 score 4.80000019073486
 seq ACFFHLFVSSLIS/FE

<400> 438	
ttgataggaa tagcattgaa tctgtaaaatt gctttgggca ctatggccat tttaataata	60
ttgattcctc ctatcc atg agc atg gca tgt ttt ttc cat ttg ttt gtg tca	112
Met Ser Met Ala Cys Phe Phe His Leu Phe Val Ser	
-15 -10 -5	
tct ctg att tcc ttt gag cag tgt ttt gka atg cta aga aaa ttg ctt	160
Ser Leu Ile Ser Phe Glu Gln Cys Phe Xaa Met Leu Arg Lys Leu Leu	
1 5 10	
aaa att ata	169
Lys Ile Ile	
15	

<210> 439
 <211> 447
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 211..447

<221> sig_peptide
 <222> 211..345
 <223> Von Heijne matrix
 score 4.69999980926514
 seq PWLEVGLFFWLHA/AP

<400> 439	
agaacaatgc tgcttggctc cctgaattca gcacccttcc tagggaatgt atgggtggat	60
cttttgccctt gcaggattct ttttcatctt tgcagggact tctggggccg gagtatgtaa	120
aactcctggg tctctgtgtg tgcctgagtg gctgctctac tgagactctg catacacagc	180
tctgtatatc ggaccawgg ccctggtggc atg ggc tca cga gga gat ccc ctg	234

	Met	Gly	Ser	Arg	Gly	Asp	Pro	Leu	
	-45					-40			
atc tgt ggg ttg caa aga tct gtg gga gaa gtg tgg ttt cct gga tgg									282
Ile Cys Gly Leu Gln Arg Ser Val Gly Glu Val Trp Phe Pro Gly Trp									
-35	-30					-25			
ggg cac aca atc act cac tgc ttc cct tgg ctg gag gtg ggg ctt ttt									330
Gly His Thr Ile Thr His Cys Phe Pro Trp Leu Glu Val Gly Leu Phe									
-20	-15					-10			
ttt tgg ctc cat gct gct cct ggg cgg gcg att gcc cta ccc cat ttt									378
Phe Trp Leu His Ala Ala Pro Gly Arg Ala Ile Ala Leu Pro His Phe									
-5	1				5			10	
tct tca ttc tct gtg ggt caa gdb gtt cac ttg gtc agt cca ttg tgr									426
Ser Ser Phe Ser Val Gly Gln Xaa Val His Leu Val Ser Pro Leu Xaa									
15	20							25	
gam ctg gat att tca gtt gaa									447
Xaa Leu Asp Ile Ser Val Glu									
30									

<210> 440
 <211> 340
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> CDS
 <222> 176..340

 <221> sig_peptide
 <222> 176..232
 <223> Von Heijne matrix
 score 4.69999980926514
 seq ELLLLLPRGLCQV/CP

 <221> misc_feature
 <222> 20,279..281
 <223> n=a, g, c or t
 Oligonucleotide

<400> 440	
agaaaagcag ccgcagttgn gccgctccac cacgccgtcc ggggtgggcct agcagtcgct	60
ccatttatcg cttgagatct ccagccttac cgcggtcga aatggacccc aactgtcct	120
gcaccactgg tgtctccwrc gcctgcaccg gtcctgcac gtgcaaagag tgcaa atg	178
	Met
cac ctc ctg caa gaa gag ctg ctg ctc ctg ctg ccc cgt ggg ctg tgc	226
His Leu Leu Gln Glu Glu Leu Leu Leu Leu Leu Pro Arg Gly Leu Cys	
-15	-10
caa gtg tgc cca cgg ctg tgt ctg caa agg gmc gtt gga gaa ctg cag	274
Gln Val Cys Pro Arg Leu Cys Leu Gln Arg Xaa Val Gly Glu Leu Gln	
1	5
mtg cnn nky cct gat gtg gga aca gct ctt ctc cca gat gtt aat aga	322
Xaa Xaa Xaa Pro Asp Val Gly Thr Ala Leu Leu Pro Asp Val Asn Arg	
15	20
aca agc tgc aca acc tgg	340
Thr Ser Cys Thr Thr Trp	

<210> 441
 <211> 409
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 292..408

<221> sig_peptide
 <222> 292..375
 <223> Von Heijne matrix
 score 4.69999980926514
 seq QLVTRLLLSPSQS/TQ

<400> 441
 agaagatggg gaaagaggaa ggaaaggatg cccagataca gggagcttta gcgatgtagt 60
 gaacggacag aagatcagga acaagttgag ttcattgtgt ggagatggca rraagatgga 120
 gattggtgag ctgagtggag aagtgccata gagcgggtgt ttgccagagt gtctgcggat 180
 tgctcatacc tgggaaggat tctttgtatg gttcccttag gctgagggag ggtatcagct 240
 ttacagacct tgtgggatta caaaagggcc accacacact cttcaaccaa t atg tgt 297
 Met Cys
 cta tct tgc att caa ggc tca ttc ttt gtt gaa att ttg cag ttg gtc 345
 Leu Ser Cys Ile Gln Gly Ser Phe Phe Val Glu Ile Leu Gln Leu Val
 -25 -20 -15
 act agg cta ttg tta tct cca tct caa agt aca cag aca cac aca cac 393
 Thr Arg Leu Leu Leu Ser Pro Ser Gln Ser Thr Gln Thr His Thr His
 -10 -5 1 5
 aca cac aca cac aca a 409
 Thr His Thr His Thr
 10

<210> 442
 <211> 320
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 203..319

<221> sig_peptide
 <222> 203..298
 <223> Von Heijne matrix
 score 4.69999980926514
 seq AILLLVXVSDKNE/QQ

<221> misc_feature
 <222> 225..227,279
 <223> n=a, g, c or t
 Oligonucleotide

```

<400> 442
cacactagaa tagactggaa caacttggat ttagtgattc cgatgcttat caggaaggtc      60
tctgttcttt tataggaaga aaaaacatag ttatttttct tttatgatac aaaggatatgc    120
tttctatgca agctggatac cagaccaaga ataataaatc acaatttcat aaggtttcta    180
agacttgata ttatatgggg at atg acc att ttg agg gaa atg tnn nca tca      232
                        Met Thr Ile Leu Arg Glu Met Xaa Xaa Ser
                        -30 -25
ctt tat gta ctt gaa gct aag gat act gct atc tta ttg ctt gtt tna      280
Leu Tyr Val Leu Glu Ala Lys Asp Thr Ala Ile Leu Leu Leu Val Xaa
-20 -15 -10
gtg agc gat aag aat gaa cag cag ctt ggg agg ggc gtg g      320
Val Ser Asp Lys Asn Glu Gln Gln Leu Gly Arg Gly Val
-5 1 5

```

```

<210> 443
<211> 256
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> 102..254

<221> sig_peptide
<222> 102..188
<223> Von Heijne matrix
      score 4.69999980926514
      seq ICCNLYFLLFCRS/SF

```

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<400> 443
cttcttttcta actcctgcat atacctttgc atttatgtag cttctggagg gcacatggag      60
gtagctcacc atggttttaa tttgcatttc tctgataatg a atg aga ctt agt tct    116
                        Met Arg Leu Ser Ser
                        -25
tcc tgt ggg ttg cct gtt aag act ttg cca ttt atc tgt tgc aat ctt      164
Ser Cys Gly Leu Pro Val Lys Thr Leu Pro Phe Ile Cys Cys Asn Leu
-20 -15 -10
tat ttc ttg ctg ttt tgt agg agt tct ttt tta tat ttt gga tat gat      212
Tyr Phe Leu Leu Phe Cys Arg Ser Ser Phe Leu Tyr Phe Gly Tyr Asp
-5 1 5
ccc att aat act tac atg tat tac aat gtt ttc tcc cac tcg gg      256
Pro Ile Asn Thr Tyr Met Tyr Tyr Asn Val Phe Ser His Ser
10 15 20

```

```

<210> 444
<211> 284
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> 17..283

<221> sig_peptide

```

<222> 17..220

<223> Von Heijne matrix

score 4.69999980926514

seq GCLLXPLLVSCLG/SL

<400> 444

tagatggcga ctccct atg tta ctg acg aga ccg gcg gtg agt gcg gga ggc 52
Met Leu Leu Thr Arg Pro Ala Val Ser Ala Gly Gly

-65

-60

gcg gas cgc ttc tct ccg ggc tct cgg ggc agg ggt tcg gac ttg gaa 100
Ala Xaa Arg Phe Ser Pro Gly Ser Arg Gly Arg Gly Ser Asp Leu Glu

-55

-50

-45

agg ggt ctg tgc ccc gcc cat ccc ggg gcc cct cct ttg ccc cgc ccc 148
Arg Gly Leu Cys Pro Ala His Pro Gly Ala Pro Pro Leu Pro Arg Pro

-40

-35

-30

-25

ccg gac cgc ctt ccc cat tca ttc tct cct acg ggg tgt ctc ctg hgc 196
Pro Asp Arg Leu Pro His Ser Phe Ser Pro Thr Gly Cys Leu Leu Xaa

-20

-15

-10

ccc ctt ctg gtc tcg tgt ttg ggg tct ctg ctt ccg gtc acc caa acc 244
Pro Leu Leu Val Ser Cys Leu Gly Ser Leu Leu Pro Val Thr Gln Thr

-5

1

5

ctg ggg tcc ttc agt gct ggt ccc tgc ttc agg acc ctc a 284
Leu Gly Ser Phe Ser Ala Gly Pro Cys Phe Arg Thr Leu

10

15

20

<210> 445

<211> 240

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 103..240

<221> sig_peptide

<222> 103..177

<223> Von Heijne matrix

score 4.69999980926514

seq ILXSLSSSVPSRA/GS

<400> 445

tcttttgtaa tgaagcatgg cagccaggcc tagcacactt ccctctgcac accatcctgc 60
tcaggcctct gtgcctcggc tgtgctgttc cttctgcttg ga atg cat tca ctg 114
Met His Ser Leu

-25

tgt cca ctt agc caa ttc cta cct att ctt tma agc ctc agt tcc agt 162
Cys Pro Leu Ser Gln Phe Leu Pro Ile Leu Xaa Ser Leu Ser Ser Ser

-20

-15

-10

gtc ccc tcg agg gca ggc agt gct ttc cca tct gcc cta ggt cca ctc 210
Val Pro Ser Arg Ala Gly Ser Ala Phe Pro Ser Ala Leu Gly Pro Leu

-5

1

5

10

tac cag cct cta ctt ggg ccc cca gca tgg 240
Tyr Gln Pro Leu Leu Gly Pro Pro Ala Trp

15

20

<210> 446
 <211> 184
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 8..184

<221> sig_peptide
 <222> 8..139
 <223> Von Heijne matrix
 score 4.69999980926514
 seq LVFLSVXLLFLLF/LV

<400> 446
 tcctttt atg cga aca caa gta tat gag ggg ttg tgt aaa aat tat ttt 49
 Met Arg Thr Gln Val Tyr Glu Gly Leu Cys Lys Asn Tyr Phe
 -40 -35
 tct ctt gct gta cta caa aga gat aga atc aaa ctg ctt ttt ttc gac 97
 Ser Leu Ala Val Leu Gln Arg Asp Arg Ile Lys Leu Leu Phe Phe Asp
 -30 -25 -20 -15
 ata ctg gtt ttt ctt tct gtt tww ctt ctc ttt ctt cta ttt ctt gtg 145
 Ile Leu Val Phe Leu Ser Val Xaa Leu Leu Phe Leu Leu Phe Leu Val
 -10 -5 1
 gat atw atg gct aat adc aca aca agt tta ggg agg ccc 184
 Asp Ile Met Ala Asn Xaa Thr Thr Ser Leu Gly Arg Pro
 5 10 15

<210> 447
 <211> 360
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 34..360

<221> sig_peptide
 <222> 34..168
 <223> Von Heijne matrix
 score 4.69999980926514
 seq LLSLAQTITTKTTA/TT

<221> misc_feature
 <222> 280
 <223> n=a, g, c or t
 Oligonucleotide

<400> 447
 aaaaactctt ttctttatcc tctttccaga aaa atg ggc caa ttc aca gct gca 54
 Met Gly Gln Phe Thr Ala Ala
 -45 -40

atg gtt ggg aga att tcc tgt ctg gga gtc tgg aaa ctg cca aga gtg	102
Met Val Gly Arg Ile Ser Cys Leu Gly Val Trp Lys Leu Pro Arg Val	
-35 -30 -25	
gaa agc tgc agc cag cca gcg agg cct ctg ttg tca ctg gcc caa aca	150
Glu Ser Cys Ser Gln Pro Ala Arg Pro Leu Leu Ser Leu Ala Gln Thr	
-20 -15 -10	
aca aca aaa aca acc gca aca aca aca aca aca aaa cat gcc acg	198
Thr Thr Lys Thr Thr Ala Thr Thr Thr Thr Thr Thr Lys His Ala Thr	
-5 1 5 10	
tgt gca ctg gca tat aca aac acg ccc aca gaa cca vrc caa gcg gac	246
Cys Ala Leu Ala Tyr Thr Asn Thr Pro Thr Glu Pro Xaa Gln Ala Asp	
15 20 25	
aag gct tca agg aga gct tct ggg ahv ctc rwv ncc gcg gcg agg cat	294
Lys Ala Ser Arg Arg Ala Ser Gly Xaa Leu Xaa Xaa Ala Ala Arg His	
30 35 40	
atc cct tgg cat ggt gcc act gca gcc cag ctc cca gcc ccc ccg cca	342
Ile Pro Trp His Gly Ala Thr Ala Ala Gln Leu Pro Ala Pro Pro Pro	
45 50 55	
tct gtc atc agc gct ctg	360
Ser Val Ile Ser Ala Leu	
60	

<210> 448
 <211> 123
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 39..122

<221> sig_peptide
 <222> 39..92
 <223> Von Heijne matrix
 score 4.69999980926514
 seq IAILFPNSGSCFA/FS

<400> 448	
cttatctgat tcacagcccg tattcagatt tgccaatt atg ttg att ttc att att	56
Met Leu Ile Phe Ile Ile	
-15	

gct att tta ttt ccc aat tca gga tca tgc ttt gca ttt agt tgt cat	104
Ala Ile Leu Phe Pro Asn Ser Gly Ser Cys Phe Ala Phe Ser Cys His	
-10 -5 1	

gtc tcc ttt ttt ttt ttt t	123
Val Ser Phe Phe Phe Phe	
5 10	

<210> 449
 <211> 193
 <212> DNA
 <213> Homo sapiens

<220>

<221> CDS
<222> 18..191

<221> sig_peptide
<222> 18..62
<223> Von Heijne matrix
score 4.69999980926514
seq RCACFPFFPFAFC/HD

<400> 449
ctctctcctg ttcggtc atg gtg aga tgt gct tgc ttc ccc ttc ttc ccc 50
Met Val Arg Cys Ala Cys Phe Pro Phe Phe Pro
-15 -10 -5
ttc gcc ttc tgc cat gac tgt aag ttt ctt ggg gcc tcc cag tca tgc 98
Phe Ala Phe Cys His Asp Cys Lys Phe Leu Gly Ala Ser Gln Ser Cys
1 5 10
ttc ttg tta agc cgg caa aac tgt gta agc aca gga kga cct tca tcc 146
Phe Leu Leu Ser Arg Gln Asn Cys Val Ser Thr Gly Xaa Pro Ser Ser
15 20 25
aaa tct gat atc aac tca agg tct gga tct tgt tca ctg gca agg gg 193
Lys Ser Asp Ile Asn Ser Arg Ser Gly Ser Cys Ser Leu Ala Arg
30 35 40

<210> 450
<211> 302
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 8..301

<221> sig_peptide
<222> 8..88
<223> Von Heijne matrix
score 4.69999980926514
seq LAPLXLVFISLLP/AP

<221> misc_feature
<222> 292
<223> n=a, g, c or t
Oligonucleotide

<400> 450
ccagcaa atg gtg agt ttg agg gta ggg gcc tct cca ttt cgg ttc cca 49
Met Val Ser Leu Arg Val Gly Ala Ser Pro Phe Arg Phe Pro
-25 -20 -15
ctg gcc ccc ctc tbt ttg gtt ttc atc tct ctt ctc cca gcc cca ttt 97
Leu Ala Pro Leu Xaa Leu Val Phe Ile Ser Leu Leu Pro Ala Pro Phe
-10 -5 1
ttt cct act ctt tcg ttt cct tgt tgc tgt gtg tcc tgg ctc ttt tct 145
Phe Pro Thr Leu Ser Phe Pro Cys Cys Cys Val Ser Trp Leu Phe Ser
5 10 15
ctt tct gtg vtt gtc tct ctg cgt ctc agt ctt tbt gtg tcc tgt tta 193

Leu	Ser	Val	Xaa	Val	Ser	Leu	Arg	Leu	Ser	Leu	Xaa	Val	Ser	Cys	Leu	
20					25				30						35	
tct	ctc	tgg	tgt	ctc	ttg	gta	ttg	ttt	ctc	tct	ccc	act	ctg	tat	gtc	241
Ser	Leu	Trp	Cys	Leu	Leu	Val	Leu	Phe	Leu	Ser	Pro	Thr	Leu	Tyr	Val	
			40					45					50			
tct	gac	tca	ttc	tgc	tca	ttc	tgt	gtc	ctc	cct	att	gct	ctc	tgt	ccc	289
Ser	Asp	Ser	Phe	Cys	Ser	Phe	Cys	Val	Leu	Pro	Ile	Ala	Leu	Cys	Pro	
			55					60					65			
can	gct	cgt	tct	t												302
Xaa	Ala	Arg	Ser													
			70													

<210> 451
 <211> 367
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 150..365

<221> sig_peptide
 <222> 150..311
 <223> Von Heijne matrix
 score 4.69999980926514
 seq PGLAFLAILTVLA/KP

<400> 451																
aaaatgatcc	atgcacacag	cctctatagg	aaagaaaaaa	aatatccaat	tgatttttctt											60
cccttttctg	cttctaaagt	ataccaaatt	tcactgtgat	cttaatatc	cccagaacag											120
acacctctga	gcagagagca	ggccttaga	atg gcc cac	ccc tgt tta	gct cca											173
			Met Ala His	Pro Cys Leu	Ala Pro											
				-50												
gca gaa cct	tct act ctt	tca caa acc	kcc cat cca	att caa aga	acc											221
Ala Glu Pro	Ser Thr Leu	Ser Gln Thr	Xaa His Pro	Ile Gln Arg	Thr											
	-45		-40		-35											
ctg aca act	ttc cct cag	gct tgg gtt	cta acc agc	agc ttt tcc	ata											269
Leu Thr Thr	Phe Pro Gln	Ala Trp Val	Leu Thr Ser	Ser Ser Phe	Ser Ile											
	-30		-25		-20											
cag cca ggc	ctt gca ttc	cta gcc att	ctc acc gtg	tta gcc aaa	ccc											317
Gln Pro Gly	Leu Ala Phe	Leu Ala Ile	Leu Thr Val	Leu Ala Lys	Pro											
		-10		-5	1											
ggs tcc tct	amc tgg agt	cct ggt cag	ttc aca cca	cac tcc ctg	ctg											365
Gly Ser Ser	Xaa Trp Ser	Pro Gly Gln	Phe Thr Pro	His Ser Leu	Leu											
	5		10		15											
gg																367

<210> 452
 <211> 349
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS

<222> 244..348

<221> sig_peptide

<222> 244..336

<223> Von Heijne matrix

score 4.69999980926514

seq HLYXSLFSSFLCS/TP

<400> 452

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ttctttcark tcttactact catccttcat ttatctcctg gatcattgcc cagagaatga      60
aagaaattgc cagtcaagcc agccaggtag gttaaactta tcctggcagt cctggagact      120
gctgcagact gactgcctga tgtccgtgcc cactgggggtt tttccctttt cagaaaggat      180
ttctccctga tctctcccca caaactctgg ctttgctttt tcatttccta agagcaactc      240
aat atg cat ttc ccc atc caa gct acc ttc sac tat tcc cct act gat      288
    Met His Phe Pro Ile Gln Ala Thr Phe Xaa Tyr Ser Pro Thr Asp
        -30          -25          -20
tct ctc tgt cat tta tat ttk tca ctc ttc tct tcc ttt ctc tgc tct      336
Ser Leu Cys His Leu Tyr Xaa Ser Leu Phe Ser Ser Phe Leu Cys Ser
    -15          -10          -5
acc cct gcc cgg g
Thr Pro Ala Arg
1
```

<210> 453

<211> 270

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 87..269

<221> sig_peptide

<222> 87..194

<223> Von Heijne matrix

score 4.69999980926514

seq SCFVPSLVTGALQ/QS

<400> 453

```
agcagtcacag agaagtgaag tgacttgccct gaagccacag agcctgcaag tgcgagggct      60
gggattccaa tccaagctct gggcca atg gct ttg cat atc cta gaa tgc gag      113
    Met Ala Leu His Ile Leu Glu Cys Glu
        -35          -30
agg aac gtt tgt ttt gta gca gtt aga cag cct gct cat gaa agc tgc      161
Arg Asn Val Cys Phe Val Ala Val Arg Gln Pro Ala His Glu Ser Cys
    -25          -20          -15
ttt gtg ccc agc ctt gtg aca ggt gct tta caa caa tcc cag aca cag      209
Phe Val Pro Ser Leu Val Thr Gly Ala Leu Gln Gln Ser Gln Thr Gln
    -10          -5          1          5
cac cca cct tgg gtt tgc cct cag gta cag ggc tcc tat cca tcc tgg      257
His Pro Pro Trp Val Cys Pro Gln Val Gln Gly Ser Tyr Pro Ser Trp
        10          15          20
aag aac aga ggg a
Lys Asn Arg Gly
```

<210> 454
 <211> 492
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 317..490

<221> sig_peptide
 <222> 317..412
 <223> Von Heijne matrix
 score 4.69999980926514
 seq RVLXLCNSRVST/RX

<221> misc_feature
 <222> 415..416
 <223> n=a, g, c or t
 Oligonucleotide

<400> 454
 taaggatatt acaaaacatt ttataaacac gtgggtctct tatgaagtac aatccaaagt 60
 ttgcatacaa tttaaaacaa aagcaagaaa tgtcacgctt tgggaacact gtttktctca 120
 cactaaaatg ttctatctga agcaagggga agtgtccaaa ttatagttca caaaatacct 180
 ttattttctc acaacaaaat catccctagt cagcggccca acattactca tttctgtcat 240
 caaaaacacc ctttctgtgg gttggtatga aatatccgca ggcatcacia gtactataag 300
 aaagggtttt ttcaaa atg tcc tgt act cac tcc tct tct aac ctg ggt aag 352
 Met Ser Cys Thr His Ser Ser Ser Asn Leu Gly Lys
 -30 -25
 ttt tct gta cac aga gag tac cgt gtc ctc mta ctg tgt aac agt agg 400
 Phe Ser Val His Arg Glu Tyr Arg Val Leu Xaa Leu Cys Asn Ser Arg
 -20 -15 -10 -5
 gtc tct ttc act cgn ntc cat gtg aag aga cca cca wac agg cta tgt 448
 Val Ser Phe Thr Arg Xaa His Val Lys Arg Pro Pro Xaa Arg Leu Cys
 1 5 10
 gtg agc agc aaa ggc tgt tta ttt cac ctg ggt gca ggc agg ct 492
 Val Ser Ser Lys Gly Cys Leu Phe His Leu Gly Ala Gly Arg
 15 20 25

<210> 455
 <211> 177
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 56..175

<221> sig_peptide
 <222> 56..112
 <223> Von Heijne matrix
 score 4.69999980926514

seq AFPLLLVIILLFQ/KQ

```
<400> 455
cacattcata agtatgagct taggctgagg atatatatcc agtgggggat gaaac atg      58
                                         Met
ctt aag aaa ttg agt gca ttt cct tta tta ttg gtt att att ttg cta      106
Leu Lys Lys Leu Ser Ala Phe Pro Leu Leu Leu Val Ile Ile Leu Leu
      -15                      -10                      -5
ttt caa aaa caa wtt gga ctt tta aaa aat tat amt tca cca cag aga      154
Phe Gln Lys Gln Xaa Gly Leu Leu Lys Asn Tyr Xaa Ser Pro Gln Arg
      1                      5                      10
cag gtg ttg ttt tgt aat cga ag      177
Gln Val Leu Phe Cys Asn Arg
15                      20
```

<210> 456

<211> 102

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 14..100

<221> sig_peptide

<222> 14..67

<223> Von Heijne matrix

score 4.69999980926514

seq CIFLAVLSKISWA/VN

```
<400> 456
ctaattgaaa agg atg tcc tat ttc cga tgt ata ttt ttg gca gtt ttg      49
      Met Ser Tyr Phe Arg Cys Ile Phe Leu Ala Val Leu
      -15                      -10
tca aaa atc agt tgg gct gta aat atg tgc agt ctt att tct ggg tcc      97
Ser Lys Ile Ser Trp Ala Val Asn Met Cys Ser Leu Ile Ser Gly Ser
      -5                      1                      5                      10
tcg gg      102
Ser
```

<210> 457

<211> 151

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 35..151

<221> sig_peptide

<222> 35..136

<223> Von Heijne matrix

score 4.59999990463257

seq LFLSISLITLYYS/SE

<400> 457
tgagttaaat tagacaactg taagagaaaa attt atg ctt tgt ata atg ttt ggt 55
Met Leu Cys Ile Met Phe Gly
-30
att gaa act aat gaa att acc aag atg aca atg tct ttt ctt ttg ttt 103
Ile Glu Thr Asn Glu Ile Thr Lys Met Thr Met Ser Phe Leu Leu Phe
-25 -20 -15
cta agt atc agt ttg ata act tta tat tat tcc tca gaa gca tgt ggg 151
Leu Ser Ile Ser Leu Ile Thr Leu Tyr Tyr Ser Ser Glu Ala Cys Gly
-10 -5 1 5

<210> 458
<211> 285
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 16..285
<221> sig_peptide
<222> 16..132
<223> Von Heijne matrix
score 4.59999990463257
seq YVFXLLAPFLTRS/SP
<221> misc_feature
<222> 251
<223> n=a, g, c or t
Oligonucleotide

<400> 458
agacctccag aaacc atg tgt caa gct cgg att gcc tta gac agg tgc aat 51
Met Cys Gln Ala Arg Ile Ala Leu Asp Arg Cys Asn
-35 -30
tta aga aca gct ttc atc ctc ttt kct ctc ata ttg tca cac tat gtg 99
Leu Arg Thr Ala Phe Ile Leu Phe Xaa Leu Ile Leu Ser His Tyr Val
-25 -20 -15
ttc yga ctt ctg gct cct ttc ctc aca aga agc tca ccc agc tgg aac 147
Phe Xaa Leu Leu Ala Pro Phe Leu Thr Arg Ser Ser Pro Ser Trp Asn
-10 -5 1 5
tct tat ggg acc ttg gca cca gag acc aca aat tcc tct ttg aag ttt 195
Ser Tyr Gly Thr Leu Ala Pro Glu Thr Thr Asn Ser Ser Leu Lys Phe
10 15 20
tct aac agc aac aat ggt att tct gac ttg gct twc ttg tat ttc tcd 243
Ser Asn Ser Asn Asn Gly Ile Ser Asp Leu Ala Xaa Leu Tyr Phe Ser
25 30 35
cac gtt anc aaa att ggt tca gca tct acc atg ggc tac ggg 285
His Val Xaa Lys Ile Gly Ser Ala Ser Thr Met Gly Tyr Gly
40 45 50

<210> 459
<211> 311

<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 15..311

<221> sig_peptide
<222> 15..86
<223> Von Heijne matrix
score 4.59999990463257
seq QGMLLAILEXCGA/IP

<400> 459
tcctcaagtt cttc atg gtc aag tcc gtc atc ttt ctt tcc ttc tgg caa 50
Met Val Lys Ser Val Ile Phe Leu Ser Phe Trp Gln
-20 -15
ggc atg ctc ctg gcc atc ctg gag rag tgt ggg gcc atc ccc aaa atc 98
Gly Met Leu Leu Ala Ile Leu Glu Xaa Cys Gly Ala Ile Pro Lys Ile
-10 -5 1
cac tcg gcc cgc gtg tcg gtg ggc gag ggc acc gtg gct gcc ggc tac 146
His Ser Ala Arg Val Ser Val Gly Glu Gly Thr Val Ala Ala Gly Tyr
5 10 15 20
cag gac ttc atc atc tgt gtg gag atg ttc ttt gca gcc ctg gcc ctg 194
Gln Asp Phe Ile Ile Cys Val Glu Met Phe Phe Ala Ala Leu Ala Leu
25 30 35
cgg cac gcc ttc acc tac aag gtc tat gct gac aag agg ctg gac gca 242
Arg His Ala Phe Thr Tyr Lys Val Tyr Ala Asp Lys Arg Leu Asp Ala
40 45 50
caa gtg cca aca tac ggc cct tac ggc cgc tgt gcc ccc atg aag agc 290
Gln Val Pro Thr Tyr Gly Pro Tyr Gly Arg Cys Ala Pro Met Lys Ser
55 60 65
atc tcc agc agc ctc aag gag 311
Ile Ser Ser Ser Leu Lys Glu
70 75

<210> 460
<211> 425
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 161..424

<221> sig_peptide
<222> 161..418
<223> Von Heijne matrix
score 4.59999990463257
seq AAAALCILILLXA/MY

<400> 460
aggccgggct gatgctgagg caatttatca tcttgatctc ccactgagtc agggagctct 60
cctgtcacca gtattgattt cagaggatgg actaaatttc ctaggatttc cattaagaat 120

Lys	Asn	Asn	Arg	Pro	Ser	Gly	Ile	Pro	Xaa	Arg	Xaa	Ser	Gly	Ser	Lys	
50						55					60					
tca	ggc	aat	aca	gct	tta	ttg	acc	atc	gyc	ggg	gct	cag	gcg	gag	gat	344
Ser	Gly	Asn	Thr	Ala	Leu	Leu	Thr	Ile	Xaa	Gly	Ala	Gln	Ala	Glu	Asp	
65					70				75					80		
gab	gct	gac	tat	tac	tgt	agt	kat	cgc	gac	cat	act	gat	aat	cgg	tgg	392
Xaa	Ala	Asp	Tyr	Tyr	Cys	Ser	Xaa	Arg	Asp	His	Thr	Asp	Asn	Arg	Trp	
			85					90					95			
gtg	ttc	ggc	ggg	ggg	acc	agg	ctg	aca	g							420
Val	Phe	Gly	Gly	Gly	Thr	Arg	Leu	Thr								
			100				105									

<210> 462
 <211> 257
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 46..255
 <221> sig_peptide
 <222> 46..105
 <223> Von Heijne matrix
 score 4.59999990463257
 seq XILTCLIFRNSEG/FQ

<400>	462																
tttttttttt	tccccaagcg	aaswtgaaca	gttgctaagt	ggaaa	atg	gag	gct	gaa									57
								Met	Glu	Ala	Glu						
								-20									
ttt	tac	atg	gkg	att	ctt	acc	tgc	ttg	atc	ttc	agg	aac	tca	gaa	ggg		105
Phe	Tyr	Met	Xaa	Ile	Leu	Thr	Cys	Leu	Ile	Phe	Arg	Asn	Ser	Glu	Gly		
	-15				-10					-5							
ttt	cag	att	gyc	cat	gtc	cag	aaa	caa	cag	tgt	ctt	ttc	aaa	aat	gag		153
Phe	Gln	Ile	Xaa	His	Val	Gln	Lys	Gln	Gln	Cys	Leu	Phe	Lys	Asn	Glu		
1			5					10					15				
aaa	gtg	gtc	gtg	ggc	tca	tgc	aac	agg	acc	atc	cag	aac	cag	cag	tgg		201
Lys	Val	Val	Val	Gly	Ser	Cys	Asn	Arg	Thr	Ile	Gln	Asn	Gln	Gln	Trp		
			20				25					30					
atg	tgg	act	gag	gat	gaa	aag	ctc	ctt	cat	gtt	aaa	tct	gca	ctg	tgc		249
Met	Trp	Thr	Glu	Asp	Glu	Lys	Leu	Leu	His	Val	Lys	Ser	Ala	Leu	Cys		
		35				40					45						
ttg	gcc	at															257
Leu	Ala																
			50														

<210> 463
 <211> 117
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS

<222> 61..117

<221> sig_peptide

<222> 61..111

<223> Von Heijne matrix

score 4.59999990463257

seq ACALCVWLCVKSC/SI

<400> 463

aataggaaga caaaagacaa aaaaaaatcc accaccacca aaatatccct ttgtacatgt 60

atg tgc gtg tgc gcg tgt gct ttg tgt gtg tgg ttg tgt gtt aaa tca 108

Met Cys Val Cys Ala Cys Ala Leu Cys Val Trp Leu Cys Val Lys Ser

-15

-10

-5

tgc agt att

117

Cys Ser Ile

1

<210> 464

<211> 142

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 39..140

<221> sig_peptide

<222> 39..101

<223> Von Heijne matrix

score 4.59999990463257

seq FIYLLAFCMPSLE/KC

<400> 464

cttattgtgg attgtggttt taattttgta tttccctg atg att agt gat gtt cag 56

Met Ile Ser Asp Val Gln

-20

cac ctt ttc ata tac ttg tta gcc ttt tgt atg cct tcc ttg gag aaa 104

His Leu Phe Ile Tyr Leu Leu Ala Phe Cys Met Pro Ser Leu Glu Lys

-15

-10

-5

1

tgt cta tac ggg tct ttg gcc cac ttt ttt ttt ttt tt

142

Cys Leu Tyr Gly Ser Leu Ala His Phe Phe Phe Phe

5

10

<210> 465

<211> 300

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 216..299

<221> sig_peptide

<222> 216..260

<223> Von Heijne matrix
 score 4.59999990463257
 seq LFRVLFSXTCALX/QD

<400> 465
 agttacttct ttgctagggt gaggaaggg tggaagcgcc tcctgcagcc acgaatatcc 60
 tccagtgcct gagagaaaac ggcctaatac aaaacgtccg cggcatacat ccattcttaa 120
 aacttgagt gctgcttttc tgggtggaaa agagcggat cagacagggt gagcagtcgg 180
 ggaacggatg aacaaagact tgcaccgtgg ccctg atg cct ttg ttc cga gtt 233
 Met Pro Leu Phe Arg Val
 -15 -10
 cta ttc agt tgw act tgt gcg ttg twa cag gac ttt aga atg cag ccc 281
 Leu Phe Ser Xaa Thr Cys Ala Leu Xaa Gln Asp Phe Arg Met Gln Pro
 -5 1 5
 tgc ccc cca acc ccc aag g 300
 Cys Pro Pro Thr Pro Lys
 10

<210> 466
 <211> 235
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 146..235
 <221> sig_peptide
 <222> 146..217
 <223> Von Heijne matrix
 score 4.59999990463257
 seq LLFYVLLFRNLYT/HT

<400> 466
 tttatatctt taattgcaag gataaaagaa ggggtgcatc tcaaaggcca tgataaatat 60
 aaaggataga aaagtacgt tgatggtgtg cccctcgata tctagaagat agcatagtcc 120
 atgcattctc agaaagatcc tatcc atg tgg tat gta gag atg tgg gtt tct 172
 Met Trp Tyr Val Glu Met Trp Val Ser
 -20
 ttt ttt cta ctt ttt tat gtg ctt ctt ttt aga aac tta tac aca cac 220
 Phe Phe Leu Leu Phe Tyr Val Leu Leu Phe Arg Asn Leu Tyr Thr His
 -15 -10 -5 1
 aca cac cac act ggg 235
 Thr His His Thr Gly
 5

<210> 467
 <211> 220
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 58..219

<221> sig_peptide
 <222> 58..147
 <223> Von Heijne matrix
 score 4.59999990463257
 seq VLVVSFVVGGLGC/NX

<221> misc_feature
 <222> 218
 <223> n=a, g, c or t
 Oligonucleotide

<400> 467
 accacaactc ccaggggtgct ccgcgtcctc gccgctgtcg ccgccgcgga gacaaag 57
 atg gct gcg aga gtc ggc gcc ttc ctc aag aat gcc tgg gac aag gag 105
 Met Ala Ala Arg Val Gly Ala Phe Leu Lys Asn Ala Trp Asp Lys Glu
 -30 -25 -20 -15
 cca gtg ctg gtc gtg tcc ttc gtc gtc ggg ggc ctc ggc tgt aat dct 153
 Pro Val Leu Val Val Ser Phe Val Val Gly Gly Leu Gly Cys Asn Xaa
 -10 -5 1
 gcc ccc att gag ccc cta ctt caa gta ctc cgt cat gat caa caa ggc 201
 Ala Pro Ile Glu Pro Leu Leu Gln Val Leu Arg His Asp Gln Gln Gly
 5 10 15
 cac gcc cta caa cta cna c 220
 His Ala Leu Gln Leu Xaa
 20

<210> 468
 <211> 462
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 154..462

<221> sig_peptide
 <222> 154..222
 <223> Von Heijne matrix
 score 4.59999990463257
 seq WTCVAPVYPACSG/RR

<400> 468
 gactgcagcc gcgagctcct ggaggcggcg ggatggaggc ggccggccgag cctggaaacc 60
 tggccgcgt caggcacatc atcctggtcc tctcaggaaa ggggggcgtt gggaaaagca 120
 ccatctccac ggagctggcc ctggcactgc gcc atg cag gca aga agg tgg gaa 174
 Met Gln Ala Arg Arg Trp Glu
 -20
 tcc tgg atg tgg acc tgt gtg gcc cca gta tac ccc gca tgc tcg ggg 222
 Ser Trp Met Trp Thr Cys Val Ala Pro Val Tyr Pro Ala Cys Ser Gly
 -15 -10 -5
 cgc agg gca rdr gct gtk sac cag tgs grr ccg cgg ctg ggc amc sgt 270
 Arg Arg Ala Xaa Ala Val Xaa Gln Xaa Xaa Pro Arg Leu Gly Xaa Xaa
 1 5 10 15

ctt cct gga ccg gga bca gag cat ctc gct cat gtc tgt ggg ctt cct	318
Leu Pro Gly Pro Gly Xaa Glu His Leu Ala His Val Cys Gly Leu Pro	
20 25 30	
gct gga gaa gcc gga cga gcc cgt ggt gtg gag agg ccc caa gaa aaa	366
Ala Gly Glu Ala Gly Arg Gly Arg Gly Val Glu Arg Pro Gln Glu Lys	
35 40 45	
cgc gct gat aaa gca gtw kgt gtc cga cgt gcc ctg ggg gga gct gga	414
Arg Ala Asp Lys Ala Val Xaa Val Arg Arg Gly Leu Gly Gly Ala Gly	
50 55 60	
cta cct ggt ggt gac acg ccc cgg gga cct ccg atg agc aca tgg cca	462
Leu Pro Gly Gly Asp Thr Pro Arg Gly Pro Pro Met Ser Thr Trp Pro	
65 70 75 80	

<210> 469
 <211> 438
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 391..438

<221> sig_peptide
 <222> 391..432
 <223> Von Heijne matrix
 score 4.59999990463257
 seq FLFFFGNSPCCGA/TG

<400> 469	
tatagtttca gttatgacat gagcacaaac atcatgattt ctgttctttt taatgcactc	60
agactggcta agaatatgtt ctgtgttggt gaatattcca tatgtatttg aaaataatat	120
atactctgct cttgttaggt tctagaaatg tcaattacct caaattctct gagagtgcag	180
ctcagttctt ctatatcctt actggtttct gcctacttgc tctgtcagtt actgagcaaa	240
aagtagcaaa gtctgcagct gtaatacatt tgtttatttc tctcattttt gttagtattt	300
gcttcattga ctttgaagct rtgttgtag catgcataca cataggatga ttatggcttc	360
ttggaaaatt gacccttta gcattatgta atg ttc ctc ttt ttc ttt ggt aac	414
Met Phe Leu Phe Phe Phe Gly Asn	
-10	

agt cca tgt tgt gga gcc aca ggg	438
Ser Pro Cys Cys Gly Ala Thr Gly	
-5 1	

<210> 470
 <211> 131
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 11..130

<221> sig_peptide
 <222> 11..85
 <223> Von Heijne matrix

score 4.59999990463257
seq SLSLSASLIIS/PS

<400> 470
atcttttcac atg ggc ctc tcc cac cat cgg gtc tca gcc cca tct tct 49
Met Gly Leu Ser His His Arg Val Ser Ala Pro Ser Ser
-25 -20 -15
ctc tct ctc tct ctc tcg gcc tcc ctc att att tct ccc tct ccc tcc 97
Leu Ser Leu Ser Leu Ser Ala Ser Leu Ile Ile Ser Pro Ser Pro Ser
-10 -5 1
gcc tct cca tct ctc ctt sct ccc cct bcc cgg g 131
Ala Ser Pro Ser Leu Leu Xaa Pro Pro Xaa Arg
5 10 15

<210> 471
<211> 211
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 115..210
<221> sig_peptide
<222> 115..183
<223> Von Heijne matrix
score 4.5
seq LSMLLRLVNSRP/PV

<400> 471
tggcgcgatc ttggctcacc gcaccttcg cctcccggt tcgagcgctt ctctgcctc 60
agcctcccga ttagcgggga tgacaggag tcaccccccac gcctggcttg gctg atg 117
Met
ttt gtg ttt tta gta ggc acg ccg tgt ctc tcc atg ttg ctc agg ctg 165
Phe Val Phe Leu Val Gly Thr Pro Cys Leu Ser Met Leu Leu Arg Leu
-20 -15 -10
gtc tcc aac tcc cga cct cct gtg atg cgc cca cct cgg cct ggg g 211
Val Ser Asn Ser Arg Pro Pro Val Met Arg Pro Pro Arg Pro Gly
-5 1 5

<210> 472
<211> 150
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 25..150
<221> sig_peptide
<222> 25..123
<223> Von Heijne matrix
score 4.5
seq VTITILFLIVSMA/LK

<400> 472
ctttattgag ggatacttta ctct atg aaa ttc act cat ttt aag tgt aca 51
Met Lys Phe Thr His Phe Lys Cys Thr
-30 -25
att cgg tta tta tta cta tat tta cag aat cct gta acc atc aca att 99
Ile Arg Leu Leu Leu Leu Tyr Leu Gln Asn Pro Val Thr Ile Thr Ile
-20 -15 -10
tta ttt tta atc gtt tcc atg gcc ctg aaa ata aac cac ata ccc aag 147
Leu Phe Leu Ile Val Ser Met Ala Leu Lys Ile Asn His Ile Pro Lys
-5 1 5
ggg 150
Gly

<210> 473
<211> 352
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 227..352
<221> sig_peptide
<222> 227..268
<223> Von Heijne matrix
score 4.5
seq SCMSLFPCCPAQS/KN

<400> 473
tatttgatta aaaaagactc ttcttgTTTT ctgttttGtc tgagttttca ttatacccac 60
ttctcaacta ccccatccca mgggtagaag tttttaaaat ttgcatattt aamattcatt 120
ttcgamttat ctgaaattaa tcaatatctc tactgtagtc ttggataatg ccaagagttt 180
aaaatgctat aatccaaaca cctgtttgga ctcaatatgt catttt atg tct tgt 235
Met Ser Cys
atg tca ctt ttc ccc tgt tgc cct gct cag agt aag aat tat atg tta 283
Met Ser Leu Phe Pro Cys Cys Pro Ala Gln Ser Lys Asn Tyr Met Leu
-10 -5 1 5
tta tta ttc att att tta ctt cca act caa ttt tta tat tca aaa tta 331
Leu Leu Phe Ile Ile Leu Leu Pro Thr Gln Phe Leu Tyr Ser Lys Leu
10 15 20
gtt aca att tgc tgt tgt ttt 352
Val Thr Ile Cys Cys Cys Phe
25

<210> 474
<211> 141
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 64..141

<221> sig_peptide
 <222> 64..105
 <223> Von Heijne matrix
 score 4.5
 seq LVCCTINSSFALG/IS

<221> misc_feature
 <222> 38
 <223> n=a, g, c or t
 Oligonucleotide

<400> 474
 tactttaagt tctagggtac gtctgcacaa cgtsrggntt tgatacatag gtatatatgt 60
 gcc atg ttg gtt tgc tgc acc atc aac tca tca ttt gca tta ggt att 108
 Met Leu Val Cys Cys Thr Ile Asn Ser Ser Phe Ala Leu Gly Ile
 -10 -5 1
 tct cgt aat gct atc cct ctg cca gcc cct ggg 141
 Ser Arg Asn Ala Ile Pro Leu Pro Ala Pro Gly
 5 10

<210> 475
 <211> 300
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 92..298

<221> sig_peptide
 <222> 92..250
 <223> Von Heijne matrix
 score 4.5
 seq ALYVICQFILIRS/GV

<400> 475
 cagattaaga gatggagaaa ggtgtagggm tgattctttt tttggtgaga cctcgcataa 60
 ctatcataaaa tttgacagtg agtatgagag a atg gga cgt ggt cct ggc ccc 112
 Met Gly Arg Gly Pro Gly Pro
 -50
 tta caa gag aga tct ctc ttt gag ama aag aga ggc gct cct cca agt 160
 Leu Gln Glu Arg Ser Leu Phe Glu Xaa Lys Arg Gly Ala Pro Pro Ser
 -45 -40 -35
 agc aat att gaa gac ttc cat gga ctc tta ccg aag gtt atc ccc atc 208
 Ser Asn Ile Glu Asp Phe His Gly Leu Leu Pro Lys Val Ile Pro Ile
 -30 -25 -20 -15
 tgt gct cta tat gtg att tgc cag ttc att cta ata agg agt gga gtc 256
 Cys Ala Leu Tyr Val Ile Cys Gln Phe Ile Leu Ile Arg Ser Gly Val
 -10 -5 1
 aac ata tca atg gag caa gtc aca gtc gtc gat gcc agt ctg gg 300
 Asn Ile Ser Met Glu Gln Val Thr Val Val Asp Ala Ser Leu
 5 10 15

<210> 476

<211> 232
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 112..231

<221> sig_peptide
 <222> 112..150
 <223> Von Heijne matrix
 score 4.5
 seq MLYCVVVVHSVCC/AV

<400> 476
 ttttaggggg gtttggttcg tttttgaact gtatacagat gaaattatac agaatgcttt 60
 ttttttggtg tatggccttt ttcactctgt agtgtatttg tgagattcat c atg ttg 117
 Met Leu
 tat tgt gta gtt gtg gtt cat tct gtt tgc tgt gca gta tac tat ttt 165
 Tyr Cys Val Val Val Val His Ser Val Cys Cys Ala Val Tyr Tyr Phe
 -10 -5 1 5
 gtg att att cat aca ata gaa cat att aca tat tta tgt atc cat tct 213
 Val Ile Ile His Thr Ile Glu His Ile Thr Tyr Leu Cys Ile His Ser
 10 15 20
 acc att cta ctg tgt gtg g 232
 Thr Ile Leu Leu Cys Val
 25

<210> 477
 <211> 236
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 124..234

<221> sig_peptide
 <222> 124..201
 <223> Von Heijne matrix
 score 4.5
 seq VFXSLFLIQLLIS/FS

<221> misc_feature
 <222> 171
 <223> n=a, g, c or t
 Oligonucleotide

<400> 477
 aagtggcagc btcagcaccc agggctgtgg taggtcacag tctctgggyk ggtctcagtg 60
 tccaacactg tagctggtgc ctgccagggt cccagtggtt ggggtcacca ggtctgaaga 120
 gag atg tgc tgg ytg cgg gya tgg ggc cag atc ctc ctg cca gtt ttc 168
 Met Cys Trp Leu Arg Xaa Trp Gly Gln Ile Leu Leu Pro Val Phe
 -25 -20 -15

cbn tcc ctc ttt ctc atc caa ttg ctt atc agc ttc tca gag aat ggt 216
 Xaa Ser Leu Phe Leu Ile Gln Leu Leu Ile Ser Phe Ser Glu Asn Gly
 -10 -5 1 5
 ttt atc cac agc ccc atg gg 236
 Phe Ile His Ser Pro Met
 10

<210> 478
 <211> 201
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 138..200

<221> sig_peptide
 <222> 138..179
 <223> Von Heijne matrix
 score 4.5
 seq CGLXILCGPWLHA/AP

<400> 478
 tctacatcac aggtkkatca gtgaaatatg tggtaagatg tacaaataag atgtgccccca 60
 ccaccagaat gatcagttct gtgaggacac gtccgtgact gtaccctctt tcagaagtgc 120
 tatcrattaa tgtgggtt atg tgt ggc ctg akk atc ctc tgt ggg cct tgg 170
 Met Cys Gly Leu Xaa Ile Leu Cys Gly Pro Trp
 -10 -5
 ctc cat gca gca cct cca tcc ccg ccg cgg g 201
 Leu His Ala Ala Pro Pro Ser Pro Pro Arg
 1 5

<210> 479
 <211> 151
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 25..150

<221> sig_peptide
 <222> 25..123
 <223> Von Heijne matrix
 score 4.5
 seq SISLLMLLXXYWS/CW

<400> 479
 acatagcatt ttatgkacta gaaa atg ttc cat gga agg gtt atg gcc atg 51
 Met Phe His Gly Arg Val Met Ala Met
 -30 -25
 ggt kat tta acc aaa cat tta aat cta aac att tct atc tca ctg ttg 99
 Gly Xaa Leu Thr Lys His Leu Asn Leu Asn Ile Ser Ile Ser Leu Leu
 -20 -15 -10

aca tct cca
Thr Ser Pro

511

<210> 481
<211> 429
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 212..427

<221> sig_peptide
<222> 212..382
<223> Von Heijne matrix
score 4.5
seq IWVRFNFLASSQA/CS

<400> 481
aggagagggga atttgtttta aaagagagaa agacattgag actgtgtaaa ggggatgttg 60
caacctttta aaatctgtga tctcagacca aattatacaa tataatctca gtaggtgccca 120
gtagtaggga aaagtgtcag ccctcgtgtc tggcactaag taccaccac cccaacccca 180
gtgatgggag cctctaaatg actgagattt a atg tct act acc tat ttg aat 232
Met Ser Thr Thr Tyr Leu Asn
-55
gag gac ttg aag aag aaa ttc agt gca gtk ata gag cag gtg ctt ttt 280
Glu Asp Leu Lys Lys Lys Phe Ser Ala Val Ile Glu Gln Val Leu Phe
-50 -45 -40 -35
gca cac tta tcc cca cta cat gtg tgg ctc cag ctc agg tct ctc tgt 328
Ala His Leu Ser Pro Leu His Val Trp Leu Gln Leu Arg Ser Leu Cys
-30 -25 -20
gag trt ttg acc tgc atc tgg gtt aga ttc aat ttt tta gcc tca agc 376
Glu Xaa Leu Thr Cys Ile Trp Val Arg Phe Asn Phe Leu Ala Ser Ser
-15 -10 -5
caa gca tgc tcc aaa tgc aac tcc tcg ttt ctc atc atg tca tcc tct 424
Gln Ala Cys Ser Lys Cys Asn Ser Ser Phe Leu Ile Met Ser Ser Ser
1 5 10
tca cc 429
Ser
15

<210> 482
<211> 385
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 145..384

<221> sig_peptide
<222> 145..261
<223> Von Heijne matrix
score 4.5

seq LIILDLLVPVIGL/IT

<400> 482

tacacgtaca gctcagcctt tctgttagct gcaacttcag tgttggtgaa ttattatgct 60
tctttgcaca ttgacttcta tgggtgcctac aacacgtcag cttgtggaat tgagctgctt 120
cctcgaaaag gtcctcgcgt gtgg atg gca ctt atc gtt cta cag cta aca 171
Met Ala Leu Ile Val Leu Gln Leu Thr

-35

ttt gga att gga tac gtt aca cta ctc cag att cat tcc atc tat tca 219
Phe Gly Ile Gly Tyr Val Thr Leu Leu Gln Ile His Ser Ile Tyr Ser
-30 -25 -20 -15

caa tta att att ttg gat ctc ttg gtt cct gta ata ggc tta atc aca 267
Gln Leu Ile Ile Leu Asp Leu Leu Val Pro Val Ile Gly Leu Ile Thr
-10 -5 1

gag cta cca tta cac atc aga gag act tta ctg ttt act tct tcc ttg 315
Glu Leu Pro Leu His Ile Arg Glu Thr Leu Leu Phe Thr Ser Ser Leu
5 10 15

att ctc aca tta aat aca gtg ttt gtc ctg gca gtg aaa ctg aar tgg 363
Ile Leu Thr Leu Asn Thr Val Phe Val Leu Ala Val Lys Leu Lys Trp
20 25 30

ttt tat tat tcc aca cga tat g 385
Phe Tyr Tyr Ser Thr Arg Tyr
35 40

<210> 483

<211> 202

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 39..200

<221> sig_peptide

<222> 39..110

<223> Von Heijne matrix

score 4.5

seq XVAXFLLTFYVIS/QV

<400> 483

catattaatg aaaagtgcc aaaactgaaa aaccaaac atg agg gta gca ggt gct 56
Met Arg Val Ala Gly Ala
-20

gca aar ttg gtg gta rct gtg gca rtg ttt tta ctg aca ttt tat gtt 104
Ala Lys Leu Val Val Xaa Val Ala Xaa Phe Leu Leu Thr Phe Tyr Val
-15 -10 -5

att tct caa gta ttt gaa ata aaa atg gat gca agt tta gga aat cta 152
Ile Ser Gln Val Phe Glu Ile Lys Met Asp Ala Ser Leu Gly Asn Leu
1 5 10

ttt gca aga tca gca ttg gac aca gct gca cgt tct aca aag cct ccg 200
Phe Ala Arg Ser Ala Leu Asp Thr Ala Ala Arg Ser Thr Lys Pro Pro
15 20 25 30

gg 202

<210> 484
 <211> 310
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 148..309

<221> sig_peptide
 <222> 148..192
 <223> Von Heijne matrix
 score 4.5
 seq TLVFLSTRQVLQC/QP

<400> 484
 gcggggctgg aggcggtggc tgcggttgcg ggaccggcac tatgctgggc cttcctacca 60
 cttatgtgtg gcttggtagt ggcctagggt ctctctccc tgctgaagtc cctctcctgc 120
 aggtggccgt ctgcccggcc cagcacc atg cac acg ctt gtg ttc ttg agc aca 174
 Met His Thr Leu Val Phe Leu Ser Thr
 -15 -10
 cgg cag gtg ctg cag tgc cag cca gct gcc tgc cag gcc ctg ccc ctg 222
 Arg Gln Val Leu Gln Cys Gln Pro Ala Ala Cys Gln Ala Leu Pro Leu
 -5 1 5 10
 ctg cca cgc gaa ctc ttc ccc ctg ctg ttc aag gtg gcc ttc atg ghc 270
 Leu Pro Arg Glu Leu Phe Pro Leu Leu Phe Lys Val Ala Phe Met Xaa
 15 20 25
 aag aag aca gtg gta ctg cgc gak ttg gta cac acg cgg g 310
 Lys Lys Thr Val Val Leu Arg Xaa Leu Val His Thr Arg
 30 35

<210> 485
 <211> 420
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 372..419

<221> sig_peptide
 <222> 372..413
 <223> Von Heijne matrix
 score 4.5
 seq TVVISCLVGECGS/WK

<400> 485
 agccggtggc agcacagcca ggacagccat ttcctcagca gccttcggta aaggcaacag 60
 attctgacgg taactgtgta tcagttggaa ttactgcact aactttgagg gccatactca 120
 aggactccaa taataaccaa gtcaatggcc ttagtggaat tacaacaatt ccgttttagca 180
 gctgttgggc caactacaca gaccttactc cccttagaac aggaaaaaat tataagattg 240
 aatttatact ggataatggt gttggggtag aatccagaac tttcagcctg ctggcagagt 300
 ctgtctctag cagtggcagc agcagcagca gcmacagcaa agcatcaact gtgggtacat 360
 atgccagat a atg act gtm gta att agc tgt ctg gtt gga gaa tgt ggc 410

Met Thr Val Val Ile Ser Cys Leu Val Gly Glu Cys Gly
-10 -5
tct tgg aaa t 420
Ser Trp Lys
1

<210> 486
<211> 226
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 10..225

<221> sig_peptide
<222> 10..150
<223> Von Heijne matrix
score 4.5
seq PIFGLLVPSQIFS/SL

<400> 486
caaccatac atg tgc aca ctc aca gac aca cac act cac gtc caa gtg cac 51
Met Cys Thr Leu Thr Asp Thr His Thr His Val Gln Val His
-45 -40 -35
aag tca aaa cct tgc cag ctc ctc tcc cct cct cca cca rsc cat ggt 99
Lys Ser Lys Pro Cys Gln Leu Leu Ser Pro Pro Pro Pro Xaa His Gly
-30 -25 -20
cct ctt ctt ctc cct atc ttt ggc ctt ctt gtg ccc tct cag att ttc 147
Pro Leu Leu Leu Pro Ile Phe Gly Leu Leu Val Pro Ser Gln Ile Phe
-15 -10 -5
agc tct ctt ctc aat tct cta cat ctg ggc ctg cct tcc ttc cca aag 195
Ser Ser Leu Leu Asn Ser Leu His Leu Gly Leu Pro Ser Phe Pro Lys
1 5 10 15
atg cca ctc atg att ttc ctc ccc cgc tgg g 226
Met Pro Leu Met Ile Phe Leu Pro Arg Trp
20 25

<210> 487
<211> 454
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 221..454

<221> sig_peptide
<222> 221..409
<223> Von Heijne matrix
score 4.5
seq QILXSTLAMKIHS/QQ

<400> 487

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agaaaatgga ggcgaatctg tatttccagt taactgctca gaagagagat gctgaagagc    60
tgtagtcgtg catccttctc accctccggt agaaagcctc ctctcatcct cagaagacta    120
ctgtcagagg atgtaggvat ggacatcccc tttgaagagg gcgtgctgag tcccagtgtc    180
gcagacatga ggctgaacc tcctaattct ctggatctta atg aca ctc atc ctc    235
                                   Met Thr Leu Ile Leu
                                   -60
gga gaa tca agc tca cag ccc caa ata tca atc ttt ctc tgg acc aaa    283
Gly Glu Ser Ser Ser Gln Pro Gln Ile Ser Ile Phe Leu Trp Thr Lys
      -55                    -50                    -45
gtg aag gat cta ttc tct ctg atg ata act tgg aca gtc cag atg aaa    331
Val Lys Asp Leu Phe Ser Leu Met Ile Thr Trp Thr Val Gln Met Lys
      -40                    -35                    -30
ttg aca tca atg tgg atg aac ttg ata ccc ccg atg aag cag att ctt    379
Leu Thr Ser Met Trp Met Asn Leu Ile Pro Pro Met Lys Gln Ile Leu
      -25                    -20                    -15
tdg agt aca ctg gcc atg aag atc cac agc caa caa aga ttc tgg cca    427
Xaa Ser Thr Leu Ala Met Lys Ile His Ser Gln Gln Arg Phe Trp Pro
      -10                    -5                    1                    5
aga gtc aga gtc tat tcc aga ata tac    454
Arg Val Arg Val Tyr Ser Arg Ile Tyr
      10                    15

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<210> 488
<211> 329
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 253..327

<221> sig_peptide
<222> 253..309
<223> Von Heijne matrix
      score 4.5
      seq VLFLNLNFQKIEE/EE

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<400> 488
cggctaattg gatgcctcca gctttgttct ttttgcttag gattgctttg gctatttggg    60
ctcctttttg ggtccatatt aatttttaaaa cagttttttc tggttttgtg aaggatgtca    120
ttggtagttt ataggaatag cahtgaatct gtagattgct ttgggcagta tggccatttt    180
aacaatatta attcttccta tctatgaata tggaatgttt ttccatgtgt ttgtgtcatc    240
tctttatacc tg atg tat aaa gaa aag ctg gta tta ttc cta ctc aat ctg    291
      Met Tyr Lys Glu Lys Leu Val Leu Phe Leu Leu Asn Leu
      -15                    -10
ttc caa aaa att gag gag gag gaa ctc ttc cct aat ga    329
Phe Gln Lys Ile Glu Glu Glu Glu Leu Phe Pro Asn
      -5                    1                    5

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<210> 489
<211> 414
<212> DNA
<213> Homo sapiens

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<220>
 <221> CDS
 <222> 149..412

<221> sig_peptide
 <222> 149..292
 <223> Von Heijne matrix
 score 4.5
 seq LELVATLPDDVQP/GP

<221> misc_feature
 <222> 396
 <223> n=a, g, c or t
 Oligonucleotide

<400> 489
 gaaagtgcag gcagctgtgg aaggcgaagt tcaatcccag agtccgcccc ctgaattggg 60
 gcctttccgg aggaggaagc tctgaaaaac agggggggccc agtgccattc cgcagggaat 120
 tgtcgcttgc gttcagctgt tctacaca atg gac tca gta cct gcc act gtg 172
 Met Asp Ser Val Pro Ala Thr Val
 -45
 cct tct atc gcc gct acc ccg ggg gac ccg gaa ctt gtg gga ccc ttg 220
 Pro Ser Ile Ala Ala Thr Pro Gly Asp Pro Glu Leu Val Gly Pro Leu
 -40 -35 -30 -25
 tct gtg ctc tac gca gcc ttc ata gcc aag ctg ctg gag cta gtt gct 268
 Ser Val Leu Tyr Ala Ala Phe Ile Ala Lys Leu Leu Glu Leu Val Ala
 -20 -15 -10
 aca ttg cct gat gat gtt cag cct ggg cct gat ttt tat ggr stg sca 316
 Thr Leu Pro Asp Asp Val Gln Pro Gly Pro Asp Phe Tyr Gly Xaa Xaa
 -5 1 5
 tgg aaa ctg tat tta tca ctg cct tct tgg gaa tkg ttc gtt tgc cat 364
 Trp Lys Leu Tyr Leu Ser Leu Pro Ser Trp Glu Xaa Phe Val Cys His
 10 15 20
 ttt ctt atg gag act gtc ctt gtt gtg aag gnt aga gta tat cwa gtc 412
 Phe Leu Met Glu Thr Val Leu Val Val Lys Xaa Arg Val Tyr Xaa Val
 25 30 35 40
 ac 414

<210> 490
 <211> 185
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 69..185

<221> sig_peptide
 <222> 69..122
 <223> Von Heijne matrix
 score 4.5
 seq AVWASVASPASIC/CG

<400> 490


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agttccggcc tccaaggggc gggcagaagt tggaacatg cggctgtcgg tcgctgcagc      60
gatctccc atg gcc gcg tat ttc gcc gta tgg gcc tcg gtc gcg agt ccc      110
      Met Ala Ala Tyr Phe Ala Val Trp Ala Ser Val Ala Ser Pro
            -15             -10             -5
gca tcc atc tgt tgc ggr amy tgg ctc aca ggg ctg gtg cgg cac gaa      158
Ala Ser Ile Cys Cys Gly Xaa Trp Leu Thr Gly Leu Val Arg His Glu
            1             5             10
cgc atc gag gca cca tgg gcg cgt ggg      185
Arg Ile Glu Ala Pro Trp Ala Arg Gly
            15             20

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<210> 491
<211> 348
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> 247..348

<221> sig_peptide
<222> 247..333
<223> Von Heijne matrix
      score 4.5
      seq ILLILQLLKXSLK/KC

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<221> misc_feature
<222> 323..324
<223> n=a, g, c or t
      Oligonucleotide

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<400> 491
ttatgtttta aaggtcacaa gtctagaata actgaattgg gaattggaaa taccttaatt      60
ctataatttg tatctaaaat taggttttcc cttttaagtt gttaattttc tatggkttgt      120
gctgcatgct ttcactttta ttagtactta cagccaaaga gatgggcaaa tgtctagaaa      180
aattaatggt ttgattcagg aatttgtgcc tagtgatggc ctccaataga gaattttcca      240
gagaga atg aag act cag ttt cta agt tgg ggc aaa ttt agt ttt tgt      288
      Met Lys Thr Gln Phe Leu Ser Trp Gly Lys Phe Ser Phe Cys
            -25             -20
ttt ggt att ctt ctt ata tta cag cta tta aaa bnn tct ctt aaa aaa      336
Phe Gly Ile Leu Leu Ile Leu Gln Leu Leu Lys Xaa Ser Leu Lys Lys
-15             -10             -5             1
tgc cgg cac ggg      348
Cys Arg His Gly
            5

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<210> 492
<211> 126
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> 5..124

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<221> sig_peptide
 <222> 5..79
 <223> Von Heijne matrix
 score 4.5
 seq LRFILPSSWDCRC/AP

<400> 492
 ctac atg ctt cct gct gtg gct gtc tcg gaa ccc gtg gtc ctc cgc ttc 49
 Met Leu Pro Ala Val Ala Val Ser Glu Pro Val Val Leu Arg Phe
 -25 -20 -15
 att ctg ccg agt tcc tgg gat tgc agg tgc gcg ccg cca ctc ctg act 97
 Ile Leu Pro Ser Ser Trp Asp Cys Arg Cys Ala Pro Pro Leu Leu Thr
 -10 -5 1 5
 ggt ttt tgt att ttt tgg ktg gag acg gg 126
 Gly Phe Cys Ile Phe Trp Xaa Glu Thr
 10 15

<210> 493
 <211> 300
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 119..298

<221> sig_peptide
 <222> 119..217
 <223> Von Heijne matrix
 score 4.40000009536743
 seq WLLMVAPRLPAGA/RD

<400> 493
 acactgcctg cctggtgcag cccatgtgac gggctcgagct ccgggccctg ctgtccctgg 60
 ccgggctatc ccagtggctt caggcacctt ctccagacct acccagaaaag atgcccg 118
 atg gat cct gca gct ccg tgg ctt ttc tgg gaa gca gcg gcc cct gct 166
 Met Asp Pro Ala Ala Pro Trp Leu Phe Trp Glu Ala Ala Ala Pro Ala
 -30 -25 -20
 ctc aag aga ccc tgg ctc ctg atg gtg gcc cca agg ttg cca gct ggt 214
 Leu Lys Arg Pro Trp Leu Leu Met Val Ala Pro Arg Leu Pro Ala Gly
 -15 -10 -5
 gct agg gac tca gga cag ttt ccc aga aaa ggc caa gcg ggc agc ccc 262
 Ala Arg Asp Ser Gly Gln Phe Pro Arg Lys Gly Gln Ala Gly Ser Pro
 1 5 10 15
 tcc agg ggc cgg gtg agg aag ctg ggg ggt gcg gtg gg 300
 Ser Arg Gly Arg Val Arg Lys Leu Gly Gly Ala Val
 20 25

<210> 494
 <211> 295
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 182..295

<221> sig_peptide
 <222> 182..274
 <223> Von Heijne matrix
 score 4.40000009536743
 seq SRLXALLSPYAFT/LX

<400> 494
 tttatacacacacacacacacacactcata ttcattacat gtgtgtactt tctggttgct 60
 tcagtaggac ttttctaggc ttctttggac tatgtgtgat attttacttc agggactgaa 120
 tttcacaact gcctactatg caactttgtg attttcttga aagcacaakt actatatata 180
 a atg aaa atg tcc acc ccc tcc ccg ctt tct aaa aaa gtg ctc aga aac 229
 Met Lys Met Ser Thr Pro Ser Pro Leu Ser Lys Lys Val Leu Arg Asn
 -30 -25 -20
 cag gtc tca aga ttg rtt gcg ttg ctt tcc cca tac gct ttc act ctg 277
 Gln Val Ser Arg Leu Xaa Ala Leu Leu Ser Pro Tyr Ala Phe Thr Leu
 -15 -10 -5 1
 sct cgt ctt gcc tca ggg 295
 Xaa Arg Leu Ala Ser Gly
 5

<210> 495
 <211> 244
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 70..243

<221> sig_peptide
 <222> 70..114
 <223> Von Heijne matrix
 score 4.40000009536743
 seq RFLLLYATQQGQA/KA

<400> 495
 ggaagtcgcg ttgtgcaggt tcgtgcccg ctggcgcggc gtggtttcac tgttacatgc 60
 cttgaagtg atg agg agg ttt ctg tta cta tat gct aca cag cag gga cag 111
 Met Arg Arg Phe Leu Leu Leu Tyr Ala Thr Gln Gln Gly Gln
 -15 -10 -5
 gca aag gcc atc gca gaa gaa atg tgt rag caa gct gtg gta cat gga 159
 Ala Lys Ala Ile Ala Glu Glu Met Cys Xaa Gln Ala Val Val His Gly
 1 5 10 15
 ttt tct gca gat ctt cac tgt att agt gaa tcc gat aag gtc tcg gtg 207
 Phe Ser Ala Asp Leu His Cys Ile Ser Glu Ser Asp Lys Val Ser Val
 20 25 30
 att cag aat aca cct act ttt gca acg ggg ggg cgg g 244
 Ile Gln Asn Thr Pro Thr Phe Ala Thr Gly Gly Arg
 35 40

<210> 496
 <211> 215
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 91..213

<221> sig_peptide
 <222> 91..171
 <223> Von Heijne matrix
 score 4.40000009536743
 seq FVNLNLCFAYTFA/LY

<400> 496
 atttaagtcc agagagcaag gtgattgcag tttctttggt cggtttgctt attttttact 60
 gcttatttct gtgtgcataa attcagcgac atg cta ata gac ata tgg tca atg 114
 Met Leu Ile Asp Ile Trp Ser Met
 -25 -20
 gtg ctt aga gaa aat ctg ttt gta aac ctg aat ctc tgt ttt gcc tac 162
 Val Leu Arg Glu Asn Leu Phe Val Asn Leu Asn Leu Cys Phe Ala Tyr
 -15 -10 -5
 aca ttt gca ttg tat tcc tgc cct gct cca act cgt tgt cct aga cca 210
 Thr Phe Ala Leu Tyr Ser Cys Pro Ala Pro Thr Arg Cys Pro Arg Pro
 1 5 10
 tcc ag 215
 Ser

<210> 497
 <211> 255
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 36..254

<221> sig_peptide
 <222> 36..89
 <223> Von Heijne matrix
 score 4.40000009536743
 seq WFPLSCSPSLPLS/IP

<400> 497
 cttttgggggt tcgctgtttc ttccctctct gctgg atg ctg tct tgc ccc tgg 53
 Met Leu Ser Cys Pro Trp
 -15
 ttt ccc cta tcc tgt tct ccc tcc ttg cct ctg agc atc cca gac tgc 101
 Phe Pro Leu Ser Cys Ser Pro Ser Leu Pro Leu Ser Ile Pro Asp Cys
 -10 -5 1
 ctg cct gcc ttc ctc tgg ccg ctg ggg ata ccc tgg cct gat gga gag 149
 Leu Pro Ala Phe Leu Trp Pro Leu Gly Ile Pro Trp Pro Asp Gly Glu
 5 10 15 20

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ggt cta aga cct tcc cgt ctt ctc cgg aca cgg gaa aac att acc cct      197
Gly Leu Arg Pro Ser Arg Leu Leu Arg Thr Arg Glu Asn Ile Thr Pro
                25                      30                      35
ctc tct tta ttc gct atg ctg agt ggc agg gag ggt gcc ccg ctc ctg      245
Leu Ser Leu Phe Ala Met Leu Ser Gly Arg Glu Gly Ala Pro Leu Leu
                40                      45                      50
gtc ccc ctg g
Val Pro Leu
                55

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<210> 498
<211> 82
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> 23..82

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<221> sig_peptide
<222> 23..61
<223> Von Heijne matrix
      score 4.40000009536743
      seq MVVVSFLASSSLP/AE

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<400> 498
ctttttcgtc tgggctgccac ac atg gta gtt gtt tcg ttt ctt gcc tcc tct      52
                        Met Val Val Val Ser Phe Leu Ala Ser Ser
                        -10                      -5
tcc ttg ccg gcg gag acc cct aag caa ggg
Ser Leu Pro Ala Glu Thr Pro Lys Gln Gly      82
                1                      5

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<210> 499
<211> 474
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> 39..473

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<221> sig_peptide
<222> 39..359
<223> Von Heijne matrix
      score 4.40000009536743
      seq IIILFVVITSRRG/SP

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<400> 499
ttcctggacc gcgctggaag ccctggcggc ggcgggccc atg ggg csc ttg gcg ctg      56
                        Met Gly Xaa Leu Ala Leu
                        -105
cyc gcc tgg ctg cag ccc agg tat agg aag aat gcg tat ctt ttc atc      104
Xaa Ala Trp Leu Gln Pro Arg Tyr Arg Lys Asn Ala Tyr Leu Phe Ile

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-100	-95	-90	
tat tac tta atc cag ttc tgt ggc cas tct tgg ata ttt gca aat atg			152
Tyr Tyr Leu Ile Gln Phe Cys Gly Xaa Ser Trp Ile Phe Ala Asn Met			
-85	-80	-75	-70
aca gtc aga ttc ttt tca ttt gga aaa gat tca atg gtt gac act ttt			200
Thr Val Arg Phe Phe Ser Phe Gly Lys Asp Ser Met Val Asp Thr Phe			
-65	-60	-55	
tat gct att gga ctt gtg atg cga ctt tgc caa tcc gta tct ctc ctg			248
Tyr Ala Ile Gly Leu Val Met Arg Leu Cys Gln Ser Val Ser Leu Leu			
-50	-45	-40	
gaa ctg ctg cac ata tat gtt ggc att gag tca aac cat ctt ctc cca			296
Glu Leu Leu His Ile Tyr Val Gly Ile Glu Ser Asn His Leu Leu Pro			
-35	-30	-25	
agg ttt ttg cag ctc aca gaa aga ata atc atc ctt ttt gtg gtg atc			344
Arg Phe Leu Gln Leu Thr Glu Arg Ile Ile Ile Leu Phe Val Val Ile			
-20	-15	-10	
acc agt cga aga gga agt cca acg aga aat atg tgg tgt gtg tgt tat			392
Thr Ser Arg Arg Gly Ser Pro Thr Arg Asn Met Trp Cys Val Cys Tyr			
-5	1	5	10
tcg tct ttg gat cta tgg ata tgg tta rgt aca ctt ata gca tgk tda			440
Ser Ser Leu Asp Leu Trp Ile Trp Leu Xaa Thr Leu Ile Ala Xaa Xaa			
15	20	25	
tca gtc ata gga ata tcc tat gct gtc ttg aca t			474
Ser Val Ile Gly Ile Ser Tyr Ala Val Leu Thr			
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<210> 500
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 <213> Homo sapiens

<220>
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 <222> 177..239

<221> sig_peptide
 <222> 177..230
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 score 4.40000009536743
 seq SLTLTALLVPSRV/QP

<400> 500	
cttcactcat ggggagagca tttctacctg acaccctccc atttctgttt tccttaccca	60
gatctacctt ctgagatatt atccttcttc agggagataa ggaaaaaaag ccacagggtc	120
ccggagagcc aggggaatgg tgagtgtttc ctgtctccat tactggctgt aacagg atg	179
	Met
gac aca ttc cct tct ctt acc ctg act gcc tta ttg gtg cct agt aga	227
Asp Thr Phe Pro Ser Leu Thr Leu Thr Ala Leu Leu Val Pro Ser Arg	
-15	-10
gtt cag ccc cag gg	241
Val Gln Pro Gln	
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<210> 501

<211> 430
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 178..429

<221> sig_peptide
 <222> 178..237
 <223> Von Heijne matrix
 score 4.40000009536743
 seq LRYVASAVFGVIG/SQ

<221> misc_feature
 <222> 17
 <223> n=a, g, c or t
 Oligonucleotide

<400> 501
 gaggtgagtc ctggrntgc gtgggtgggg cggagagcat tatctgcggc tccgattttg 60
 cagattctgg ctgaggcgtt cgtgatgtca gcagcagccg agacgggctt gttaaaggcc 120
 gggtgctagg gctgggggaa ctcagattgc ttcacctgtg gtatcagaca tcacaac 177
 atg ggg ctc acc aag cag tac cta cgc tat gtt gct agt gcg gtc ttt 225
 Met Gly Leu Thr Lys Gln Tyr Leu Arg Tyr Val Ala Ser Ala Val Phe
 -20 -15 -10 -5
 ggc gtt atc ggc agc caa aaa ggt aat att gtc ttt gtg aca ctt cgt 273
 Gly Val Ile Gly Ser Gln Lys Gly Asn Ile Val Phe Val Thr Leu Arg
 1 5 10
 ggt gag aaa gga cgt tat gtg gca gta cca gct tgt gaa cac gtt ttc 321
 Gly Glu Lys Gly Arg Tyr Val Ala Val Pro Ala Cys Glu His Val Phe
 15 20 25
 atc wgg gac tta agg aaa gga gag aag att ctt atc ctt cag ggg ctt 369
 Ile Xaa Asp Leu Arg Lys Gly Glu Lys Ile Leu Ile Leu Gln Gly Leu
 30 35 40
 aaa caa gaa gtt act tgc tta tgc ccc tcc cca gat ggg cta cac tta 417
 Lys Gln Glu Val Thr Cys Leu Cys Pro Ser Pro Asp Gly Leu His Leu
 45 50 55 60
 gct gtt ggg tat g 430
 Ala Val Gly Tyr

<210> 502
 <211> 413
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 333..413

<221> sig_peptide
 <222> 333..404
 <223> Von Heijne matrix
 score 4.40000009536743

seq VFFSVLYVQQGLS/SQ

<221> misc_feature

<222> 7,359

<223> n=a, g, c or t
Oligonucleotide

<400> 502

agggasnggc	agtgatcacg	caagccggag	cggcgggctg	acgttggacg	agctgccagg	60
tagctgaaag	caggcagcca	ggcagccgag	acacttccca	gcgattccag	cctgggctcc	120
gcagaagcct	cgctgaatcc	cagccagctg	gttctaacct	tccagaatcg	caatcccttc	180
tccccacagc	cagccctcgc	cgagcaagca	gcaggatggt	tgcagtgtcg	cgcccagggc	240
tctgagactg	agcctgccat	ccactcgcac	gcctttcttt	cagggctttt	cggctgttgg	300
ctacactgat	gtgaccccc	tccctttttg	ga atg atg	ggg atc ttt ttg gtg		353
			Met Met	Gly Ile Phe Leu Val		

-20

tat gtn gga ttt gtt ttc ttt tcc gtt tta tat	gta caa caa ggg ctt	401
Tyr Val Gly Phe Val Phe Phe Ser Val Leu Tyr	Val Gln Gln Gly Leu	
-15	-10	-5

tct tct caa gca	413
Ser Ser Gln Ala	
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<210> 503

<211> 167

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 26..166

<221> sig_peptide

<222> 26..91

<223> Von Heijne matrix
score 4.40000009536743
seq WVLDPALLLTCLT/FP

<400> 503

gaatcggaca	acttaaagtc	tcgat	atg agc ctc gga ttg cat tcg aac tcc	52
			Met Ser Leu Gly Leu His Ser Asn Ser	
			-20	-15

tgg gtt cta gac cca gct ctg cta cta act tgt ctg acc ttc ccc att	100	
Trp Val Leu Asp Pro Ala Leu Leu Leu Thr Cys Leu Thr Phe Pro Ile		
-10	-5	1

tat aaa ctg ttg tgg gtg aga ggt ggg acw agg wga act ctr wgr gcv	148	
Tyr Lys Leu Leu Trp Val Arg Gly Gly Thr Arg Xaa Thr Leu Xaa Ala		
5	10	15

ctg cac tcg gcg cgg acg g	167
Leu His Ser Ala Arg Thr	
20	25

<210> 504

<211> 420

<212> DNA
 <213> Homo sapiens

 <220>
 <221> CDS
 <222> 217..420

 <221> sig_peptide
 <222> 217..396
 <223> Von Heijne matrix
 score 4.40000009536743
 seq MWVXCXFCFVLC/FE

 <221> misc_feature
 <222> 47..48,368..369,373
 <223> n=a, g, c or t
 Oligonucleotide

<400> 504
 ggktccgctc cctggggcgc acgtcagtca ggaggcggaa gcgcagnnga ggcgggaagg 60
 ttgtagtgcc gcgagttgag ctctctttgc ctaagtggtc gcgccccctt taagagcagc 120
 gattgtaagg agaggcggtc ccggtgtcct cgggtcccag gtgattgtga agtgctgacc 180
 aattgccact ggacatactt gaaacaaaat aggaaa atg gca gca aac tct tca 234
 Met Ala Ala Asn Ser Ser
 -60 -55
 gga caa ggt ttt caa aac aaa aat aga gtt gca atc ttg gca gaa ctg 282
 Gly Gln Gly Phe Gln Asn Lys Asn Arg Val Ala Ile Leu Ala Glu Leu
 -50 -45 -40
 aca aag aga aaa gaa aac tac tta tgc aga acc agt ctt caa caa atc 330
 Thr Lys Arg Lys Glu Asn Tyr Leu Cys Arg Thr Ser Leu Gln Gln Ile
 -35 -30 -25
 atc ctg gar cta ggt att gac act ata atg tgg gtt tnn tgt ntg ttt 378
 Ile Leu Glu Leu Gly Ile Asp Thr Ile Met Trp Val Xaa Cys Xaa Phe
 -20 -15 -10
 tgt ttt gtt ttg ttt tgt ttt gag acg gag tct cgc cct gtc 420
 Cys Phe Val Leu Phe Cys Phe Glu Thr Glu Ser Arg Pro Val
 -5 1 5

<210> 505
 <211> 457
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> CDS
 <222> 43..456

 <221> sig_peptide
 <222> 43..147
 <223> Von Heijne matrix
 score 4.40000009536743
 seq PAPLLFLPPAAPG/GE

 <221> misc_feature

<222> 416..417

<223> n=a, g, c or t
Oligonucleotide

<400> 505

gtagtcggat agttggcggg tggttgagtg gaagcggtcg cc atg tcc gcg ggg 54
Met Ser Ala Gly
-35
agc gcg aca cat cct gga gct ggc ggg cgc cgc agc aaa tgg gac caa 102
Ser Ala Thr His Pro Gly Ala Gly Gly Arg Arg Ser Lys Trp Asp Gln
-30 -25 -20
cca gct cca gcc cca ctt ctc ttc ctc ccg cca gcg gcc cca ggt ggg 150
Pro Ala Pro Ala Pro Leu Leu Phe Leu Pro Pro Ala Ala Pro Gly Gly
-15 -10 -5 1
gag gtc acc agc agt ggg gga agt cct ggg gsc acc aca gct gct cct 198
Glu Val Thr Ser Ser Gly Gly Ser Pro Gly Xaa Thr Thr Ala Ala Pro
5 10 15
tca gga gcc ttg gat gct gct gct gct gtg gct gcc aag att aat gcc 246
Ser Gly Ala Leu Asp Ala Ala Ala Val Ala Ala Lys Ile Asn Ala
20 25 30
atg ctc atg gca aaa ggg aag ctg aaa cca act cag rat gct tct gag 294
Met Leu Met Ala Lys Gly Lys Leu Lys Pro Thr Gln Xaa Ala Ser Glu
35 40 45
aag ctt cag gct cct ggc aaa ggc cta act agc aat aaa agc aag gat 342
Lys Leu Gln Ala Pro Gly Lys Gly Leu Thr Ser Asn Lys Ser Lys Asp
50 55 60 65
gac ctg gtg gta gct gaa gta gaa att aat gat gtg cct ctc aca tgt 390
Asp Leu Val Val Ala Glu Val Glu Ile Asn Asp Val Pro Leu Thr Cys
70 75 80
agg aac ttg ctg act cga gga cag ann caa gac gag atc agc cga ctt 438
Arg Asn Leu Leu Thr Arg Gly Gln Xaa Gln Asp Glu Ile Ser Arg Leu
85 90 95
agt ggg gct gca gta tca a 457
Ser Gly Ala Ala Val Ser
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<210> 506

<211> 315

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 141..314

<221> sig_peptide

<222> 141..203

<223> Von Heijne matrix
score 4.40000009536743
seq IRAVCLSGGSCWG/GV

<400> 506

ctctttctgt cttgattttt ctgtgtgtct ctctgcgtct tgtctatttg ttttctctct 60
ttcttctctg tggccctccc ctttgtctct tcctttctgt tttctcctgt agttctcct 120

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cttctctccc ctgattgctc atg agt ccc ctt gat cag gct gta ata cgt gct      173
                Met Ser Pro Leu Asp Gln Ala Val Ile Arg Ala
                -20                -15
gtg tgt ctc agt gga ggt tcc tgc tgg gga gga gtc cgt tgt ctt gtg      221
Val Cys Leu Ser Gly Gly Ser Cys Trp Gly Gly Val Arg Cys Leu Val
-10                -5                1                5
cgt ggg ggc ccg aac ata ggc cct gca gcc cag ctg ctt ggg ggc att      269
Arg Gly Gly Pro Asn Ile Gly Pro Ala Ala Gln Leu Leu Gly Gly Ile
                10                15                20
cca ctc tgc tgg cca cca gct gtg act gca ggt gaa gtg aaa ctg c      315
Pro Leu Cys Trp Pro Pro Ala Val Thr Ala Gly Glu Val Lys Leu
                25                30                35

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<210> 507
<211> 208
<212> DNA
<213> Homo sapiens

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<220>
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<222> 152..208

<221> sig_peptide
<222> 152..196
<223> Von Heijne matrix
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      seq SFHFIXFLPFWA/EX

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<221> misc_feature
<222> 201..202
<223> n=a, g, c or t
      Oligonucleotide

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<400> 507
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cgtcgagcct gcgcactctg cctgagaccc tcgaccagc ccggtcctg tcctcctgta      120
ttcctgcagt ccttttaagg aagaaaagtg a atg aac tca ttt cat ttt att      172
                Met Asn Ser Phe His Phe Ile
                -15                -10
tss ttc ctc cct ttc ccc tgg gct gaa wnn gcg cag      208
Xaa Phe Leu Pro Phe Pro Trp Ala Glu Xaa Ala Gln
                -5                1

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<210> 508
<211> 169
<212> DNA
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<220>
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<222> 65..169

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<221> sig_peptide
<222> 65..151

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<223> Von Heijne matrix
 score 4.40000009536743
 seq LLSTHTWTDALA/FS

<400> 508
 atacagacac ccagrsagga ccctgaacac acagacaggc acagggaccc ctgtgcccac 60
 aggg atg ggc tgg cac tca cat agt tcc caa ggc gtg caw gca atg cct 109
 Met Gly Trp His Ser His Ser Ser Gln Gly Val Xaa Ala Met Pro
 -25 -20 -15
 ctg ctg ctg tcc aca cac acc tgg aca gac aca gcc ctg gca ttc agc 157
 Leu Leu Leu Ser Thr His Thr Trp Thr Asp Thr Ala Leu Ala Phe Ser
 -10 -5 1
 aca cac aca cac 169
 Thr His Thr His
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<210> 509
 <211> 118
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 12..116
 <221> sig_peptide
 <222> 12..77
 <223> Von Heijne matrix
 score 4.40000009536743
 seq WFLRSWTPQTAG/RV

<400> 509
 caattcaagt c atg crg gct gtg aga aac gcg ggg tcg tgg ttc ctg cgg 50
 Met Xaa Ala Val Arg Asn Ala Gly Ser Trp Phe Leu Arg
 -20 -15 -10
 tcc tgg act tgg ccc cag aca gcc ggc agg gtc gtg gcc aga rsg ccg 98
 Ser Trp Thr Trp Pro Gln Thr Ala Gly Arg Val Val Ala Arg Xaa Pro
 -5 1 5
 gcc ggg acc atc tgc aca gg 118
 Ala Gly Thr Ile Cys Thr
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<210> 510
 <211> 402
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 334..402
 <221> sig_peptide
 <222> 334..378
 <223> Von Heijne matrix

score 4.40000009536743
seq ALFILVSISLFYA/LF

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<400> 510
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cacctggcac gtgcccttca aatgtctcca ctgcgtcttt gcctttccct tttctgttgc      120
gtgccatcat tccgattccg attttaacag caacctgctg atttcctgcc atagtttcct      180
actttccatt ctgagcccct ttaatccact tataacaatat aactactccc tgaattattt      240
ggtcatacca cttgtatctg ccgaaccctt attcctcccc tgggggtacgt tttccactaa      300
acacacacag ggaaatgcca ccaaatagc tct atg tgt gcc ttg ttc att ctt      354
                               Met Cys Ala Leu Phe Ile Leu
                               -15                               -10
gtt tcc att tct ttg ttt tat gca ctt ttt atc tct cca tcc ata caa      402
Val Ser Ile Ser Leu Phe Tyr Ala Leu Phe Ile Ser Pro Ser Ile Gln
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<210> 511
<211> 343
<212> DNA
<213> Homo sapiens

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<221> CDS
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<221> sig_peptide
<222> 159..317
<223> Von Heijne matrix
score 4.40000009536743
seq NLVLYFLVHLLFS/LS

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<400> 511
cagaggcttt tatttgcata aatgtcggac cgtcttagct ctcttgtgaa aggaactttt      60
tgccatatta tagtggctca ccttacctcc tggaatgcat tctggcctca agtctgtacc      120
tagcattgat agaggaagcc cagcctgggtg tgcacagc atg tac ctg gtg tgc aca      176
                               Met Tyr Leu Val Cys Thr
                               -50
aca tgc acc tgg tgt gta ttt tct gaa atg ttt gtt cat gga tta aac      224
Thr Cys Thr Trp Cys Val Phe Ser Glu Met Phe Val His Gly Leu Asn
                               -45                               -40                               -35
atc act cag ctc gtg ctg agc cag ctg gat tac ttt ttc cat tcc aat      272
Ile Thr Gln Leu Val Leu Ser Gln Leu Asp Tyr Phe Phe His Ser Asn
                               -30                               -25                               -20
ctg aca aac ttg gtc ttg tat ttc tta gtc cat tta ctt ttt tcc ctt      320
Leu Thr Asn Leu Val Leu Tyr Phe Leu Val His Leu Leu Phe Ser Leu
                               -15                               -10                               -5                               1
agc ctg ttt atg ccg ctg acg gg      343
Ser Leu Phe Met Pro Leu Thr
                               5
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<210> 512
<211> 420
<212> DNA
<213> Homo sapiens

<220>
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 <222> 7..420

 <221> sig_peptide
 <222> 7..240
 <223> Von Heijne matrix
 score 4.40000009536743
 seq FWWWLGSLXVTWL/IH

<221> misc_feature
 <222> 93,100,137..138
 <223> n=a, g, c or t
 Oligonucleotide

<400> 512
 taagtg atg aag ctg aaa tta tac cta tgt ata tta ggt ccc tgg ggc 48
 Met Lys Leu Lys Leu Tyr Leu Cys Ile Leu Gly Pro Trp Gly
 -75 -70 -65
 tgc aak rkc aaa gta cca cta att ggg ttt ctt aaa aga ata aan hta 96
 Cys Xaa Xaa Lys Val Pro Leu Ile Gly Phe Leu Lys Arg Ile Xaa Xaa
 -60 -55 -50
 tat nwt ctc aca gtt ctg aaa cct agd agt ctg ara tca ann tca gca 144
 Tyr Xaa Leu Thr Val Leu Lys Pro Xaa Ser Leu Xaa Ser Xaa Ser Ala
 -45 -40 -35
 ggg ttg gtt cct tct gag gac tct aaa aaa gaa tct gtt tca tgc ctc 192
 Gly Leu Val Pro Ser Glu Asp Ser Lys Lys Glu Ser Val Ser Cys Leu
 -30 -25 -20
 tct cct agg ttc tgg tgg tgg ctg gga agc ctg akt gtt act tgg ctt 240
 Ser Pro Arg Phe Trp Trp Trp Leu Gly Ser Leu Xaa Val Thr Trp Leu
 -15 -10 -5
 ata cat gca tca ctc cag tct ctg tct cct ttt tct cat gcc att ttc 288
 Ile His Ala Ser Leu Gln Ser Leu Ser Pro Phe Ser His Ala Ile Phe
 5 10 15
 tca tgt gtc tct gtg ttt tcc ttt gct tat aag gat acc agt cat att 336
 Ser Cys Val Ser Val Phe Ser Phe Ala Tyr Lys Asp Thr Ser His Ile
 20 25 30
 gaa tta ggg cct gct cta ata acc tca tct caa tta cct ctg caa gga 384
 Glu Leu Gly Pro Ala Leu Ile Thr Ser Ser Gln Leu Pro Leu Gln Gly
 35 40 45
 acc aat ttc caa ata atg tca cac tca cat gta gca 420
 Thr Asn Phe Gln Ile Met Ser His Ser His Val Ala
 50 55 60

<210> 513
 <211> 324
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 219..323

<221> sig_peptide
 <222> 219..317
 <223> Von Heijne matrix
 score 4.40000009536743
 seq LKLLFLILILIAG/YR

<400> 513
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 acaaaatcag atgctccaaa tggtcagttg atgatgatac caatcaaaga aaactaagga 120
 ggaagaaaaa gaaaacagga aagagaggag gcaacaggaa aatcggcctt cgtccttcag 180
 tctacgcttg aaattgccag ggatggataa atctgaag atg aat gaa aaa aag aaa 236
 Met Asn Glu Lys Lys Lys
 -30

cta ctg gga acg gaa cag aaa caa aaa aaa agg atg gga aat ctg aag 284
 Leu Leu Gly Thr Glu Gln Lys Gln Lys Lys Arg Met Gly Asn Leu Lys
 -25 -20 -15
 ctg cta ttt ctt att ctg atc tta ata gca gga tac agg g 324
 Leu Leu Phe Leu Ile Leu Ile Leu Ile Ala Gly Tyr Arg
 -10 -5 1

<210> 514
 <211> 303
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 212..301

<221> sig_peptide
 <222> 212..292
 <223> Von Heijne matrix
 score 4.40000009536743
 seq SALMLPLGCAVRT/RM

<400> 514
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 ctcccccatc gcaaccacaca ggagggtttc cctcactctg cctcctccaw cgcaccccca 120
 kggagggtgtt ttccctcact gggtctgttg gtggcgggtg cagcaatccg agtcacatgg 180
 caccagagta tgtcacgggt ggcggatctg a atg ggg ctg cag agc ctc aca 232
 Met Gly Leu Gln Ser Leu Thr
 -25

ctt cca gtg tct tgc agc cct tct gcc ctg atg ctt ccc ttg gga tgt 280
 Leu Pro Val Ser Cys Ser Pro Ser Ala Leu Met Leu Pro Leu Gly Cys
 -20 -15 -10 -5
 gct gtc cgc acg cgc atg ctt ga 303
 Ala Val Arg Thr Arg Met Leu
 1

<210> 515
 <211> 455
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 342..455

<221> sig_peptide
 <222> 342..434
 <223> Von Heijne matrix
 score 4.40000009536743
 seq LTTLESLAGSVXS/EQ

<400> 515
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 acatgtatca gtgtgttgat ttgcacaaac caataaaagc cctacatttt ttggaaatgg 120
 atcccctagat ttcaagcatg tataatcact caaagtggat atgatcacag gcattcttct 180
 cttgagctca gcaaaactat gcctaccaac accgaagaga agtcaaagat ttttatgaaa 240
 aaaaattgca gatgatgttg gtgagataat aggatatgag caatgaaccc ttgggtgggg 300
 ttccagggca cttaaattgc ctcgtgtctt gagtccttaa g atg gac tca aac aaa 356
 Met Asp Ser Asn Lys
 -30
 aaa tta gta tta tca ata aca ggt aat act gtg tgg att cta aca aca 404
 Lys Leu Val Leu Ser Ile Thr Gly Asn Thr Val Trp Ile Leu Thr Thr
 -25 -20 -15
 tta gaa tca tta gct ggc agt gtc aam tct gaa caa gat ttg tca gct 452
 Leu Glu Ser Leu Ala Gly Ser Val Xaa Ser Glu Gln Asp Leu Ser Ala
 -10 -5 1 5
 tat 455
 Tyr

<210> 516
 <211> 360
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 196..360

<221> sig_peptide
 <222> 196..336
 <223> Von Heijne matrix
 score 4.40000009536743
 seq SFXXCLFLXLXS/EM

<221> misc_feature
 <222> 330..332
 <223> n=a, g, c or t
 Oligonucleotide

<400> 516
 aagagcgttg ggcagatata gtctgtagat atttttgaaa cgtcttttggg tttgtcccat 60
 ttgggggttg ctcagcttct tgaatctgta ggttttgggg atcccccamc ctgcaaattt 120
 ggtgatattt ttgctcttat ttctkcaagt gaacttgaaa tcccaccctg ttggttttct 180
 ccttctaaga ctctg atg acg tgt atg tta gcc tgt agg tgt agt ctc amg 231
 Met Thr Cys Met Leu Ala Cys Arg Cys Ser Leu Xaa

					-45						-40						
ggt	ccc	caa	gat	ttt	cgt	ttc	tgc	tct	gtc	ttt	tct	ctg	ttg	ctc	aag		279
Gly	Pro	Gln	Asp	Phe	Arg	Phe	Cys	Ser	Val	Phe	Ser	Leu	Leu	Leu	Lys		
-35					-30					-25					-20		
ttg	ggt	aat	ttc	tat	ttt	tct	ttt	wct	dtc	tgt	ctw	ttt	ctw	dta	ctd		327
Leu	Gly	Asn	Phe	Tyr	Phe	Ser	Phe	Xaa	Xaa	Cys	Leu	Phe	Leu	Xaa	Leu		
			-15					-10						-5			
wyn	nnt	tct	gag	atg	gag	tcm	cac	tct	ttc	agc							360
Xaa	Xaa	Ser	Glu	Met	Glu	Ser	His	Ser	Phe	Ser							
			1				5										

<210> 517
 <211> 453
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 113..451
 <221> sig_peptide
 <222> 113..307
 <223> Von Heijne matrix
 score 4.40000009536743
 seq FIEAALLIHGSAC/VY

<400> 517																	
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accctcgga	aggcagccct	gcggtccctt	tgccgccctg	tccctcccgg	ac atg gag												118
					Met Glu												
					-65												
gac gtg	gag gcg	cgc ttc	gcc cac	ctc ttg	cag ccc	atc cgc	gac ctc										166
Asp Val	Glu Ala	Arg Phe	Ala His	Leu Leu	Gln Pro	Ile Arg	Asp Leu										
	-60			-55		-50											
acc aag	aac tgg	gag gtg	gac gtg	gcg gcc	cag ctg	ggc gag	tat ctg										214
Thr Lys	Asn Trp	Glu Val	Asp Val	Ala Ala	Gln Leu	Gly Glu	Tyr Leu										
	-45			-40		-35											
gag gag	ctg gat	cag atc	tgc att	tct ttt	gac gaa	ggc aag	acc aca										262
Glu Glu	Leu Asp	Gln Ile	Cys Ile	Ser Phe	Asp Glu	Gly Lys	Thr Thr										
	-30		-25		-20												
atg aac	ttc att	gag gca	gcg ttg	ttg atc	cat ggc	tct gcc	tgc gtc										310
Met Asn	Phe Ile	Glu Ala	Ala Leu	Leu Ile	His Gly	Ser Ala	Cys Val										
	-15		-10		-5		1										
tac agt	aag aag	gtg gaa	tac ctc	tac tca	ctc gtc	tac cag	gcc ctt										358
Tyr Ser	Lys Lys	Val Glu	Tyr Leu	Tyr Ser	Leu Val	Tyr Gln	Ala Leu										
	5		10		15												
gat ttc	atc tct	gga aag	agg cg	gcc aag	cag ctc	tct tcg	gtg cag										406
Asp Phe	Ile Ser	Gly Lys	Arg Arg	Ala Lys	Gln Leu	Ser Ser	Val Gln										
	20		25		30												
gag gac	agg gcc	aat ggg	gtt gca	gct ccg	ggg tcc	cca gga	ggc ag										453
Glu Asp	Arg Ala	Asn Gly	Val Ala	Ala Pro	Gly Ser	Pro Gly	Gly										
	35		40		45												

<210> 518

<211> 245
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 185..244

<221> sig_peptide
 <222> 185..229
 <223> Von Heijne matrix
 score 4.40000009536743
 seq VSYLILTLLHVQT/AV

<400> 518
 agttttcttc agaacagagg ctgagctcga agcgccgggc agtacagtga gggagagccg 60
 aggggaaccag cgcggtgcct agcggaactc cagggctgga atcccagagac acaagtgcac 120
 ctgctagctg ttagcacttg gcagacggag ttctcctcta gggtagttct aactttgggt 180
 aata atg ttt gtc agc tac ctg ata tta aca ttg ctc cac gtt caa aca 229
 Met Phe Val Ser Tyr Leu Ile Leu Thr Leu Leu His Val Gln Thr
 -15 -10 -5
 gca gtg tta gca aga c 245
 Ala Val Leu Ala Arg
 1 5

<210> 519
 <211> 275
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 96..275

<221> sig_peptide
 <222> 96..170
 <223> Von Heijne matrix
 score 4.40000009536743
 seq IFLLYFKFWGTCA/ER

<400> 519
 ttgtttttta gaaaaatgaa taatttcttt ttatattatt ctgttacatt ttttccccac 60
 ttaatagaac gtccagaaaa tctttgcatc tcaga atg cct gaa gct gcc ttg 113
 Met Pro Glu Ala Ala Leu
 -25 -20
 ttc ttg ttt ttt tta ttc att ttt tta tta tac ttt aag ttc tgg ggt 161
 Phe Leu Phe Phe Leu Phe Ile Phe Leu Leu Tyr Phe Lys Phe Trp Gly
 -15 -10 -5
 aca tgt gca gaa cgt gca ggt ttg tta cat agg tat act cgt gcc atg 209
 Thr Cys Ala Glu Arg Ala Gly Leu Leu His Arg Tyr Thr Arg Ala Met
 1 5 10
 gag gtt tgc tgc acc cat caa cca tca tct aca tta ggt att tct cct 257
 Glu Val Cys Cys Thr His Gln Pro Ser Ser Thr Leu Gly Ile Ser Pro
 15 20 25

aat gct ctc ctt ccc cta
 Asn Ala Leu Leu Pro Leu
 30 35

275

<210> 520
 <211> 182
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 91..180

<221> sig_peptide
 <222> 91..159
 <223> Von Heijne matrix
 score 4.40000009536743
 seq LCMHLSIHPXXCA/CI

<400> 520
 gtctgagcgg cacagacgag atctcgatcg aaggcgagat ggcggacgtg ctagatcttc 60
 acgaggctgg gggcgaagat ttcgccatgg atg agg atg ggg acg aga gca tcc 114
 Met Arg Met Gly Thr Arg Ala Ser
 -20
 ccg cct ctg tgc atg cat ctg tcc atc cat ccc cky mtc tgt gca tgc 162
 Pro Pro Leu Cys Met His Leu Ser Ile His Pro Xaa Xaa Cys Ala Cys
 -15 -10 -5 1
 atc tgt cca tcc atc cag gg 182
 Ile Cys Pro Ser Ile Gln
 5

<210> 521
 <211> 218
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 104..217

<221> sig_peptide
 <222> 104..211
 <223> Von Heijne matrix
 score 4.40000009536743
 seq XVCVCVCVCVCVC/VC

<221> misc_feature
 <222> 145,151,174
 <223> n=a, g, c or t
 Oligonucleotide

<400> 521
 atttatgtag gcaggtggat gccaaactgcc agtgcagggt ggcataagtt agcgttccaa 60
 agttaagcta tgggtgcattc caaatccatt cacacttagg aga atg tac cca aga 115

													Met	Tyr	Pro	Arg	
																	-35
gtg	tgg	gga	tgt	ttt	caa	tta	ctg	cat	ttn	ctt	can	bga	aca	aga	acs		163
Val	Trp	Gly	Cys	Phe	Gln	Leu	Leu	His	Xaa	Leu	Xaa	Xaa	Thr	Arg	Thr		
		-30					-25					-20					
aca	ggt	aag	tnw	gtg	tgt	gtg	tgt	gtg	tgt	gtg	tgt	gtg	tgt	gtg	tgt		211
Thr	Gly	Lys	Xaa	Val	Cys	Val	Cys	Val	Cys	Val	Cys	Val	Cys	Val	Cys		
	-15					-10					-5						
gtg	tgt	g															218
Val	Cys																
1																	

<210> 522
 <211> 313
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 12..311
 <221> sig_peptide
 <222> 12..53
 <223> Von Heijne matrix
 score 4.40000009536743
 seq AAVVLAATRLRG/SG

<400> 522	
ggagacgcaa g atg gcg gct gtg gtg ctg gcg gcg acg cgg ttg ctg cgg	50
Met Ala Ala Val Val Leu Ala Ala Thr Arg Leu Leu Arg	
	-10
	-5
ggc tcg ggt tct tgg ggc tgt tcg cgg ctg agg ttt gga cct cct gcg	98
Gly Ser Gly Ser Trp Gly Cys Ser Arg Leu Arg Phe Gly Pro Pro Ala	
1 5 10 15	
tac aga cgg ttt agt agt ggt ggt gcc tat ccc aac atc ccc ctc tct	146
Tyr Arg Arg Phe Ser Ser Gly Gly Ala Tyr Pro Asn Ile Pro Leu Ser	
20 25 30	
tct ccc tta cct gga gta ccc aag cct gtt ttt gct aca gtt gat gga	194
Ser Pro Leu Pro Gly Val Pro Lys Pro Val Phe Ala Thr Val Asp Gly	
35 40 45	
cag gaa aag ttt gaa acc aaa gta acc aca ttg gat aat ggg ctt cgc	242
Gln Glu Lys Phe Glu Thr Lys Val Thr Thr Leu Asp Asn Gly Leu Arg	
50 55 60	
gtg gca tct cag aat aag ttt gga cag ttt tgt aca gta gga att ctt	290
Val Ala Ser Gln Asn Lys Phe Gly Gln Phe Cys Thr Val Gly Ile Leu	
65 70 75	
atc aat tca gga tcg aga tat ga	313
Ile Asn Ser Gly Ser Arg Tyr	
80 85	

<210> 523
 <211> 502
 <212> DNA
 <213> Homo sapiens

500
450
400
350
300
250
200
150
100
50
0

<220>
<221> CDS
<222> 324..500

<221> sig_peptide
<222> 324..398
<223> Von Heijne matrix
score 4.30000019073486
seq ALYLSLNLYFANS/LY

<221> misc_feature
<222> 284,469..470,472
<223> n=a, g, c or t
Oligonucleotide

<400> 523
gtctaggctc ttcaagttag gattcatatc tatgacatgt gctgtacagt gcttctactg 60
tgaggtagtc tcccagacag aaaccacatg ggccttcagg catagatggc cagtaaataa 120
ttactttaca gtgggtgtcat ttcttaggag acmcagagtr agaccttaag tgagatctta 180
cctacctcct cccatccaat ctatccaac aaggttgac ctaaagcagc cttgagctta 240
ataatgatgt gtgttagaac aaggatactg agattagact aagntgggtc tttaagtcag 300
ccgtctctga caaagggcac aca atg tac tgt ctg arg tgt gtg gag aaa ata 353
Met Tyr Cys Leu Xaa Cys Val Glu Lys Ile
-25 -20
gca aaa gct ctt tat ctc agc ctt aat tta tat ttt gca aat tca ctt 401
Ala Lys Ala Leu Tyr Leu Ser Leu Asn Leu Tyr Phe Ala Asn Ser Leu
-15 -10 -5 1
tat tat atg tgt gtg tgt tca tac ata tac ttt tat tta tkt att tat 449
Tyr Tyr Met Cys Val Cys Ser Tyr Ile Tyr Phe Tyr Leu Xaa Ile Tyr
5 10 15
ktk tat kkt tta ata aaa ann dng tct tat tat gtt gcc cag act ggt 497
Xaa Tyr Xaa Leu Ile Lys Xaa Xaa Ser Tyr Tyr Val Ala Gln Thr Gly
20 25 30
ctc aa 502
Leu

<210> 524
<211> 118
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 11..118

<221> sig_peptide
<222> 11..97
<223> Von Heijne matrix
score 4.30000019073486
seq SAVFLTAVFSSHS/WL

<400> 524
atctttgttg atg tgt cag ctc cgc agg ggt ttg ggg aaa cgg ccg ctg 49

Met Cys Gln Leu Arg Arg Gly Leu Gly Lys Arg Pro Leu
-25 -20
agt gag gcg tcg gct gtg ttt ctc acc gcg gtc ttt tcc tcc cac tct 97
Ser Glu Ala Ser Ala Val Phe Leu Thr Ala Val Phe Ser Ser His Ser
-15 -10 -5
tgg ctg gtt gga ccc cgc tat 118
Trp Leu Val Gly Pro Arg Tyr
1 5

<210> 525
<211> 276
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 176..274

<221> sig_peptide
<222> 176..268
<223> Von Heijne matrix
score 4.30000019073486
seq LTFCLIDLSNVDS/GX

<400> 525
cctgagttct agtttgattg cactgtgggc tgagagacag ttgtttataa tttctgttct 60
tttacgtttg ctgaggagag ctttacttcc aactatgtgg tcgattttgg aataggtgtg 120
gtgcggtgct gaaaaaatg tatattctgt tgatttgggg tggagagttc tgtag atg 178
Met
tct gtt agg tcc act tgg tgc aga gct cag ttc aat tcc tgg gta tcc 226
Ser Val Arg Ser Thr Trp Cys Arg Ala Gln Phe Asn Ser Trp Val Ser
-30 -25 -20 -15
ttg tta act ttc tgc ctc att gat ctg tct aat gtt gac agt ggg amg 274
Leu Leu Thr Phe Cys Leu Ile Asp Leu Ser Asn Val Asp Ser Gly Xaa
-10 -5 1
gg 276

<210> 526
<211> 366
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 103..366

<221> sig_peptide
<222> 103..261
<223> Von Heijne matrix
score 4.30000019073486
seq LRLTWLVAAGLEG/RV

<400> 526
tcactacttc tcccccgac tccttggtag tctgttagtg ggagatcctt gttgccgtcc 60

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cttcgcctcc ttcaccgccg cagacccctt caagttctag tc atg gtg agt ggg      114
                                   Met Val Ser Gly
                                   -50
gtt ccc tcg ggg ctg ggg aag agt gcg cgt ccc agg gga cgg cgg gcc      162
Val Pro Ser Gly Leu Gly Lys Ser Ala Arg Pro Arg Gly Arg Arg Ala
-45                                -40                                -35
cgg aaa cta ctg cct gca cct cgg gcc gcg ccc agg aca gct cca gac      210
Arg Lys Leu Leu Pro Ala Pro Arg Ala Ala Pro Arg Thr Ala Pro Asp
-30                                -25                                -20
tac ccc ggg ccc ctc cgg tta acc tgg ctt gtg gcg gcc ggg ctg gaa      258
Tyr Pro Gly Pro Leu Arg Leu Thr Trp Leu Val Ala Ala Gly Leu Glu
-15                                -10                                -5
ggt cga gtt cac ttg gca gac acc agt tcg ggc cgg aaa acc tgg ccc      306
Gly Arg Val His Leu Ala Asp Thr Ser Ser Gly Arg Lys Thr Trp Pro
1                                5                                10                                15
ggg tgc ggc cat cag tgg aaa tgg aaa gcc ctc ttg atc cta gtg agg      354
Gly Cys Gly His Gln Trp Lys Trp Lys Ala Leu Leu Ile Leu Val Arg
20                                25                                30
gct ttc ccc gca
Ala Phe Pro Ala
35

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<210> 527
<211> 428
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> 316..426

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<221> sig_peptide
<222> 316..408
<223> Von Heijne matrix
      score 4.30000019073486
      seq VCSSLRSXRPCWC/DG

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<400> 527
catttcctaa tctctgcatt ttccagcaag taagtgggtg tgacttggtg ctttcaagta      60
tgttttgtct aaaattcata gatgctgaac tgtgtatatt tgttgtcaag tttgaaaggt      120
acttgggttt ttgggggtgt taggaggtag ggtggatggt actattaaat acatttagac      180
tttttaaaat aagtgttaact gatcatttcc aacaaatatt tactatgtcc atacttgtgc      240
tccaaaagac aattctgtct tcctcttgag atacatgtct cggggcccct gtaggtctgg      300
tctgagaggg tcccc atg ggt ggc tgt gtc wgc tgg cgc ttt ctt gga cac      351
                                   Met Gly Gly Cys Val Xaa Trp Arg Phe Leu Gly His
                                   -30                                -25                                -20
tcc tct gct ctc agg act gtg tgt agc agt ctg cgc tca gya agg cca      399
Ser Ser Ala Leu Arg Thr Val Cys Ser Ser Leu Arg Ser Xaa Arg Pro
-15                                -10                                -5
tgt tgg tgt gat ggg ctt cgg ctc aga tg
Cys Trp Cys Asp Gly Leu Arg Leu Arg
1                                5

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<210> 528

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<211> 400
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 83..400

<221> sig_peptide
 <222> 83..235
 <223> Von Heijne matrix
 score 4.30000019073486
 seq STCLLRALSSELC/AP

<400> 528
 gacacggaag tagctccgaa caggaagagg acgaaaaaaaa taaccgtccg cgacgccgag 60
 acaaaccgga cccgcaacca cc atg aac agc aaa ggt caa tat cca aca cag 112
 Met Asn Ser Lys Gly Gln Tyr Pro Thr Gln
 -50 -45
 cca acc tac cct gtg cag cct cct ggg aat tcc agt ata ccc tca gac 160
 Pro Thr Tyr Pro Val Gln Pro Pro Gly Asn Ser Ser Ile Pro Ser Asp
 -40 -35 -30
 ctt gca tct tcc tca ggc tcc acc cta tac cga tgc tcc acc tgc cta 208
 Leu Ala Ser Ser Ser Gly Ser Thr Leu Tyr Arg Cys Ser Thr Cys Leu
 -25 -20 -15 -10
 ctc aga gct cta tcg tcc gag ctt tgt gca ccc agg ggc tgc cac agt 256
 Leu Arg Ala Leu Ser Ser Glu Leu Cys Ala Pro Arg Gly Cys His Ser
 -5 1 5
 ccc cac cat gtc agc cgc att tcc tgg acc ctc tct gta tct tcc cat 304
 Pro His His Val Ser Arg Ile Ser Trp Thr Leu Ser Val Ser Ser His
 10 15 20
 ggc cca gtc tgt ggc tgt tgg gcc ttt agg ttc cac aat ccc cat ggc 352
 Gly Pro Val Cys Gly Cys Trp Ala Phe Arg Phe His Asn Pro His Gly
 25 30 35
 tta tta tcc agt cgg tcc cat cta tcc amc tgg ctc cac agt gct ggt 400
 Leu Leu Ser Ser Arg Ser His Leu Ser Xaa Trp Leu His Ser Ala Gly
 40 45 50 55

<210> 529
 <211> 244
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 68..244

<221> sig_peptide
 <222> 68..133
 <223> Von Heijne matrix
 score 4.30000019073486
 seq LFFETGSPSVAQS/GV

<400> 529

<210> 531
 <211> 406
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 284..406

<221> sig_peptide
 <222> 284..361
 <223> Von Heijne matrix
 score 4.30000019073486
 seq AXYLLVGLFPLKC/HX

<221> misc_feature
 <222> 384
 <223> n=a, g, c or t
 Oligonucleotide

<400> 531
 taatatatgt magaatagca gggaccatgt cttctgttca atatkgatc ctgagcacct 60
 agtattttaag taggtatttc agtaaataat gtaacatata taataaataa tattaatatt 120
 tgttgactaa atgaatttag gtctggacct tgatggctta atgtctttct aaaaatctac 180
 ttccatatct aagcctttct tgactacttt cgcctttttc tgtgaactta aaagtcttta 240
 ttcattgttt gccgcatgct aaacatttac aaaagtaatc ctt atg tca tct gaa 295
 Met Ser Ser Glu
 -25
 att ttc taw ktt dtk cak att gck tat gct tda tat ttg cta gtt ggt 343
 Ile Phe Xaa Xaa Xaa Xaa Ile Ala Tyr Ala Xaa Tyr Leu Leu Val Gly
 -20 -15 -10
 ctt ttc cct cta aaa tgc cac wag agt hat ttt tct aag tna caa atc 391
 Leu Phe Pro Leu Lys Cys His Xaa Ser Xaa Phe Ser Lys Xaa Gln Ile
 -5 1 5 10
 tca tca ttt gtg gaa 406
 Ser Ser Phe Val Glu
 15

<210> 532
 <211> 212
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 23..211

<221> sig_peptide
 <222> 23..76
 <223> Von Heijne matrix
 score 4.30000019073486
 seq LTVTLGRLASACS/HS

<400> 532

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gtttccggcc gaggctgcgg cc atg gca gca tct tcc ctg acg gtc acc tta      52
                        Met Ala Ala Ser Ser Leu Thr Val Thr Leu
                        -15                               -10
ggg cgg ctg gcg tcc gcg tgc agc cac agc atc ctg aga cct tcg ggg      100
Gly Arg Leu Ala Ser Ala Cys Ser His Ser Ile Leu Arg Pro Ser Gly
                        -5                               1           5
ccc gga gca gcc tcc ctt tgg tct gct tct cga agg ttc aat tca cag      148
Pro Gly Ala Ala Ser Leu Trp Ser Ala Ser Arg Arg Phe Asn Ser Gln
                        10                               15           20
agc act tca tat cta cca gga tat gtt cvt aaa aca tcc ctg agt tca      196
Ser Thr Ser Tyr Leu Pro Gly Tyr Val Xaa Lys Thr Ser Leu Ser Ser
25                               30                               35           40
cca cct tgg ccg agg g
Pro Pro Trp Pro Arg
                        45

```

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<210> 533
<211> 149
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> 76..147

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<221> sig_peptide
<222> 76..129
<223> Von Heijne matrix
      score 4.30000019073486
      seq CICSCLFFSQYLX/XS

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<400> 533
tatagtgat tataatcaag tgtaggcttc ctgaattttg acatcctttt agaacttggg      60
tctggaattc cagaa atg tta att gct gct tgt att tgt tct tgt ttg ttt      111
                        Met Leu Ile Ala Cys Ile Cys Ser Cys Leu Phe
                        -15                               -10
ttt agc cag tat ttg gsy ytt tct aat cca gcc gcg gg      149
Phe Ser Gln Tyr Leu Xaa Xaa Ser Asn Pro Ala Ala
-5                               1           5

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<210> 534
<211> 145
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> 56..145

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<221> sig_peptide
<222> 56..103
<223> Von Heijne matrix
      score 4.30000019073486
      seq WVLSYMWQSASLG/FS

```

<400> 534
 tgggctactc atggywagat aagacttaca cttctgaaag aggccttaga gtttc atg 58
 Met
 aag tgc tgg gtt ctc agc tac atg tgg cag agt gca tct ctg ggt ttt 106
 Lys Cys Trp Val Leu Ser Tyr Met Trp Gln Ser Ala Ser Leu Gly Phe
 -15 -10 -5 1
 agt aac agg att aaa tct mac ttg aga cct cca gca ggc 145
 Ser Asn Arg Ile Lys Ser Xaa Leu Arg Pro Pro Ala Gly
 5 10

<210> 535
 <211> 384
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 81..383
 <221> sig_peptide
 <222> 81..287
 <223> Von Heijne matrix
 score 4.30000019073486
 seq GIRLSCVLSHLQA/WD

<400> 535
 aaatcctcag cagatTTTTG ttcaagagct gcttccagat tggcttctag ctgccagtgt 60
 gaccttgggc agaaccttca atg tct gtg ggg ctg tgt ttt ctt atc tgg caa 113
 Met Ser Val Gly Leu Cys Phe Leu Ile Trp Gln
 -65 -60
 atg gga att atg cts ttg cct cgg gaa tgt tgg aag gtc aaa gac agt 161
 Met Gly Ile Met Leu Leu Pro Arg Glu Cys Trp Lys Val Lys Asp Ser
 -55 -50 -45
 aag aag tac aaa agc tgc aga gaa tca gta ctg cct gca caa gca tgt 209
 Lys Lys Tyr Lys Ser Cys Arg Glu Ser Val Leu Pro Ala Gln Ala Cys
 -40 -35 -30
 aca gga gag tcc cct gtc tta tct gga gtc agg gtt ctg ggg atc cgc 257
 Thr Gly Glu Ser Pro Val Leu Ser Gly Val Arg Val Leu Gly Ile Arg
 -25 -20 -15
 ctc tcg tgc gtg tta tcc cat ctc caa gcc tgg gac tcc tgg gac aat 305
 Leu Ser Cys Val Leu Ser His Leu Gln Ala Trp Asp Ser Trp Asp Asn
 -10 -5 1 5
 cag aag gtg tgc tac ctg ggt gca ccc tgc ttt ggg aaa agg ctg agt 353
 Gln Lys Val Cys Tyr Leu Gly Ala Pro Cys Phe Gly Lys Arg Leu Ser
 10 15 20
 cca acc acc tgg ctc act ttt tgg gtg gga c 384
 Pro Thr Thr Trp Leu Thr Phe Trp Val Gly
 25 30

<210> 536
 <211> 207
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 78..206

<221> sig_peptide
 <222> 78..119
 <223> Von Heijne matrix
 score 4.30000019073486
 seq FAFLAGCSGSLW/SR

<400> 536
 aactttaccc agatatacta tatgccaaac aatgtttgtc accagggata ccacaacaga 60
 aaacaaatac actaaaa atg ttc gct ttc ctg gcc ggg tgc agt ggc tca 110
 Met Phe Ala Phe Leu Ala Gly Cys Ser Gly Ser
 -10 -5
 tgc ctg tgg tcc cgg cac ttc ggg aga ctg cgg cgg gcg gct ccc ttg 158
 Cys Leu Trp Ser Arg His Phe Gly Arg Leu Arg Arg Ala Ala Pro Leu
 1 5 10
 agc cca gag ttt gag acc ggc ctg ggt aac atg gtg gaa ccc caa tgg g 207
 Ser Pro Glu Phe Glu Thr Gly Leu Gly Asn Met Val Glu Pro Gln Trp
 15 20 25

<210> 537
 <211> 394
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 268..393
 <221> sig_peptide
 <222> 268..318
 <223> Von Heijne matrix
 score 4.30000019073486
 seq FLFVPHLISCNWC/EP

<400> 537
 ttagcaaadc acagatgaag gtctcattac tatatgcaga gggtgccata agttacaadc 60
 cctttgtgcc tctggctgct ccaacatcac agatgccatc ctgaatgctc taggtcagaa 120
 ctgcccacgg cttaggtaaa catttcttgt ttagctcaaa aaaatcatag aacaaaagtt 180
 tccttcaccc atatttcttc cttggaactt tggaatttta aggtaggcac tgcagacgct 240
 ttgaaatitt aaggtagtcc ctttttag atg ccc acc tac ttc ctt ttt gta cct 294
 Met Pro Thr Tyr Phe Leu Phe Val Pro
 -15 -10
 cat ttg att tca tgt aat tgg tgt gaa cca agg ggt aac aat ccc caa 342
 His Leu Ile Ser Cys Asn Trp Cys Glu Pro Arg Gly Asn Asn Pro Gln
 -5 1 5
 att cca cta ctt gct atc cat act aga aaa aag aat caa cat ttt att 390
 Ile Pro Leu Leu Ala Ile His Thr Arg Lys Lys Asn Gln His Phe Ile
 10 15 20
 act t 394
 Thr

25

<210> 538
<211> 415
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 237..413

<221> sig_peptide
<222> 237..317
<223> Von Heijne matrix
score 4.30000019073486
seq LTSVSLXXXXXXG/SV

<221> misc_feature
<222> 308..309,375
<223> n=a, g, c or t
Oligonucleotide

<400> 538
gaatcctcgc aaagaattgg caatgtcgtt gcctttctct ggcggaaggc tggcwactac 60
cctttgaatt tggaatgtat gtcacacagt tctagagtag aatgcaaact cagcactgtc 120
ctctttgaac caaaatgtct ccaaaaacaa gattctaatt tatacttaat atttcccca 180
gaagcccaat cattaagcc acctttccag gaacagaagt gtttttgaca ctgtga atg 239
Met
ctt tgg acc agt ttc cag aat cct ctt cag gta gtg ctt ctc acc agc 287
Leu Trp Thr Ser Phe Gln Asn Pro Leu Gln Val Val Leu Leu Thr Ser
-25 -20 -15
gtt tcc ctt ttd aww wtg gbn ndc mta ggt tca gtc cga atc awk cta 335
Val Ser Leu Xaa Xaa Xaa Xaa Xaa Gly Ser Val Arg Ile Xaa Leu
-10 -5 1 5
tct cac tgg tca agc tca gcc ttc ttc ttc ctd att cwb nck kyw hwt 383
Ser His Trp Ser Ser Ser Ala Phe Phe Phe Leu Ile Xaa Xaa Xaa Xaa
10 15 20
ctt tca cat gtg aca aaa caa atg cat ttg aa 415
Leu Ser His Val Thr Lys Gln Met His Leu
25 30

<210> 539
<211> 160
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 66..158

<221> sig_peptide
<222> 66..107
<223> Von Heijne matrix
score 4.30000019073486

seq LTCLCGCFIVLLV/CV

<400> 539
tacattcaag gtagtattg atatgcatgt atttgatcct gtcattgtgt tgtagctgt 60
ttatt atg ctg act tgt ttg tgt ggt tgc ttt ata gtg tta ctt gtc tgt 110
Met Leu Thr Cys Leu Cys Gly Cys Phe Ile Val Leu Leu Val Cys
-10 -5 1
gta ctt aaa tgt gtt ttt gta gtg gct agt aat ggc ctt ttc ttt cct 158
Val Leu Lys Cys Val Phe Val Val Ala Ser Asn Gly Leu Phe Phe Pro
5 10 15
tt 160

<210> 540
<211> 327
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 207..326

<221> sig_peptide
<222> 207..293
<223> Von Heijne matrix
score 4.30000019073486
seq HLSILAFVAIAFG/VL

<400> 540
catttttttc atgtgttttt ttggctgcat aaatgtcttc ttttgagaag tgtctgttca 60
tgtccctcgc ccactttttg atggggttgt ttgttttttt cttgtaaatt tgtttgagtt 120
cattgtagat tctggatatt agccctttgt cagatgagta ggttgcgaaa attttctccc 180
atgttgtagg ttgcctgttc actctg atg gta gtt tct ttt gct gtg cag aag 233
Met Val Val Ser Phe Ala Val Gln Lys
-25
ctc ttt agt tta att aga tcc cat ttg tca att ttg gct ttt gtt gcc 281
Leu Phe Ser Leu Ile Arg Ser His Leu Ser Ile Leu Ala Phe Val Ala
-20 -15 -10 -5
att gct ttt ggt gtt ttg gac atg aag tcc ttg ccc acg cca ggg g 327
Ile Ala Phe Gly Val Leu Asp Met Lys Ser Leu Pro Thr Pro Gly
1 5 10

<210> 541
<211> 396
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 84..395

<221> sig_peptide
<222> 84..278
<223> Von Heijne matrix
score 4.30000019073486

seq FFSRLGATSVXRA/CT

<221> misc_feature

<222> 271,328,344..345,347

<223> n=a, g, c or t
Oligonucleotide

<400> 541

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cttctgcact cacagccgaa ggaaagcagc aggttggggc ttcttgtggc caacttcaga      60
gcctgtcacc aggaaaggtg agc atg gga gga agg aag atg gcg aca gat gaa      113
                Met Gly Gly Arg Lys Met Ala Thr Asp Glu
                -65                -60

gaa aat gtc tat ggt tta gaa gag aac gct cag tcc cgg cag gag tcc      161
Glu Asn Val Tyr Gly Leu Glu Glu Asn Ala Gln Ser Arg Gln Glu Ser
-55                -50                -45                -40
acg cgg agg ctc atc ctt gtt ggg aga aca ggg gcc ggg aag agc gcc      209
Thr Arg Arg Leu Ile Leu Val Gly Arg Thr Gly Ala Gly Lys Ser Ala
                -35                -30                -25
act ggg aac agc atc ctg ggc cag aga cgg ttc ttc tcc agg ctg ggg      257
Thr Gly Asn Ser Ile Leu Gly Gln Arg Arg Phe Phe Ser Arg Leu Gly
                -20                -15                -10
gcc acg tct gtg anc agg gcc tgc acc acg grh agc cgc agg tgg gac      305
Ala Thr Ser Val Xaa Arg Ala Cys Thr Thr Xaa Ser Arg Arg Trp Asp
                -5                1                5
aag tgc cac gtg gaa gtc gtr gnd ctm gga cat vwk can nmh ggg aag      353
Lys Cys His Val Glu Val Val Xaa Leu Gly His Xaa Xaa Xaa Gly Lys
10                15                20                25
tgt cca aga cag atc ctg gct gtg agg aga gag gtc act gct a      396
Cys Pro Arg Gln Ile Leu Ala Val Arg Arg Glu Val Thr Ala
                30                35
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<210> 542

<211> 247

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 8..247

<221> sig_peptide

<222> 8..100

<223> Von Heijne matrix
score 4.30000019073486
seq ALALTXTLTPAG/EH

<221> misc_feature

<222> 78,182,194

<223> n=a, g, c or t
Oligonucleotide

<400> 542

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atcaata atg cag ctt caa gtt ctg ggg aga ccg cag ggg gcc ccc cag      49
                Met Gln Leu Gln Val Leu Gly Arg Pro Gln Gly Ala Pro Gln
```


	-30		-25		-20		
ctg gct ccc cag gcc ttg gct cta act bmk acc ctc ctc cca gcc cca							97
Leu Ala Pro Gln Ala Leu Ala Leu Thr Xaa Thr Leu Leu Pro Ala Pro							
	-15		-10		-5		
gga gaa cac gat tck ccr atg stc att ggc cag ttt ccc cwa aac cct							145
Gly Glu His Asp Ser Pro Met Xaa Ile Gly Gln Phe Pro Xaa Asn Pro							
1 5 10 15							
ccc tcc gag cac ccg ggc gcc agt ccc agg cgg wmr ngg acg ggc tgg							193
Pro Ser Glu His Pro Gly Ala Ser Pro Arg Arg Xaa Xaa Thr Gly Trp							
	20		25		30		
nra ccc caa agc tgg gac cgg agg gtg agc ccg gca gag gca gag aca							241
Xaa Pro Gln Ser Trp Asp Arg Arg Val Ser Pro Ala Glu Ala Glu Thr							
	35		40		45		
cgc agg							247
Arg Arg							

<210> 543
 <211> 221
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 87..221

<221> sig_peptide
 <222> 87..209
 <223> Von Heijne matrix
 score 4.30000019073486
 seq HLFTLGFLCSLCP/HP

<221> misc_feature
 <222> 154
 <223> n=a, g, c or t
 Oligonucleotide

<400> 543	
tgctatgttc aatcttgtac aggtcttttg tggacatatg gtctcactcc tcttaggtat	60
ataccgagta gtgaaactgc cagggtc atg gga gta tac acg tgt cca att ttt	113
	Met Gly Val Tyr Thr Cys Pro Ile Phe
	-40 -35
gtg cat tac tac gag aac cat gga cca acc ccw agt ttc cnt gcc ttt	161
Val His Tyr Tyr Glu Asn His Gly Pro Thr Pro Ser Phe Xaa Ala Phe	
	-30 -25 -20
att tcc ttt cat cta ttt act ttg ggc ttt ctt tgt tcc cta tgc ccc	209
Ile Ser Phe His Leu Phe Thr Leu Gly Phe Leu Cys Ser Leu Cys Pro	
	-15 -10 -5
cac ccc cac ggg	221
His Pro His Gly	
1	

<210> 544
 <211> 375
 <212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 307..375

<221> sig_peptide

<222> 307..354

<223> Von Heijne matrix

score 4.30000019073486

seq SVSCSSSLWVSLS/KD

<221> misc_feature

<222> 302

<223> n=a, g, c or t

Oligonucleotide

<400> 544

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tcaatggaag aaggagwaaa aagagaagag gaaaatggga ccaatactgc tgatcatgtt      60
cgaaattcca gttgggcaaa aaacggctcc taccaagggtg ctcttcataa cgcctctgaa    120
gaagccacag aacaaaacat acgagctggt acccaggcag ttttgcaggt ggatcacttt    180
atggctatgt ttaaaaataa aataatcatt aaatatttct gttcagtatt tcagtataca    240
gtatactttt cacaatataa aaatagaagc ttaatactgg gcattcatac tttttaaaga    300
gmatga atg aag aaa tcg gtt tcc tgc tgt agt tct cta tgg gta agt      348
      Met Lys Lys Ser Val Ser Cys Cys Ser Ser Leu Trp Val Ser
      -15                -10                -5
ctt agt aaa gac gag aat gct gaa atg      375
Leu Ser Lys Asp Glu Asn Ala Glu Met
      1                5
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<210> 545

<211> 376

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 260..376

<221> sig_peptide

<222> 260..349

<223> Von Heijne matrix

score 4.30000019073486

seq TVLLSGSPRAVVS/AV

<400> 545

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tagtggacag cccaagctgc ttctcttaga atggctgtgg cttcacaagt gatgagaaga      60
gcatgcgctt gatttcagat cccattaca agctcataat gaatgagtca caggagaaag    120
gtgrgacttg gggcccttgc gtgcctgatg ggaagctcct gcmaccccg ggagcccctc    180
cagactgtcc ttgccacact ggctgcactg gcctctttat gccaacccag tgaggacagg    240
ttctgagggg cctggacag atg ctg ctg ccc cta gcc atg gct gga cga tgt      292
      Met Leu Leu Pro Leu Ala Met Ala Gly Arg Cys
      -30                -25                -20
tat aca gcc aag cac agc acw gtg ctg ctc tca gga agc cca agg gct      340
```

Tyr Thr Ala Lys His Ser Thr Val Leu Leu Ser Gly Ser Pro Arg Ala
-15 -10 -5
gtg gtc agt gca gtg gtg atg gtg ggc aca ggg tgc 376
Val Val Ser Ala Val Val Met Val Gly Thr Gly Cys
1 5

<210> 546
<211> 109
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 30..107

<221> sig_peptide
<222> 30..86
<223> Von Heijne matrix
score 4.30000019073486
seq LRAFLLSVPLGKG/SA

<400> 546
cccacagcct tccctggtgt gcctgcagt atg cca tcc tgc tgc tac ctt agg 53
Met Pro Ser Cys Cys Tyr Leu Arg
-15
gct ttt ctg ctc tct gtc cct ctg ggg aaa ggc tca gcc ctt aag gat 101
Ala Phe Leu Leu Ser Val Pro Leu Gly Lys Gly Ser Ala Leu Lys Asp
-10 -5 1 5
ccc gtg ct 109
Pro Val

<210> 547
<211> 306
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 3..305

<221> sig_peptide
<222> 3..74
<223> Von Heijne matrix
score 4.19999980926514
seq LLLSSLWIVCLH/LD

<400> 547
at atg gtt gct gac aag gag gtg cag aca agg acc ctc ttg ctt tcc 47
Met Val Ala Asp Lys Glu Val Gln Thr Arg Thr Leu Leu Leu Ser
-20 -15 -10
tca cta tgg ata gtc tgt tgc ctc cat cta gat tct ctt att tca rrr 95
Ser Leu Trp Ile Val Cys Cys Leu His Leu Asp Ser Leu Ile Ser Xaa
-5 1 5
aaa tat cct ctc cat gca att agg aga tat tta tcg acg ctg aga aac 143

Lys	Tyr	Pro	Leu	His	Ala	Ile	Arg	Arg	Tyr	Leu	Ser	Thr	Leu	Arg	Asn	
	10						15					20				
caa	aga	gcc	gaa	gaa	cag	gtt	gca	cgt	ttt	caa	aaa	ata	cct	aat	ggg	191
Gln	Arg	Ala	Glu	Glu	Gln	Val	Ala	Arg	Phe	Gln	Lys	Ile	Pro	Asn	Gly	
	25					30				35						
gaa	aat	gag	aca	atg	att	cct	gta	ttg	aca	tca	aaa	aaa	gca	agt	gaa	239
Glu	Asn	Glu	Thr	Met	Ile	Pro	Val	Leu	Thr	Ser	Lys	Lys	Ala	Ser	Glu	
40				45				50					55			
tta	cca	gtc	agt	gaa	gtt	gca	agc	att	ctc	caa	gct	gat	ctt	cag	aat	287
Leu	Pro	Val	Ser	Glu	Val	Ala	Ser	Ile	Leu	Gln	Ala	Asp	Leu	Gln	Asn	
				60				65					70			
ggt	cta	aaa	caa	tgt	gaa	g										306
Gly	Leu	Lys	Gln	Cys	Glu											
	75															

<210> 548
 <211> 148
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 89..148
 <221> sig_peptide
 <222> 89..130
 <223> Von Heijne matrix
 score 4.19999980926514
 seq HICLFFSFSXXFX/LF

<400> 548	
aggatagctg aaaggagttc atctaactgg agtcccacta gaagtaagaa acccctattg	60
tttatttttt aataatgtaa tttttatt atg cat att tgt ctt ttt ttt tct	112
Met His Ile Cys Leu Phe Phe Ser	
-10	
ttt tct ttw wct ttt tkt ctt ttc ttt ttt ttt ttt	148
Phe Ser Xaa Xaa Phe Xaa Leu Phe Phe Phe Phe Phe	
-5 1 5	

<210> 549
 <211> 374
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 240..374
 <221> sig_peptide
 <222> 240..296
 <223> Von Heijne matrix
 score 4.19999980926514
 seq ILARLCRMQTCWC/LS

```

<400> 549
tacattcggc ccggccatgg cagcggcgcc cctgaaagtg tgcattcgtg gctcggggaa      60
ctgggggttca gctgttgcaa aarkrattgg taataatgtc aagaaacttc agaaatttgc      120
ctccacagtc aagatgtggg tcttttraar aaamcrgkkr akkggcagra aactgacaga      180
catcataaat aatgaccatg aaaatgtaaa atatcttcct ggacacaagc tgccagaaa      239
atg tgg ttg cca tgt caa atc tta gcg agg ctg tgc agg atg cag acc      287
Met Trp Leu Pro Cys Gln Ile Leu Ala Arg Leu Cys Arg Met Gln Thr
          -15                      -10                      -5

tgc tgg tgt ttg tca ttc ccc acc agt tca ttc aca gaa tct gtg atg      335
Cys Trp Cys Leu Ser Phe Pro Thr Ser Ser Phe Thr Glu Ser Val Met
          1                      5                      10

aga tca ctg gga gag tgc cca aga aag cgc tgg ggg ggg      374
Arg Ser Leu Gly Glu Cys Pro Arg Lys Arg Trp Gly Gly
          15                      20                      25

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<210> 550
<211> 476
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> 147..476

<221> sig_peptide
<222> 147..398
<223> Von Heijne matrix
      score 4.19999980926514
      seq VTILVSLALAFLA/CI

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<400> 550
agacacacgc gaggcgctgt cctttcagca ccacaagctc gggctgagga gggaggactc      60
ctggccgtcc tcctcckett caaattggct tgaatctgct ctgaccccc acgagtgcag      120
cacagtctgg gaagaaaggc gtaagg atg gwg aag ctg arc agt aac ccc agc      173
                      Met Xaa Lys Leu Xaa Ser Asn Pro Ser
                      -80

gag aag gga acc aag ccg cct tca gtt gag gat ggc ttc cag acc gtc      221
Glu Lys Gly Thr Lys Pro Pro Ser Val Glu Asp Gly Phe Gln Thr Val
-75                      -70                      -65                      -60

cct ctc atc act ccg ttg gag gtt aat cac tta cag ctg cct gct cca      269
Pro Leu Ile Thr Pro Leu Glu Val Asn His Leu Gln Leu Pro Ala Pro
          -55                      -50                      -45

gaa aag gtg att gtg aag aca aga acg gaa tat cag ccg gaa cag aag      317
Glu Lys Val Ile Val Lys Thr Arg Thr Glu Tyr Gln Pro Glu Gln Lys
          -40                      -35                      -30

aac aaa ggg aag ttc cgg gtg cca aaa atc gct gaa ttt acg gtc acc      365
Asn Lys Gly Lys Phe Arg Val Pro Lys Ile Ala Glu Phe Thr Val Thr
          -25                      -20                      -15

atc ctt gtc agc ctg gcc cta gct ttc ctt gcg tgc atc gtg ttc ctg      413
Ile Leu Val Ser Leu Ala Leu Ala Phe Leu Ala Cys Ile Val Phe Leu
          -10                      -5                      1                      5

gtg gtt tac aaa gcc ttc acc tat gat cac agc tgc cca gag gat tcg      461
Val Val Tyr Lys Ala Phe Thr Tyr Asp His Ser Cys Pro Glu Asp Ser
          10                      15                      20

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tct atr agc acc ggg
 Ser Xaa Ser Thr Gly
 25

476

<210> 551
 <211> 231
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 77..229

<221> sig_peptide
 <222> 77..139
 <223> Von Heijne matrix
 score 4.19999980926514
 seq EVLSLLFXCIYWG/QY

<400> 551
 catcctcatc ttcttctctt cttgttactt tggatatttg ctgaaaggct gtcagttgct 60
 ccacacaact tataaa atg ttc ats gcc gca gca gga gta gag gtc ctg agc 112
 Met Phe Xaa Ala Ala Ala Gly Val Glu Val Leu Ser
 -20 -15 -10
 ctc cta ttt ttc tgc atc tac tgg ggt caa tat gcc acc gat ggc att 160
 Leu Leu Phe Xaa Cys Ile Tyr Trp Gly Gln Tyr Ala Thr Asp Gly Ile
 -5 1 5
 ggc aac gag agt gtg aag atc ttg gcc aag ctg ctc ttc tcc tcc agc 208
 Gly Asn Glu Ser Val Lys Ile Leu Ala Lys Leu Leu Phe Ser Ser Ser
 10 15 20
 ttc ctc atc ttc ctg ctg atg gg 231
 Phe Leu Ile Phe Leu Leu Met
 25 30

<210> 552
 <211> 229
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 125..229

<221> sig_peptide
 <222> 125..202
 <223> Von Heijne matrix
 score 4.19999980926514
 seq FLSFLSFFFFSFF/LF

<400> 552
 agtttcactc cgaaagtsct tcttacagag caactccaag gatgggctga aaagcacata 60
 gagaaaaatgg aacagtgcga agttggaagg tccgtgcggg tggcagcgcc agtgtgggga 120
 tgag atg ctc aca gga cgg ttt tta ggc ggc tca caa ggg ttt ttt ctt 169
 Met Leu Thr Gly Arg Phe Leu Gly Gly Ser Gln Gly Phe Phe Leu

	-25		-20		-15												
tct	ttt	ctt	tct	ttc	ttt	ttt	ttt	tcc	ttt	ttc	ctt	ttc	ctt	ycr	ttt		217
Ser	Phe	Leu	Ser	Phe	Phe	Phe	Phe	Ser	Phe	Phe	Leu	Phe	Leu	Xaa	Phe		
	-10					-5					1				5		
ttt	ttt	ttt	ttt														229
Phe	Phe	Phe	Phe														

<210> 553
 <211> 232
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 110..232
 <221> sig_peptide
 <222> 110..193
 <223> Von Heijne matrix
 score 4.19999980926514
 seq FVFMSKLLLLFSFS/FL

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acgatcagat	ctgakra	gaa	ttgagcccc	aaaagcagtt	atcagactat	ttgaaataaa											60
gatttatatt	caccttta	aat	aacaatgtac	cattaataac	acataattac	atg ttt att											118
						Met Phe Ile											
tkr taw rak	atg aaa	cag wcr	ttt cat	att ata	gac ttt	gtt ttc	atg										166
Xaa Xaa Xaa	Met Lys	Gln Xaa	Phe His	Ile Ile	Asp Phe	Val Phe	Met										
-25		-20		-15		-10											
agt aaa ctt	tta tta	ttt tca	ttt tca	ttt tta	ara aaa	gcr cgc	atg										214
Ser Lys Leu	Leu Leu	Phe Ser	Phe Ser	Phe Leu	Xaa Lys	Ala Arg	Met										
	-5			1		5											
awt aca gca	gca cct	ggg															232
Xaa Thr Ala	Ala Pro	Gly															
	10																

<210> 554
 <211> 141
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 31..141
 <221> sig_peptide
 <222> 31..84
 <223> Von Heijne matrix
 score 4.19999980926514
 seq HILTAVLPLVSHQ/QN

<400> 554																	
ttacattcct	cacttctag	t	ggtttgatta	atg gtc	aca cca	gta cac	atc ctg										54
				Met Val	Thr Pro	Val His	Ile Leu										

-15

aca gcc gtg ctt cca ctt gtg tct cac cag	caa aac cat ctg ggt gga	102
Thr Ala Val Leu Pro Leu Val Ser His Gln	Gln Asn His Leu Gly Gly	
-10	-5 1 5	
agg ttt gca tct ctg gga tcc tca ggc att agg cac ggg		141
Arg Phe Ala Ser Leu Gly Ser Ser Gly Ile Arg His Gly		
10	15	

<210> 555
 <211> 376
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 319..375

<221> sig_peptide
 <222> 319..363
 <223> Von Heijne matrix
 score 4.19999980926514
 seq ILHLATLLNLFIS/SN

<221> misc_feature
 <222> 144..145,202,276..277
 <223> n=a, g, c or t
 Oligonucleotide

<400> 555

ttctatttct gtgaagaatg tcacagaatg cagtctacat attgcataga atctgtagat	60
tgcattgggt agcatggaca ttttaacaat attgattctt ccaattcatg aacatgaaat	120
atctttccat tttttgaggt ctanncaatc tcttttatca gtgtkctcta attctgatta	180
tagagatctt tcacatcttt gnttcaagtt gattcctacg tatttcactt tatttgtggc	240
tggtgtaa at gggattactt tttgcatttc tttchnnsaa ttgttcagtc agcatacagg	300
aatgatactg atttttgt atg ttg att tta cat ctt gca act tta cta aat	351
Met Leu Ile Leu His Leu Ala Thr Leu Leu Asn	
-15 -10 -5	

ttg ttt atc agt tct aac agt ttt g	376
Leu Phe Ile Ser Ser Asn Ser Phe	
1	

<210> 556
 <211> 279
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 199..279

<221> sig_peptide
 <222> 199..243
 <223> Von Heijne matrix
 score 4.19999980926514

seq LASFGPFRSSCFA/AR

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<400> 556
cccttggttac tgctacccat cctacctgca ccctgctttt tccctcttgs cacgcttttt      60
ttcctctccc tcttaccccc accctgtaca aaatgcataa aggatggaaa aactactgca      120
gccagaagtc tttgaatgag gcatcaatgg atgaatattt aggcagctta gggctgtttc      180
gaaagctgac tgccaagg atg cct ctt gcc tct ttc ggg cca ttt cg g agc      231
                        Met Pro Leu Ala Ser Phe Gly Pro Phe Arg Ser
                        -15                        -10                        -5
agt tgt ttt gca gcc agg tcc atc att tgg aaa tca gga agg caa ggg      279
Ser Cys Phe Ala Ala Arg Ser Ile Ile Trp Lys Ser Gly Arg Gln Gly
                        1                        5                        10
```

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<210> 557
<211> 340
<212> DNA
<213> Homo sapiens
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<220>
<221> CDS
<222> 233..340

<221> sig_peptide
<222> 233..325
<223> Von Heijne matrix
      score 4.19999980926514
      seq FLLSFLSFRSPLC/HH
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<400> 557
caaagaaatt agtgggctaaa cgtagagaaa ttaagatgaa ggaactggca catggagcca      60
ctgtgtacta taaagtattt ttattggtat ttagtcttgc tgttattgtt gctaattgatt      120
gtattgaata attaccagct gttgttagtt atttgaaatt aggtgcctaa agcaacctct      180
catcttgacg aaagtcacat ttcttgaaac tttttaaaaa cttgcttgaa ac atg gag      238
                        Met Glu
                        -30
act tgg aat ggg acg tct atc ata gta gca cat ctg ara tcc ttc tca      286
Thr Trp Asn Gly Thr Ser Ile Ile Val Ala His Leu Xaa Ser Phe Ser
                        -25                        -20                        -15
ttc ctg ctg tca ttt ctg tcc ttt cgc agt cca ctt tgt cac cac ccc      334
Phe Leu Leu Ser Phe Leu Ser Phe Arg Ser Pro Leu Cys His His Pro
                        -10                        -5                        1
ctc ggg      340
Leu Gly
      5
```

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<210> 558
<211> 365
<212> DNA
<213> Homo sapiens
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<220>
<221> CDS
<222> 288..365
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<221> sig_peptide
 <222> 288..329
 <223> Von Heijne matrix
 score 4.19999980926514
 seq QFLSLIFASCSST/TP

<400> 558
 acatttgcaa ccttggccat ctgtccagaa cctgctccca cctcaggccc aggccaaccg 60
 tgcactgctg caatgggctc tgagctggag acggcgatgg agaccctcat caacgtgttc 120
 cacgcccact cgggcaaaga gggggacaag tacaagctga gcaagaagga gctgaaagag 180
 ctgctgcaga cggagctctc tggcttcctg gatgtgaaag agcttatgct gtaggcaaca 240
 gaagccctca agacttttga ggaggcctag aagagtccca taattca atg cag ttc 296
 Met Gln Phe
 ctc tcg ctc atc ttt gcc tcc tgc tcc tca acc acc ccc tta cct ctg 344
 Leu Ser Leu Ile Phe Ala Ser Cys Ser Ser Thr Thr Pro Leu Pro Leu
 -10 -5 1 5
 amt cag tgc tgt acc ctt ccc 365
 Xaa Gln Cys Cys Thr Leu Pro
 10

<210> 559
 <211> 354
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 103..354

<221> sig_peptide
 <222> 103..261
 <223> Von Heijne matrix
 score 4.19999980926514
 seq VLALVCHSASISV/FP

<400> 559
 aatattataa tgaggctctg caggggcttg aacttaggtc cctgtaaggg agctactgtt 60
 ccctggtatg acccactcta gctgagctgt gcagagactg ag atg gtc acc tca 114
 Met Val Thr Ser
 -50
 aag agc agg gga ccc ckt gtc cag act ctg ggg cat gct ggc aac ctg 162
 Lys Ser Arg Gly Pro Xaa Val Gln Thr Leu Gly His Ala Gly Asn Leu
 -45 -40 -35
 agg agt ctg cgg gag tgg cct gat ctg tgc tgc ttg agg ctt ttt gtc 210
 Arg Ser Leu Arg Glu Trp Pro Asp Leu Cys Cys Leu Arg Leu Phe Val
 -30 -25 -20
 cca gat cac act gta ctt gct ctg gtg tgc cac agc gca tcc atc tct 258
 Pro Asp His Thr Val Leu Ala Leu Val Cys His Ser Ala Ser Ile Ser
 -15 -10 -5
 gtc ttc cct tct cag gtc acc tgc aga ctc cca agg aca ggg tca cat 306
 Val Phe Pro Ser Gln Val Thr Cys Arg Leu Pro Arg Thr Gly Ser His
 1 5 10 15
 ccc atc tgc gtc atc tct caa ggt gcc ttt cac gat cct cac cca aat 354
 Pro Ile Cys Val Ile Ser Gln Gly Ala Phe His Asp Pro His Pro Asn

20

25

30

<210> 560
 <211> 328
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 168..326

<221> sig_peptide
 <222> 168..248
 <223> Von Heijne matrix
 score 4.19999980926514
 seq RLVVLFASPXVRP/AS

<221> misc_feature
 <222> 230
 <223> n=a, g, c or t
 Oligonucleotide

<400> 560
 attaagggac aataatggcc gctttcaagg tgtggatttt ggctccttga gcctgtctga 60
 gcgaggggtg gcagcgccgg cgccccagaa tccgggacag aaagggctbc aagagtcgcg 120
 cttggtgmga gaaatcccag atcctgtgat gggggacacc agtgagg atg cct cga 176
 Met Pro Arg
 -25
 tcc atc gat ksg aag gca ctg atc tgg act gtc agg ttg gtg gtc tta 224
 Ser Ile Asp Xaa Lys Ala Leu Ile Trp Thr Val Arg Leu Val Val Leu
 -20 -15 -10
 ttt gcn agt cca awa gtg cgg cca gcg agc agc atg tct tca agg ctc 272
 Phe Ala Ser Pro Xaa Val Arg Pro Ala Ser Ser Met Ser Ser Arg Leu
 -5 1 5
 ctg ctc ccc gsc ctt cat tac tcg gac tgg act tgc tgg ctt cct gaa 320
 Leu Leu Pro Xaa Leu His Tyr Ser Asp Trp Thr Cys Trp Leu Pro Glu
 10 15 20
 cgg aga ga 328
 Arg Arg
 25

<210> 561
 <211> 341
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 69..341

<221> sig_peptide
 <222> 69..230
 <223> Von Heijne matrix
 score 4.19999980926514

seq TVVFLTLLSVVIL/IF

<221> misc_feature

<222> 270..272,321..322

<223> n=a, g, c or t
Oligonucleotide

<400> 561

ccttcaccag cagcccgctc gactggaaag atctgcctct tctccaagaa actcaaccac 60
tagtgaca atg acc agc ctc ctg act act cct tct cca aga gaa gaa ctg 110

Met Thr Ser Leu Leu Thr Thr Pro Ser Pro Arg Glu Glu Leu

-50

-45

atg acc acc cca att tta cag ccc act gag gcc ctg tcc cca gaa gat 158

Met Thr Thr Pro Ile Leu Gln Pro Thr Glu Ala Leu Ser Pro Glu Asp

-40

-35

-30

-25

gga gcc agc aca gca ctc att gca gtt gtt atc acc gtt gtc ttc ctc 206

Gly Ala Ser Thr Ala Leu Ile Ala Val Val Ile Thr Val Val Phe Leu

-20

-15

-10

acc ctg ctc tcg gtc gtg atc ttg atc ttc ttt tac ctg tac aag aac 254

Thr Leu Leu Ser Val Val Ile Leu Ile Phe Phe Tyr Leu Tyr Lys Asn

-5

1

5

aaa ggc agc tac gtm nnn tat gaa cct aca gaa ggt gag ccc agt gcc 302

Lys Gly Ser Tyr Val Xaa Tyr Glu Pro Thr Glu Gly Glu Pro Ser Ala

10

15

20

atc gtc cag atg gag adw nnc ttg gcc aag ggc agc gag 341

Ile Val Gln Met Glu Xaa Xaa Leu Ala Lys Gly Ser Glu

25

30

35

<210> 562

<211> 484

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 334..483

<221> sig_peptide

<222> 334..387

<223> Von Heijne matrix
score 4.19999980926514
seq LIYLVSSFLALNQ/AS

<400> 562

gttagttggg cagggctgaa gtgtatgtgg tgaggaaaag aggctcctac tgtagacagc 60

cttggttctac agatcctccc agaaatctct gggccagggtg gaaccacaggg tcagagaggg 120

atgggagaga ggtttaattt tccatgataa ataaaaatct ataaaaataat aaacaagaga 180

aaagagattg gaaacagcca ggttgagca gtgagtgaat aaggaaacct ggctgccctc 240

tccagattcc ccaggctctc agagaagatc agcagaaagt ctgcaagass ctaagaacca 300

tcagccctca gctgcacctc ctcccctcca agg atg aca aag gcg sgv ctc atc 354

Met Thr Lys Ala Xaa Leu Ile

-15

tat ttg gtc agc agc ttt ctt gcc cta aat cag gcc agc ctc atc agt 402

Tyr Leu Val Ser Ser Phe Leu Ala Leu Asn Gln Ala Ser Leu Ile Ser

-10	-5	1	5	
cgc tgt gac ttg gcc cag gtg ctg cag ctg gag gac ttg gat ggg ttt				450
Arg Cys Asp Leu Ala Gln Val Leu Gln Leu Glu Asp Leu Asp Gly Phe				
	10	15	20	
gag ggt tac tcc ctg agt gac tgg ctg tgc tgg c				484
Glu Gly Tyr Ser Leu Ser Asp Trp Leu Cys Trp				
	25	30		

<210> 563
 <211> 229
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 122..229

<221> sig_peptide
 <222> 122..190
 <223> Von Heijne matrix
 score 4.19999980926514
 seq QLILLGIFRGIRH/QI

<400> 563	
gaaaggcctc gaaggcagcg tcctactcga ccaccaaggc aagacaagcc acctckattt	60
agacggctaa gagagagga ggctgcttca aaatcaaagtg aggtggtagc agtgcccaca	120
a atg gca cag tta ata atg tgg ctc aag aac cag tta ata ctc ttg ggg	169
Met Ala Gln Leu Ile Met Trp Leu Lys Asn Gln Leu Ile Leu Leu Gly	
	-20 -15 -10
ata ttt cgg gga ata aga cac cag att tat cta atc aga act ctt cag	217
Ile Phe Arg Gly Ile Arg His Gln Ile Tyr Leu Ile Arg Thr Leu Gln	
	-5 1 5
atc agg caa tgg	229
Ile Arg Gln Trp	
10	

<210> 564
 <211> 352
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 80..352

<221> sig_peptide
 <222> 80..169
 <223> Von Heijne matrix
 score 4.19999980926514
 seq LAXTSLTCSVSG/VS

<400> 564	
actttctgag agtcctggac ctctgtgca agaacatgaa acatctgtgg ttcttccttc	60
tcctggtggc aggtccag atg ggt cct gtc cca ggt gca gct gca gga gtm	112

	Met	Gly	Pro	Val	Pro	Gly	Ala	Ala	Ala	Gly	Val	
	-30					-25					-20	
rgg ccc ayg amt ggc gaa ctt gcg grg acc ctg tcc ctc acc tgc agt												160
Xaa Pro Xaa Xaa Gly Glu Leu Ala Xaa Thr Leu Ser Leu Thr Cys Ser												
	-15					-10					-5	
gtc tct ggt gtc tcc atc act agt tat tac tgg agc tgg atc cgc car												208
Val Ser Gly Val Ser Ile Thr Ser Tyr Tyr Trp Ser Trp Ile Arg Gln												
	1					5					10	
gcc cca ggg aag ggg ccg gag tgg atc ggg cdk atc gat cat agc ggg												256
Ala Pro Gly Lys Gly Pro Glu Trp Ile Gly Xaa Ile Asp His Ser Gly												
	15					20					25	
gat acc gac tac aat ccc tcc ctc cag agt cga gtc acc ctc tca gtg												304
Asp Thr Asp Tyr Asn Pro Ser Leu Gln Ser Arg Val Thr Leu Ser Val												
	30					35					40	
gac acg tcg aag aac cag ttc tca ctg agg ttg ctt tct gtg agc gca												352
Asp Thr Ser Lys Asn Gln Phe Ser Leu Arg Leu Leu Ser Val Ser Ala												
	50					55					60	

<210> 565
 <211> 201
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 85..201

<221> sig_peptide
 <222> 85..192
 <223> Von Heijne matrix
 score 4.1999980926514
 seq LPLFLCPLGMVET/SF

<400> 565	
agttctgctg tgtgagccgg ggcacaaaga gccctctgca ctagcgccgc agaccgcgga	60
ccagttggag gcatctgtcc accc atg tgg ttc cag aca cgt tca tgt ggc	111
	Met Trp Phe Gln Thr Arg Ser Cys Gly
	-35 -30
cac cat gac ccc gtc ggc atc aca ggg gta acc aag gtg atc ctc cct	159
His His Asp Pro Val Gly Ile Thr Gly Val Thr Lys Val Ile Leu Pro	
	-25 -20 -15
ctc ttc ctg tgt cca ctg ggg atg gta gag acc agc ttc ggg	201
Leu Phe Leu Cys Pro Leu Gly Met Val Glu Thr Ser Phe Gly	
	-10 -5 1

<210> 566
 <211> 422
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 87..422

<221> sig_peptide
 <222> 87..413
 <223> Von Heijne matrix
 score 4.19999980926514
 seq LVFLLMYLFPRQL/LI

<400> 566
 ctctcccgct tctctcgctg tgaagatggc gctctccagg gtcttcaaag cttcaccttt 60
 ctccaaaggc agatgtgaag aacttg atg tct tat gtg gta acc aag aca aaa 113
 Met Ser Tyr Val Val Thr Lys Thr Lys
 -105
 gcg att aat ggg aaa tac cat cgt ttc ttg ggt cgt cat ttc ccc cgc 161
 Ala Ile Asn Gly Lys Tyr His Arg Phe Leu Gly Arg His Phe Pro Arg
 -100 -95 -90 -85
 ttc tat gtc ctg tac aca atc ttc atg aaa gga ttg cag atg tta tgg 209
 Phe Tyr Val Leu Tyr Thr Ile Phe Met Lys Gly Leu Gln Met Leu Trp
 -80 -75 -70
 gct gat gcc aaa aag gct aga aga ata aag aca aat atg tgg aag cac 257
 Ala Asp Ala Lys Lys Ala Arg Arg Ile Lys Thr Asn Met Trp Lys His
 -65 -60 -55
 aat ata aag ttt cat caa ctt cca tac cgg gag atg gag cat ttg aga 305
 Asn Ile Lys Phe His Gln Leu Pro Tyr Arg Glu Met Glu His Leu Arg
 -50 -45 -40
 cag ttc cgc caa gac gtc acc aag tgt ctt ttc cta ggt att att tcc 353
 Gln Phe Arg Gln Asp Val Thr Lys Cys Leu Phe Leu Gly Ile Ile Ser
 -35 -30 -25
 att cca cct ttt gcc aac tac ctg gtc ttc ttg cta atg tac ctg ttt 401
 Ile Pro Pro Phe Ala Asn Tyr Leu Val Phe Leu Leu Met Tyr Leu Phe
 -20 -15 -10 -5
 ccc agg caa cta ctg atc agg 422
 Pro Arg Gln Leu Leu Ile Arg
 1

<210> 567
 <211> 218
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 48..218

<221> sig_peptide
 <222> 48..104
 <223> Von Heijne matrix
 score 4.19999980926514
 seq LSLPSFLCTCCQF/FP

<400> 567
 tttcctttct gttttgggag ggaagtggag ggagttcttt tttcttt atg tat aat 56
 Met Tyr Asn
 tat tac ttc ctt tca ttg ccg agt ttt ctt tgt acc tgt tgt caa ttc 104
 Tyr Tyr Phe Leu Ser Leu Pro Ser Phe Leu Cys Thr Cys Cys Gln Phe
 -15 -10 -5

[illegible]

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<220>
<221> CDS
<222> 2..244

<221> sig_peptide
<222> 2..238
<223> Von Heijne matrix
      score 4.19999980926514
      seq LLLVSLLEHLSHV/HE
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<210> 569
<211> 142
<212> DNA
<213> Homo sapiens
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356

<222> 78..128

<223> Von Heijne matrix

score 4.19999980926514

seq CFALCIILICVMS/CR

<400> 569

cacattagtt ttgaaactag ctctaatttc tcctaccagg aggaatttct tccttcttgg 60

caatactgtg gtattta atg gta ttt tac tgt ttt gca ctt tgt att ata 110

Met Val Phe Tyr Cys Phe Ala Leu Cys Ile Ile

-15 -10

ctt att tgt gtt atg tct tgt cgc cac ctg gg 142

Leu Ile Cys Val Met Ser Cys Arg His Leu

-5 1

<210> 570

<211> 207

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 12..206

<221> sig_peptide

<222> 12..140

<223> Von Heijne matrix

score 4.09999990463257

seq VLITQLCLGKGQS/EP

<400> 570

tcaatccttg a atg ctc tgg gag act gat ttg agt acc aat aaa act cca 50

Met Leu Trp Glu Thr Asp Leu Ser Thr Asn Lys Thr Pro

-40 -35

gtc tcc tgc aca gct ggc tct gcg tgt gct ctt tct cta ttg caa ttc 98

Val Ser Cys Thr Ala Gly Ser Ala Cys Ala Leu Ser Leu Leu Gln Phe

-30 -25 -20 -15

cct gtc ttg ata act cag ctc tgt cta ggc aaa ggg caa agt gaa ccc 146

Pro Val Leu Ile Thr Gln Leu Cys Leu Gly Lys Gly Gln Ser Glu Pro

-10 -5 1

att ggg cca tta caa gat ttt gtg tct ttg gaa agc act tca cat ttt 194

Ile Gly Pro Leu Gln Asp Phe Val Ser Leu Glu Ser Thr Ser His Phe

5 10 15

tat tct ttt ttt t 207

Tyr Ser Phe Phe

20

<210> 571

<211> 373

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 276..371

<221> sig_peptide
 <222> 276..335
 <223> Von Heijne matrix
 score 4.09999990463257
 seq LWCCSPSSRTSSS/LS

<221> misc_feature
 <222> 251
 <223> n=a, g, c or t
 Oligonucleotide

<400> 571
 attctgcagc caactttggt caccatctcc gcaatgcctt ggacgtcctg catagagagg 60
 tgcccagagt cctggtcaac ctctgtggact tcctgaaccc cactatsrtg cggcaggtgt 120
 tcctgggrra cccagacaag tgcccagtg cagcaggccag cgttttgtgt aactgcgttc 180
 tgaccctgcg ggagaactcc caagagctag ccaggctggr ggccttcagc cgagcctacc 240
 ggagcagcat nbcgagctgg tggggtcagg ccgct atg aca cgc agg agg act 293
 Met Thr Arg Arg Arg Thr
 -20 -15
 tct ctg tgg tgc tgc agc cct tct tcc aga aca tcc agc tcc ctg tcc 341
 Ser Leu Trp Cys Cys Ser Pro Ser Ser Arg Thr Ser Ser Ser Leu Ser
 -10 -5 1
 tgg cgg atg ggc tcc cag ata cgt cct tct tt 373
 Trp Arg Met Gly Ser Gln Ile Arg Pro Ser
 5 10

<210> 572
 <211> 195
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 134..193

<221> sig_peptide
 <222> 134..187
 <223> Von Heijne matrix
 score 4.09999990463257
 seq WCFHAVFFTVCVC/VR

<400> 572
 gtgacaaagt accacagact ggggtggttga aacacagaaa tttattttct cacaatttcg 60
 gaggtcttag aagtctgaga tcaaggtggt ggcaggtttg gtttattcta aggcctttct 120
 ctatggcttg tag atg gcc ttc tat ctc tgg tgt ttt cat gcg gtc ttt 169
 Met Ala Phe Tyr Leu Trp Cys Phe His Ala Val Phe
 -15 -10
 ttc act gtg tgt gtg tgt gtg cgg gg 195
 Phe Thr Val Cys Val Cys Val Arg
 -5 1

<210> 573
 <211> 352

<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 173..352

<221> sig_peptide
<222> 173..271
<223> Von Heijne matrix
score 4.09999990463257
seq PLIHLLTSLGHSTC/FR

<400> 573
tcattcttgg gtgtttctcg cagaggggga tttggcaggg tcataggaca atagtggagg 60
gaaggtcagc agataaacia gtgaacaaag gtttctgggt ttcctaggca gargaccctt 120
gcgcccttcc gcagtgtttg tgtccctggg tacttgagat tagggagtgg tg atg act 178
Met Thr
ctt aac gag cat gct gcc ttc aag cat ctg ttt aac aaa gca cat ctt 226
Leu Asn Glu His Ala Ala Phe Lys His Leu Phe Asn Lys Ala His Leu
-30 -25 -20
gca cca ccc tta atc cat tta acb ctg agt gga cac agc aca tgt ttc 274
Ala Pro Pro Leu Ile His Leu Thr Leu Ser Gly His Ser Thr Cys Phe
-15 -10 -5 1
aga gag cac agg gtt ggg ggc aag gtc ata gat gaa cag cat ccc aag 322
Arg Glu His Arg Val Gly Gly Lys Val Ile Asp Glu Gln His Pro Lys
5 10 15
gca gaa gaa tct ttc tta gta cag gag ggg 352
Ala Glu Glu Ser Phe Leu Val Gln Glu Gly
20 25

<210> 574
<211> 121
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 35..121

<221> sig_peptide
<222> 35..112
<223> Von Heijne matrix
score 4.09999990463257
seq SLASFLLLTFLPS/LP

<400> 574
accttccttc tctccttctt tccttccttc cttc atg tct ttc tct tcc tct ctc 55
Met Ser Phe Ser Ser Ser Leu
-25 -20
cct cca tct ctc cct cct tcc ctc gct tcc ttc ctc ctt ttg acc ttc 103
Pro Pro Ser Leu Pro Pro Ser Leu Ala Ser Phe Leu Leu Leu Thr Phe
-15 -10 -5
ctt cct tcc ctc cct cgg 121

Leu Pro Ser Leu Pro Arg

1

<210> 575

<211> 391

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 77..391

<221> sig_peptide

<222> 77..214

<223> Von Heijne matrix

score 4.09999990463257

seq GCAPLRWVPQIRG/CP

<221> misc_feature

<222> 31..32,314

<223> n=a, g, c or t

Oligonucleotide

<400> 575

aaaaactgts sagacttttg cccgtccatt nncrctatct ctccccactc tgggtgtcct 60

acccaaggcg ctgtct atg cgt gcc cag gcc ctg tcc tgc gga tac cca gct 112

Met Arg Ala Gln Gly Leu Ser Cys Gly Tyr Pro Ala

-45

-40

-35

cgc ccc ttg cag ccc ttt tta gag cat ctc gcg gcc tct ggc atc acc 160

Arg Pro Leu Gln Pro Phe Leu Glu His Leu Ala Gly Ser Gly Ile Thr

-30

-25

-20

aag cgc aca gcc ccg gcc tgc gct ccc cta agg tgg gtc cct cag atc 208

Lys Arg Thr Ala Pro Gly Cys Ala Pro Leu Arg Trp Val Pro Gln Ile

-15

-10

-5

cgg gcc tgt cca tta acc agg ctg gcc caa aga gcc gca gac act cga 256

Arg Gly Cys Pro Leu Thr Arg Leu Ala Gln Arg Gly Ala Asp Thr Arg

1

5

10

acc cgg gaa aac tta ttt tat tct cgg ttc ccg ggg ttg cag ctg cca 304

Thr Arg Glu Asn Leu Phe Tyr Ser Arg Phe Pro Gly Leu Gln Leu Pro

15

20

25

30

gcg gct gak nac agt gcg tcc gct ttg tct ctc tgc act ccc cgc agc 352

Ala Ala Xaa Xaa Ser Ala Ser Ala Leu Ser Leu Cys Thr Pro Arg Ser

35

40

45

ccc cct ctc ccg ctt cct ctc ccg att aac tcc ccc ggg 391

Pro Pro Leu Pro Leu Pro Leu Pro Ile Asn Ser Pro Gly

50

55

<210> 576

<211> 288

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 133..288

<221> sig_peptide

<222> 133..243

<223> Von Heijne matrix

score 4.09999990463257

seq SISFLPFQASIFG/KT

<400> 576

aaaggcacag cgcgggcgca ggcgcccaga ggcgacagga gacctcaggc ccagactcca 60
ctccccagct gtgaaaggac tgctggccag accccaagc tagcccgcca ggcctccata 120
gagctgcca gc atg gct gca tcc agt acc agt cat ctt aaa aat aaa aca 171
Met Ala Ala Ser Ser Thr Ser His Leu Lys Asn Lys Thr
-35 -30 -25
aaa acc ttc ctt gcc ccc atg acc aac tgc cac tca att tcc ttt ctt 219
Lys Thr Phe Leu Ala Pro Met Thr Asn Cys His Ser Ile Ser Phe Leu
-20 -15 -10
cct ttc caa gca agt att ttt gga aag act cgt ctg cag tca ctg agg 267
Pro Phe Gln Ala Ser Ile Phe Gly Lys Thr Arg Leu Gln Ser Leu Arg
-5 1 5
cct tcc cac cct tac ccc cac 288
Pro Ser His Pro Tyr Pro His
10 15

<210> 577

<211> 264

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 134..262

<221> sig_peptide

<222> 134..250

<223> Von Heijne matrix

score 4.09999990463257

seq FXSCXCVSTLAYT/KG

<400> 577

attacacagt agaggaggga agctaaagga agtctatgga caggtgaggg agggkgagac 60
tggggaattt tctgattgtt cagaggaatc ttgaagatga tggaaatata agatgtgcta 120
aagtttcccta gta atg ccc aag gat gct gac ctg gct ttc agt gct tca 169
Met Pro Lys Asp Ala Asp Leu Ala Phe Ser Ala Ser
-35 -30
ttg ttt gaa aga gca gag tcc ctt tat act ctg att tca aaa ttt ktt 217
Leu Phe Glu Arg Ala Glu Ser Leu Tyr Thr Leu Ile Ser Lys Phe Xaa
-25 -20 -15
tct tgt dtk tgt gtg tct acc ttg gca tat act aaa gga agg ggg gg 264
Ser Cys Xaa Cys Val Ser Thr Leu Ala Tyr Thr Lys Gly Arg Gly
-10 -5 1

<210> 578

<211> 205

<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 115..204

<221> sig_peptide
<222> 115..198
<223> Von Heijne matrix
score 4.09999990463257
seq MPFLFLTLFHCLG/RR

<221> misc_feature
<222> 94
<223> n=a, g, c or t
Oligonucleotide

<400> 578
ttagaaaata cagwtgatgt ttaatagtga tcttgtatcc tatacccttg caaactccac 60
ttcttagttc cagttacttt attgtasytt tttnhttgty ytttactgtg tgtg atg 117
Met
ttt gtg aat aga acc tgt ttt aat tct tcc ttt cca atc tgg atg cct 165
Phe Val Asn Arg Thr Cys Phe Asn Ser Ser Phe Pro Ile Trp Met Pro
-25 -20 -15
ttt ctt ttt ctt aca tta ttc cac tgc tta gga cgt cgg g 205
Phe Leu Phe Leu Thr Leu Phe His Cys Leu Gly Arg Arg
-10 -5 1

<210> 579
<211> 214
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 25..213

<221> sig_peptide
<222> 25..135
<223> Von Heijne matrix
score 4.09999990463257
seq HFLXAVSASSSXA/CL

<400> 579
gcctcctctw gcgctgtcct gtta atg gyg ggc agt agc cgc tgm vkg gga 51
Met Xaa Gly Ser Ser Arg Xaa Xaa Gly
-35 -30
ttg cag ata acc gct tcc cgc acg ggg aaa gtc tac cct gcc tgc cac 99
Leu Gln Ile Thr Ala Ser Arg Thr Gly Lys Val Tyr Pro Ala Cys His
-25 -20 -15
ttt ctg skc gcc gtc agc gcc agt agc tcg cma gca tgt ctg tgg tac 147
Phe Leu Xaa Ala Val Ser Ala Ser Ser Ser Xaa Ala Cys Leu Trp Tyr
-10 -5 1

cgc cca atm gct cgc aga ccg gct ggc ccc ggg ggg tca ctc agt tcg	195
Arg Pro Ile Ala Arg Arg Pro Ala Gly Pro Gly Gly Ser Leu Ser Ser	
5 10 15 20	
gca caa gta cat cca gca g	214
Ala Gln Val His Pro Ala	
25	

<210> 580
 <211> 328
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 28..327

<221> sig_peptide
 <222> 28..105
 <223> Von Heijne matrix
 score 4.09999990463257
 seq VTFWLLCRICTFG/FH

<400> 580	
tgttttgtgat cagtatccaa aggcaaa atg att ttg ttt gac cat tta cat tgt	54
Met Ile Leu Phe Asp His Leu His Cys	
-25 -20	
tca gca tca gga gtg act ttc tgg ttg ctt tgc agg atc tgt acg ttt	102
Ser Ala Ser Gly Val Thr Phe Trp Leu Leu Cys Arg Ile Cys Thr Phe	
-15 -10 -5	
ggg ttt cat ggt ttt tct aaa tac aca gtt tca cgt gga aca cag cag	150
Gly Phe His Gly Phe Ser Lys Tyr Thr Val Ser Arg Gly Thr Gln Gln	
1 5 10 15	
ggg gca gga avg tgv dgt gga tta cac cag aac tgg gaa cag tgg agg	198
Gly Ala Gly Xaa Xaa Xaa Gly Leu His Gln Asn Trp Glu Gln Trp Arg	
20 25 30	
ggg ctt gtt ggg aag tct agt tct gcc gca gtt gtt ttc tgc ctt acs	246
Gly Leu Val Gly Lys Ser Ser Ser Ala Ala Val Val Phe Cys Leu Thr	
35 40 45	
ttt gac ttg gtt acc agc ttt caa tta gca agt gca att gaa agt aca	294
Phe Asp Leu Val Thr Ser Phe Gln Leu Ala Ser Ala Ile Glu Ser Thr	
50 55 60	
cat ttc cat gct ggg cgc gat ggc tca cac ctg t	328
His Phe His Ala Gly Arg Asp Gly Ser His Leu	
65 70	

<210> 581
 <211> 356
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 264..356

<221> sig_peptide
 <222> 264..350
 <223> Von Heijne matrix
 score 4.09999990463257
 seq LLLFPASLRLLCV/HP

<221> misc_feature
 <222> 146
 <223> n=a, g, c or t
 Oligonucleotide

<400> 581
 gtckcatttt gcctttgwaa tggaagtcac ttccaagtgt ctgttctcta ggttttcctt 60
 tttttctctt ttagaaattg gacacttcaa taaaatttgt aattacgtcc atctgwtga 120
 htattwgmatt tyratgksca tatctnstgc cagattgtaa actccgcgag tgcacataatc 180
 agatccatta tggttctcat catatcccta gtcctagcg cagtgcgggg cacgtataag 240
 tgctcgaaag ctcccacgtg gtg atg gag cta agc ttg ccc cct tcc atg tgt 293
 Met Glu Leu Ser Leu Pro Pro Ser Met Cys
 -25 -20
 gac tac cca amt ttc tgt ctc ctc ctc ttc ccg gcc tct ctc aga ctc 341
 Asp Tyr Pro Xaa Phe Cys Leu Leu Leu Phe Pro Ala Ser Leu Arg Leu
 -15 -10 -5
 ctc tgt gtg cat ccc 356
 Leu Cys Val His Pro
 1

<210> 582
 <211> 239
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 159..239

<221> sig_peptide
 <222> 159..218
 <223> Von Heijne matrix
 score 4.09999990463257
 seq TVGCAGLAGSCR/IS

<400> 582
 agttcctggg ctcccgcgga gsatgagacg ttgtgaatta gatgtgagaa gagggacgct 60
 tgggtctgca ccaccaagac cccacaggat cgatgcaccc acccctgctg atgaccatga 120
 ccatctaaar gggaaacatc atttgagggg ccctactc atg gat cag aag ccc ctc 176
 Met Asp Gln Lys Pro Leu
 -20 -15
 ttc act gtg ggg tgt gct ggg ttg gcg ggc agt tgc cgt gga atc agt 224
 Phe Thr Val Gly Cys Ala Gly Leu Ala Gly Ser Cys Arg Gly Ile Ser
 -10 -5 1
 ttc ctc agg acc cgc 239
 Phe Leu Arg Thr Arg
 5

<210> 583
 <211> 144
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> CDS
 <222> 8..142

 <221> sig_peptide
 <222> 8..76
 <223> Von Heijne matrix
 score 4.09999990463257
 seq FILLLLIQDLTMS/PT

<400> 583
 ttttaaa atg tca gtt aat gmt att ttt att ttc tat ttt atc tta tta 49
 Met Ser Val Asn Xaa Ile Phe Ile Phe Tyr Phe Ile Leu Leu
 -20 -15 -10
 tta ttg ata caa gat ctc act atg tca ccc act gct gga atg cag tgg 97
 Leu Leu Ile Gln Asp Leu Thr Met Ser Pro Thr Ala Gly Met Gln Trp
 -5 1 5
 cat aat cat ggc cca cca caa gcc ttg cct tgc cca ctg aga abc cc 144
 His Asn His Gly Pro Pro Gln Ala Leu Pro Cys Pro Leu Arg Xaa
 10 15 20

<210> 584
 <211> 282
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> CDS
 <222> 47..280

 <221> sig_peptide
 <222> 47..181
 <223> Von Heijne matrix
 score 4.09999990463257
 seq ICLGSPLAECLLG/XX

<221> misc_feature
 <222> 183,210
 <223> n=a, g, c or t
 Oligonucleotide

<400> 584
 ccttggttaa gccgtgatcg tgacctcacc atgtgtagac agtgag atg tca ttt 55
 Met Ser Phe
 -45
 ctc aat gtg gac atc aca gat tgc ctg tat aac ccc agt gtg tgt ccc 103
 Leu Asn Val Asp Ile Thr Asp Cys Leu Tyr Asn Pro Ser Val Cys Pro
 -40 -35 -30
 gtg gct cag agc agt ctg acc tgt gac ttc ata gat ggt atc tgc ttg 151

Val	Ala	Gln	Ser	Ser	Leu	Thr	Cys	Asp	Phe	Ile	Asp	Gly	Ile	Cys	Leu	
-25						-20					-15					
ggg	tcg	cct	ttg	gct	gag	tgt	ctg	ctt	ggt	gna	gwa	wkw	ksc	att	ttk	199
Gly	Ser	Pro	Leu	Ala	Glu	Cys	Leu	Leu	Gly	Xaa	Xaa	Xaa	Xaa	Ile	Xaa	
-10					-5				1				5			
ggr	atc	aat	rns	cym	tgc	ttt	ccg	tgt	ggt	gtg	aag	tgc	gca	ggt	gtg	247
Gly	Ile	Asn	Xaa	Xaa	Cys	Phe	Pro	Cys	Gly	Val	Lys	Cys	Ala	Gly	Val	
		10					15						20			
gtc	ttg	ggg	ctg	agc	acc	ctg	tgg	tat	ggt	gta	gc					282
Val	Leu	Gly	Leu	Ser	Thr	Leu	Trp	Tyr	Val	Val						
	25						30									

<210> 585
 <211> 388
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 242..388

<221> sig_peptide
 <222> 242..352
 <223> Von Heijne matrix
 score 4.09999990463257
 seq FTFLSPSFHSHVHL/SE

<400>	585																				
tgc	att	ttt	ta	aaa	tag	cta	ga	agaaa	aga	act	tta	aat	at	tcc	aaa	aaca	aataaaa	atat	60		
aa	atg	ttt	ga	gg	tg	aggg	at	ccca	atta	cc	tg	att	ttg	gt	tatt	att	c	attgt	tata	120	
gt	ttt	caaaa	tat	ca	cat	gt	ac	cccc	aaaa	tat	gt	aaa	aac	tg	tt	ata	tac	aa	ataa	180	
ca	aa	act	aaa	aata	ac	ag	ct	gtg	caa	ac	at	ttt	aaa	agg	ct	tg	ctt	ta	atgg	gtt	240
c	atg	aaa	gta	gga	aag	gac	tct	ctg	gag	tct	tta	cca	tct	tta	tgt	gag				289	
Met	Lys	Val	Gly	Lys	Asp	Ser	Leu	Glu	Ser	Leu	Pro	Ser	Leu	Cys	Glu						
	-35					-30				-25											
aaa	cac	att	ggt	ccc	agt	ggt	ctc	ttt	acc	ttt	ctt	agt	cca	tcc	ttt					337	
Lys	His	Ile	Gly	Pro	Ser	Gly	Leu	Phe	Thr	Phe	Leu	Ser	Pro	Ser	Phe						
	-20					-15				-10											
cac	tct	gta	cat	ctt	tct	gaa	ctc	aat	gaa	tta	tac	act	att	gct	gcc					385	
His	Ser	Val	His	Leu	Ser	Glu	Leu	Asn	Glu	Leu	Tyr	Thr	Ile	Ala	Ala						
	-5			1				5						10							
ggg																				388	
Gly																					

<210> 586
 <211> 436
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 346..435

<221> sig_peptide

<222> 346..396
 <223> Von Heijne matrix
 score 4.09999990463257
 seq VLISASLLRASQL/KI

<221> misc_feature
 <222> 170
 <223> n=a, g, c or t
 Oligonucleotide

<400> 586
 tgtgctgtgt ggtaggaga aggagggatg ggagagagaa ggggaaggaa tgaggcatgg 60
 agagagatca caaccatcgt ctcaatgaag cagcagcaca cacagggatg tgtggtcgwc 120
 ccaagttcag gggagagagt ttaaaggcgg gatgatcata tgtgaagdhc tggcagcacc 180
 aatatggcac tgtcaaagta aaagagaaat agatctgaac tggattttta tgagaataat 240
 agcaaattatt aacatttctt agatagtttg atatttattc tgggaagtatc gctaccaaca 300
 tcaacatctg ggaaagcdag tgggcatcaa aatcctacct ggcta atg gaa agc aaa 357
 Met Glu Ser Lys
 -15
 gtt tta atc agt gca tca ctc cta cgg gcc tct caa tta aaa ata aaa 405
 Val Leu Ile Ser Ala Ser Leu Leu Arg Ala Ser Gln Leu Lys Ile Lys
 -10 -5 1
 tgr aac aaa atg aca aac ttc tta att ttg t 436
 Xaa Asn Lys Met Thr Asn Phe Leu Ile Leu
 5 10

<210> 587
 <211> 378
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 24..377

<221> sig_peptide
 <222> 24..95
 <223> Von Heijne matrix
 score 4.09999990463257
 seq RLPMLSLFRGSHX/XF

<400> 587
 tcctgtcctg ggcgtacgtc aag atg gcg gcg tct gta tta aac acc gtg ctg 53
 Met Ala Ala Ser Val Leu Asn Thr Val Leu
 -20 -15
 agg cgg ctt cct atg cta tct ctc ttc cga ggt tct cay vvg rbg ttc 101
 Arg Arg Leu Pro Met Leu Ser Leu Phe Arg Gly Ser His Xaa Xaa Phe
 -10 -5 1
 agg ttc ccc tcc aga ctc ttt gca cca aag ctc cct ctg agg aag att 149
 Arg Phe Pro Ser Arg Leu Phe Ala Pro Lys Leu Pro Leu Arg Lys Ile
 5 10 15
 ctt tgt cct cag ttc cca ttt ctc ctt ata agg atg agc cct gga aat 197
 Leu Cys Pro Gln Phe Pro Phe Leu Leu Ile Arg Met Ser Pro Gly Asn
 20 25 30

<211> 210
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 138..209

<221> sig_peptide
 <222> 138..179
 <223> Von Heijne matrix
 score 4.09999990463257
 seq LASPCVLVQGSX/SL

<221> misc_feature
 <222> 78,80,118
 <223> n=a, g, c or t
 Oligonucleotide

<400> 589
 gaagataata ataatgatta ttataataat gatgatgatt ccaaggaaaa aacctacagc 60
 gaatgttcca tttctacsn gcacgcagac actctcccta acactgataa cctgagcncc 120
 cagcactgga cggaaga atg ctg gcg tct ccg tgt gta ctg gtt cag ggt 170
 Met Leu Ala Ser Pro Cys Val Leu Val Gln Gly
 -10 -5
 tct ggs bcc agc ctt gtc agg acc ccc tgg tgt cca gag c 210
 Ser Gly Xaa Ser Leu Val Arg Thr Pro Trp Cys Pro Glu
 1 5 10

<210> 590
 <211> 178
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 40..177

<221> sig_peptide
 <222> 40..96
 <223> Von Heijne matrix
 score 4.09999990463257
 seq ILLLLITIIYSYL/ES

<400> 590
 acaaggactg aaccagaagg aagaggacag agcaaagcc atg aac atc atc cta 54
 Met Asn Ile Ile Leu
 -15
 gaa atc ctt ctg ctt ctg atc acc atc atc tac tcc tac ttg gag tcg 102
 Glu Ile Leu Leu Leu Leu Ile Thr Ile Ile Tyr Ser Tyr Leu Glu Ser
 -10 -5 1
 ttg gtg aag ttt ttc att cct cag agg aga aaa tct gtg gct ggg gag 150
 Leu Val Lys Phe Phe Ile Pro Gln Arg Arg Lys Ser Val Ala Gly Glu
 5 10 15

att gtt ctc att act gga gct ggg cat g
 Ile Val Leu Ile Thr Gly Ala Gly His
 20 25

178

<210> 591
 <211> 308
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 149..307

<221> sig_peptide
 <222> 149..265
 <223> Von Heijne matrix
 score 4.09999990463257
 seq PSLIAGLFGCLA/GY

<221> misc_feature
 <222> 272
 <223> n=a, g, c or t
 Oligonucleotide

<400> 591
 gcgagacggc tgggcgccga gtgggacagc gctggtgcgg agactgcttc cggactccag 60
 gtaccgcgct tggcggcagc tggccccaga cttctgtctt ttcaagmkgc aagtraargc 120
 tcggggctgc rraattgcaa ccttgcca atg gac ctg atc ggt ttt ggt tat 172
 Met Asp Leu Ile Gly Phe Gly Tyr
 -35
 gca gcc ctc gtg aca ttt gga agc att ttt gga tat aag cdg aga ggt 220
 Ala Ala Leu Val Thr Phe Gly Ser Ile Phe Gly Tyr Lys Xaa Arg Gly
 -30 -25 -20
 ggt gtt ccg tct ttg att gct ggt ctt ttt gtd gga tgt ttg gcc ggc 268
 Gly Val Pro Ser Leu Ile Ala Gly Leu Phe Val Gly Cys Leu Ala Gly
 -15 -10 -5 1
 tat nsa gct tac cgt gtc tcc aat gac aaa cga gat gta a 308
 Tyr Xaa Ala Tyr Arg Val Ser Asn Asp Lys Arg Asp Val
 5 10

<210> 592
 <211> 219
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 16..219

<221> sig_peptide
 <222> 16..72
 <223> Von Heijne matrix
 score 4.09999990463257
 seq XTFLAAXRRLVTG/QT

<400> 592
acagttcatc cggaa atg gag ggg gtc gct ttv btc acc ttc ctc gct gcg 51
Met Glu Gly Val Ala Xaa Xaa Thr Phe Leu Ala Ala
-15 -10
sgg cgg cgg ttg gta acc ggt cag acc agc ccg aga ggg acc tgg tgc 99
Xaa Arg Arg Leu Val Thr Gly Gln Thr Ser Pro Arg Gly Thr Trp Cys
-5 1 5
ctg tac cca ggc ttc tgt cgc tct gtc gcc tgc gct atg ccc tgc tgt 147
Leu Tyr Pro Gly Phe Cys Arg Ser Val Ala Cys Ala Met Pro Cys Cys
10 15 20 25
agt cac agg agc tgt aga gag gac ccc ggt aca tct gaa agc cgg gaa 195
Ser His Arg Ser Cys Arg Glu Asp Pro Gly Thr Ser Glu Ser Arg Glu
30 35 40
atg gtg cgt gtg cgg gac cac ggg 219
Met Val Arg Val Arg Asp His Gly
45

<210> 593
<211> 215
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 105..215
<221> sig_peptide
<222> 105..167
<223> Von Heijne matrix
score 4
seq IGLIGLTVPCGWG/SL

<400> 593
aggaacattt tttattttat ttttatagag atagggtctc tttctgtagc ccaagctgga 60
gtactgtctt agtctgtttt tatgctgctg ataacgacat accc atg act ggg caa 116
Met Thr Gly Gln
-20
ttt aca aaa gaa ata ggt tta att gga ctt aca gtt cca tgt ggc tgg 164
Phe Thr Lys Glu Ile Gly Leu Ile Gly Leu Thr Val Pro Cys Gly Trp
-15 -10 -5
gga agc ctc ata acc atg gca gaa ggc agg gag gag caa gtc acg tct 212
Gly Ser Leu Ile Thr Met Ala Glu Gly Arg Glu Glu Gln Val Thr Ser
1 5 10 15
ggg 215
Gly

<210> 594
<211> 161
<212> DNA
<213> Homo sapiens

<220>
<221> CDS

<222> 89..160

<221> sig_peptide

<222> 89..130

<223> Von Heijne matrix

score 4

seq HLGFIILSFHGLIA/NF

<400> 594

ctccatagtt ttaccttctc caggatgttg tatagatgga attgtacagt atgtagcctt 60

ttcacattgg cttctttcac taaataac atg cat tta gga ttc att ctt tct 112

Met His Leu Gly Phe Ile Leu Ser

-10

ttc cat ggt ttg ata gct aat ttc ttt ttt tgt ctg aat gca cca gcg g 161

Phe His Gly Leu Ile Ala Asn Phe Phe Phe Cys Leu Asn Ala Pro Ala

-5

1

5

10

<210> 595

<211> 396

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 317..394

<221> sig_peptide

<222> 317..376

<223> Von Heijne matrix

score 4

seq GCVAAGVVIGAGA/AT

<221> misc_feature

<222> 149

<223> n=a, g, c or t

Oligonucleotide

<400> 595

actcttccta tagcccagag ggcgagagg cctgtggcct gggggaagga ggacgaggtt 60

ctgcctggmt cccagcagga cgctgtgcca tttgggaaca aaggaatagt ctgcctggaa 120

tccctgcaga tcttggggcc ggaggcagnt ccaacccttg gagcaggaag aaacgcaaag 180

ttgtcaagaa ccaagtcgag ctgcctcaga gccggcccg c agtagctgca gactccgccc 240

gcgacgtgtg cgcgcttctc tgggccagag cgagcctgtt ttgtgctcgg gttaagagat 300

ttgtccbagc tatacc atg ggc cgc act cgg gaa gct ggc tgc gtg gcc gct 352

Met Gly Arg Thr Arg Glu Ala Gly Cys Val Ala Ala

-20

-15

-10

ggg gtg gtt atc ggg gct ggt gct gct act gtg tat aca gac tg 396

Gly Val Val Ile Gly Ala Gly Ala Ala Thr Val Tyr Thr Asp

-5

1

5

<210> 596

<211> 407

<212> DNA

<213> Homo sapiens

<220>
 <221> CDS
 <222> 228..407

<221> sig_peptide
 <222> 228..341
 <223> Von Heijne matrix
 score 4
 seq FKPXSCLSLLSNX/DY

<400> 596
 tgagttttat gmttgattta tatcttttgg ttacaagtc tttgtcagat atatgatttg 60
 caaatatttt ctactctgg gtaggttggtc tttttacttt ctgataatg tcctcttttg 120
 ttgcttggtg tatctccttt tttgtttttt attcttttta aagttatctc ttacaggaag 180
 gattcctttt ttcttaaaaa agtttttcaa ttcttttttt ttttgag atg gag tct 236
 Met Glu Ser
 cac tct gtc gcc cag gct agg atg cgg ysg caw aat ctc agc tca ctg 284
 His Ser Val Ala Gln Ala Arg Met Arg Xaa Xaa Asn Leu Ser Ser Leu
 -35 -30 -25 -20
 caa cct ctg ccg cct ggg ttc aag cca tts tcc tgc ctm agc ctc ctg 332
 Gln Pro Leu Pro Pro Gly Phe Lys Pro Xaa Ser Cys Leu Ser Leu Leu
 -15 -10 -5
 agt aay tsa gat tac agg cat gca cca cca ttc ctg gct aat ttt kgw 380
 Ser Asn Xaa Asp Tyr Arg His Ala Pro Pro Phe Leu Ala Asn Phe Xaa
 1 5 10
 att ttt cat aga gat gga gtt tca cca 407
 Ile Phe His Arg Asp Gly Val Ser Pro
 15 20

<210> 597
 <211> 274
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 90..272

<221> sig_peptide
 <222> 90..254
 <223> Von Heijne matrix
 score 4
 seq LHQGLCLPQRVHC/SL

<400> 597
 gctgaccgrg cgcacscgc ccccgsggcc atcttccga ccgcgagccg tccaggtctc 60
 agtgctrtgc cccccccaga gcctagagg atg ttt cat ggg atc cca gcc acg 113
 Met Phe His Gly Ile Pro Ala Thr
 -55 -50
 ccg ggc ata gga gcc cct ggg aac aag ccg gag ctg tat gag gta cga 161
 Pro Gly Ile Gly Ala Pro Gly Asn Lys Pro Glu Leu Tyr Glu Val Arg
 -45 -40 -35
 caa cat ggc aga gct gtt tgc ggt ggt gaa gac aat gca agc cct gga 209

Gln	His	Gly	Arg	Ala	Val	Cys	Gly	Gly	Glu	Asp	Asn	Ala	Ser	Pro	Gly	
-30						-25					-20					
gaa	ggc	cta	cat	caa	gga	ctg	tgt	ctc	ccc	cag	cga	gta	cac	tgc	agc	257
Glu	Gly	Leu	His	Gln	Gly	Leu	Cys	Leu	Pro	Gln	Arg	Val	His	Cys	Ser	
-15					-10					-5				1		
ctg	ctc	ccg	gct	cct	gg											274
Leu	Leu	Pro	Ala	Pro												
					5											

<210> 598
 <211> 417
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 343..417
 <221> sig_peptide
 <222> 343..408
 <223> Von Heijne matrix
 score 4
 seq LFLSVLNFLFLLS/FS

<400>	598																
gcatctagaa	gtacaagttg	atgattattg	tccatttgat	agagacactg	gaaggggtgc											60	
agtgtaaaca	ctggccatgt	gaagattgag	cctgttgatg	gtttcttttg	tatcatagga											120	
tgccacgtca	ccaactaggg	aattctgccc	aatcagttga	gccaaatagt	gctgtcctat											180	
tgtaaaattg	tttaaatctgt	gtgcttggtg	gtgtgcttgt	cagaatttgt	gaatcataga											240	
attgttttaa	ctggaagaag	accccccaaga	tcattctgctt	caacccttc	cttcctctct											300	
tttccagaga	ggttgactt	tacttgagct	gtgactagga	tt atg cca	cat tct											354	
				Met	Pro	His	Ser										
				-20													
ttt gta agt	tgt aac cta	ttt ttg tct	gtr ttg aat	ttc ctt	ttt ttg											402	
Phe Val Ser	Cys Asn Leu	Phe Leu Ser	Val Leu Asn	Phe Leu Phe	Leu												
	-15		-10		-5												
cta agc	ttt agc	aca														417	
Leu Ser	Phe Ser	Thr															
		1															

<210> 599
 <211> 329
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 240..329
 <221> sig_peptide
 <222> 240..317
 <223> Von Heijne matrix
 score 4
 seq HHLLLSTLATIAG/NI

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<400> 599
agaagactgg aactcagcaa gaaagtgatg aaaatgctct gagacataga aactctagac      60
ggcagcatag aaatggaaga aaaataccca gccagatcca gctcagagcc aagaaaatgt      120
acacaccaga tccccagcat tcccaattat cacaaaaggt gccttaattt ctatctacaa      180
gacaacccta caatcctcac aggccctgag ctcagtatag aaagttttct ggagtccat      239
atg gct gtt ttt ctc caa aag agg aaa cac aca atg aga cac cac cta      287
Met Ala Val Phe Leu Gln Lys Arg Lys His Thr Met Arg His His Leu
   -25                -20                -15
ctc ctc agt aca ctg gct act ata gca ggc aac att tac aga      329
Leu Leu Ser Thr Leu Ala Thr Ile Ala Gly Asn Ile Tyr Arg
-10                -5                1

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<210> 600
<211> 311
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> 169..309

<221> sig_peptide
<222> 169..246
<223> Von Heijne matrix
      score 4
      seq PVAVEALLRAVFG/VV

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<400> 600
acagaggcgg caagactagg gtggaggaaa gctcaagggc catcgctggg tgcttcgggtg      60
gcgggcagaa acgggactgg cagtgccac acgtgtgcgt tctccccgtc cgcccgaagg      120
agctacctgt gcaccctgcc tccggctctc ctgagcagag agatcctg atg gct gac      177
                                   Met Ala Asp
                                   -25
tca gaa gca ctc ccc tcc ctt gct ggg gac cca gtg gct gtg gaa gcc      225
Ser Glu Ala Leu Pro Ser Leu Ala Gly Asp Pro Val Ala Val Glu Ala
   -20                -15                -10
ttg ctc cgg gcc gtg ttt ggg gtt gtt gtg gat gag gcc att cag aaa      273
Leu Leu Arg Ala Val Phe Gly Val Val Val Asp Glu Ala Ile Gln Lys
   -5                1                5
gga acc agt gtc tcc cag aag gtc tgc smg tgg aag ga      311
Gly Thr Ser Val Ser Gln Lys Val Cys Xaa Trp Lys
10                15                20

```

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<210> 601
<211> 420
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> 159..419

<221> sig_peptide

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<222> 159..266
 <223> Von Heijne matrix
 score 4
 seq LAELPVSSPLCHA/VL

<221> misc_feature
 <222> 365..366
 <223> n=a, g, c or t
 Oligonucleotide

<400> 601
 ctaagccttt tctaccctct tctcaaagta gagccgaata tgattcagag gagagtctgg 60
 gaagtgatga tgatgacaat gatgatgatg atgatgtttt agcatcagat ttccatctcc 120
 aggaacattc taattcaaat tcatatagtt ggtccttg atg cgg ttg gcg atg gtg 176
 Met Arg Leu Ala Met Val
 -35
 caa ttg gtg ctc aac aat ttg aag act ttt tat ccc ttc gca gat cat 224
 Gln Leu Val Leu Asn Asn Leu Lys Thr Phe Tyr Pro Phe Ala Asp His
 -30 -25 -20 -15
 gat ctt gca gag ctt cca gtt agt tca cct ctt tgt cat gcg gtt cta 272
 Asp Leu Ala Glu Leu Pro Val Ser Ser Pro Leu Cys His Ala Val Leu
 -10 -5 1
 aaa act ctt caa tgt tgg gaa caa gtt ctt ctc cga cga ctt gaa atc 320
 Lys Thr Leu Gln Cys Trp Glu Gln Val Leu Leu Arg Arg Leu Glu Ile
 5 10 15
 cat ggt ggg cca cct caa aat tat atc gca agt cat acc gcc gan nag 368
 His Gly Gly Pro Pro Gln Asn Tyr Ile Ala Ser His Thr Ala Xaa Xaa
 20 25 30
 agt ttg tct gca ggt cct gca att ctt cgc cac aaa gct tta ctg gaa 416
 Ser Leu Ser Ala Gly Pro Ala Ile Leu Arg His Lys Ala Leu Leu Glu
 35 40 45 50
 cct a 420
 Pro

<210> 602
 <211> 463
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 311..463

<221> sig_peptide
 <222> 311..370
 <223> Von Heijne matrix
 score 4
 seq LFILXYFXXYTLS/SG

<221> misc_feature
 <222> 353..354
 <223> n=a, g, c or t
 Oligonucleotide

1. The first step is to identify the problem or question that needs to be addressed. This involves understanding the context and the specific requirements of the task.

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<220>  
<221> CDS  
<222> 37..195
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<220>

<221> CDS
<222> 63..425

<221> sig_peptide
<222> 63..140
<223> Von Heijne matrix
score 4
seq LLRELRYLSAATG/HP

<221> misc_feature
<222> 174
<223> n=a, g, c or t
Oligonucleotide

<400> 606
ggaggagggg ttttcagggt cgtaggacgc cgttgggcac cacgctcgga gaagacagga 60
ca atg gcg gcc tta ggg tcc ccg tcg cac act ttt cga gga ctt ctg 107
Met Ala Ala Leu Gly Ser Pro Ser His Thr Phe Arg Gly Leu Leu
-25 -20 -15
cgg gag ttg cgc tac ctg agc gcg gcc acc ggc cac cct atc gcg aca 155
Arg Glu Leu Arg Tyr Leu Ser Ala Ala Thr Gly His Pro Ile Ala Thr
-10 -5 1 5
ccg cgg cct atc ggt acc ntt gtg aag gct ttc cgt gca cat cgg gtc 203
Pro Arg Pro Ile Gly Thr Xaa Val Lys Ala Phe Arg Ala His Arg Val
10 15 20
acc agt gaa aag ttg tgc aga gcc caa cat gag ctt cat ttc caa gct 251
Thr Ser Glu Lys Leu Cys Arg Ala Gln His Glu Leu His Phe Gln Ala
25 30 35
gcc acc tat ctg tgc ctg ctg cgt asa tcc gga aac atg tgg ccc tac 299
Ala Thr Tyr Leu Cys Leu Leu Arg Xaa Ser Gly Asn Met Trp Pro Tyr
40 45 50
atc agg aat ttc atg gca agg gtg agc gct cgg tgg agg agt ctg ctg 347
Ile Arg Asn Phe Met Ala Arg Val Ser Ala Arg Trp Arg Ser Leu Leu
55 60 65
gct tgg tgg gtc tca agt tgc ccc atc agc ctg gag gga agg gct ggg 395
Ala Trp Trp Val Ser Ser Cys Pro Ile Ser Leu Glu Gly Arg Ala Gly
70 75 80 85
agc cat gaa cat gga gaa tat cct tgg atg c 426
Ser His Glu His Gly Glu Tyr Pro Trp Met
90 95

<210> 607
<211> 161
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 71..160

<221> sig_peptide
<222> 71..154
<223> Von Heijne matrix
score 4

seq VSLFLLVLYHYA/AV

<400> 607
 agttccggtc caggtctctg acttcgggct tggtcgctgg tggcgtcgga gccgagccgg 60
 actggtcagg atg atc acg gac gtg cag ctc gcc atc ttc gcc aac atg 109
 Met Ile Thr Asp Val Gln Leu Ala Ile Phe Ala Asn Met
 -25 -20
 ctg ggc gtg tcg ctc ttc ttg ctt gtc gtt ctc tat cac tac gcg gcc 157
 Leu Gly Val Ser Leu Phe Leu Leu Val Val Leu Tyr His Tyr Ala Ala
 -15 -10 -5 1
 gtg g 161
 Val

<210> 608
 <211> 357
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 283..357
 <221> sig_peptide
 <222> 283..336
 <223> Von Heijne matrix
 score 4
 seq LSFLCSLSQNALN/IS

<400> 608
 tgaaccttgc ttttatacaa atcacttttt tggtatttga ggaacaagat aacattttct 60
 tggcaggatt actatagtcc ccccaacaag ctctaccama gaagataata gaacttattg 120
 agcttaaatg aattatagga magttcctga aaagtccaar gtaaagtgtga agagaaccgg 180
 attctcttaa cctcacccaa cccagcactt gattctccct tgtttcctgg ttttcataca 240
 cacactggga aaggamaagg aagaagaaac aaggatgtcg tt atg gct gaa gga 294
 Met Ala Glu Gly
 -15
 gct ttg agc ttc ctt tgc tct tta tcg caa aat gca ttg aat att tcc 342
 Ala Leu Ser Phe Leu Cys Ser Leu Ser Gln Asn Ala Leu Asn Ile Ser
 -10 -5 1
 ctc att tct cgt aag 357
 Leu Ile Ser Arg Lys
 5

<210> 609
 <211> 201
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 133..201
 <221> sig_peptide
 <222> 133..180

<223> Von Heijne matrix
 score 4
 seq SFLLCFTLVGTQL/RN

<400> 609
 ttatatgttc tgcttatggg actttgcatg ttctacaaac tacaagtatc tttttctact 60
 ctgaattgaa tttagctctg tttacgggtt tcttttctgt gagcagaagt tcttaatgat 120
 tactgtagtc aa atg tat cca tct ttt ctt tta tgc ttc aca ctc gta ggg 171
 Met Tyr Pro Ser Phe Leu Leu Cys Phe Thr Leu Val Gly
 -15 -10 -5
 act cag tta aga aat tct tcc tta gcc atg 201
 Thr Gln Leu Arg Asn Ser Ser Leu Ala Met
 1 5

<210> 610
 <211> 281
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 223..279

<221> sig_peptide
 <222> 223..267
 <223> Von Heijne matrix
 score 4
 seq SCTVGCATASSWG/CT

<400> 610
 accgccttcc cacatcggat cgcaggggtc ccaaaatggc gagtgagact gcgggggactc 60
 gctgagcagc ggagggggag cgtgcagarm mgctgcggcc ctcacagtcc ggagcccggc 120
 cgtgccgtgc cgtaggaac atgcactttt ccattcccga aaccgagtcc cgcagcgggg 180
 acagcggcgg ctccgcctac gtggcctata acattcacgt ga atg gag tcc tgc 234
 Met Glu Ser Cys
 -15
 act gtc ggg tgc gct aca gcc agc tcc tgg ggc tgy acg agc agg gg 281
 Thr Val Gly Cys Ala Thr Ala Ser Ser Trp Gly Cys Thr Ser Arg
 -10 -5 1

<210> 611
 <211> 241
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 28..240

<221> sig_peptide
 <222> 28..156
 <223> Von Heijne matrix
 score 4
 seq AAWCSLVLSFCRL/HK

<223> Von Heijne matrix
 score 3.90000009536743
 seq RMCILQLLSAVLY/RF

<400> 613
 catttctatk aaaatacaaa ttttaaggctg tagatttaaat atgtagtatg ttcattrrgt 60
 tccaaataca ttctaatttc cactgtgatt tctwctttga ctcmtgaawt atttagvagg 120
 tgwttttgwh ttabdwattt ctgactgtat ggggattttc tagttagttt wctactctta 180
 atttgtcttc agagamaata ctccacaaga tttcagtcctt tcaattttgt tgcaacttgc 240
 tacaaacttg gcctaac atg ttg cat ttt wta tat atg atc caw gtg tgc 290
 Met Leu His Phe Xaa Tyr Met Ile Xaa Val Cys
 -25 -20
 ttg gaa aga atg tgc att ctg caa ttg ttg agt gct gtg ttg tat aga 338
 Leu Glu Arg Met Cys Ile Leu Gln Leu Leu Ser Ala Val Leu Tyr Arg
 -15 -10 -5 1
 ttt g 342
 Phe

<210> 614
 <211> 154
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 48..152
 <221> sig_peptide
 <222> 48..137
 <223> Von Heijne matrix
 score 3.90000009536743
 seq VGLLDTPLGAVSA/HH

<221> misc_feature
 <222> 17
 <223> n=a, g, c or t
 Oligonucleotide

<400> 614
 agtcggagcg aaggvcntgg cggasagaac ggattgcagg gtcagcc atg tca tct 56
 Met Ser Ser
 -30
 gag cct ccc cca cca cca cag ccc ccc acc cat caa gct tca gtc ggg 104
 Glu Pro Pro Pro Pro Pro Gln Pro Pro Thr His Gln Ala Ser Val Gly
 -25 -20 -15
 ctg ctg gac acc ccc ctc gga gcc gtg agc gct cac cat ccc ctc tgc 152
 Leu Leu Asp Thr Pro Leu Gly Ala Val Ser Ala His His Pro Leu Cys
 -10 -5 1 5
 cc 154

<210> 615
 <211> 272
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 185..271

<221> sig_peptide
 <222> 185..244
 <223> Von Heijne matrix
 score 3.90000009536743
 seq FLTSISFLALVLW/NV

<400> 615
 caactataat agctttttaaa cttgtttctc tttccttttc cttcatttca gtccatctta 60
 ttatctttga caaaataatt tctctgatgc ctgactgcct gccccccaac aacaaagctt 120
 ttattatact tcttaactaa tcaactatwm cyttacccat ctagccaaag tagactaccc 180
 atat atg ttt ctt gac cat gtc agg ttt tta acc tcc ata tct ttt ctt 229
 Met Phe Leu Asp His Val Arg Phe Leu Thr Ser Ile Ser Phe Leu
 -20 -15 -10
 gct ctg gtc ctg tgg aat gtc ttt ctc aac tct acc cgt ctg g 272
 Ala Leu Val Leu Trp Asn Val Phe Leu Asn Ser Thr Arg Leu
 -5 1 5

<210> 616
 <211> 114
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 36..113

<221> sig_peptide
 <222> 36..92
 <223> Von Heijne matrix
 score 3.90000009536743
 seq PALLTSSELPALA/SQ

<400> 616
 aggttttttag tcttgacctc ttgacctgct tatag atg aga gaa aag cca caa 53
 Met Arg Glu Lys Pro Gln
 -15
 cca gcg ctc ctg act tca agt gar ctg cct gcc ttg gcc tct caa ata 101
 Pro Ala Leu Leu Thr Ser Ser Glu Leu Pro Ala Leu Ala Ser Gln Ile
 -10 -5 1
 cat tgc cgc gtc c 114
 His Cys Arg Val
 5

<210> 617
 <211> 171
 <212> DNA
 <213> Homo sapiens

<220>

<221> CDS
<222> 56..169

<221> sig_peptide
<222> 56..133
<223> Von Heijne matrix
score 3.90000009536743
seq VPVLCIWRAWLRA/EV

<400> 617
aaaatgacga tttctcagga aatcatttcg actcctcttt ccctgcccaa ggagg atg 58
Met
ccc cac aac cac ttg gag gga gat gct ttg ctg aga gtc cct gtc ctc 106
Pro His Asn His Leu Glu Gly Asp Ala Leu Leu Arg Val Pro Val Leu
-25 -20 -15 -10
tgc atc tgg aga gct tgg ctc aga gct gag gtg gga ggg agg gct cct 154
Cys Ile Trp Arg Ala Trp Leu Arg Ala Glu Val Gly Gly Arg Ala Pro
-5 1 5
ctt cca ggt cgc atg gg 171
Leu Pro Gly Arg Met
10

<210> 618
<211> 240
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 160..240
<221> sig_peptide
<222> 160..225
<223> Von Heijne matrix
score 3.90000009536743
seq CLFWIXLPPHTCT/HT

<400> 618
caaaaaggaa aactgataat atcttaaaaa taatatattaa ctgagtgcg gagaaagggg 60
attgaaatgt gagctccttt atatttttagc ttgcccacgt cattgttttt ccctcagaaa 120
ctgtgaaata ctttaaatat gagttgttgg gaaagttaa atg aaa aat act ctt 174
Met Lys Asn Thr Leu
-20
tat tat aat ttt tgt tta ttt tgg att ytc cta cct ccc cac aca tgc 222
Tyr Tyr Asn Phe Cys Leu Phe Trp Ile Xaa Leu Pro Pro His Thr Cys
-15 -10 -5
aca cac aca gac aca cat 240
Thr His Thr Asp Thr His
1 5

<210> 619
<211> 257
<212> DNA
<213> Homo sapiens

<220>
 <221> CDS
 <222> 97..255

<221> sig_peptide
 <222> 97..201
 <223> Von Heijne matrix
 score 3.90000009536743
 seq CTFLSLSLHPWGG/FF

<400> 619
 acttcagaac tgggggagag ggagaggact ggaggcggga ggggtggccgc tggccagtgc 60
 gcactctttc ctctgcatcc ccttccctgc ggcccc atg tgc ctg aac ccc gcc 114
 Met Cys Leu Asn Pro Ala
 -35 -30
 tgc tcg gga ccg ctt tcc ctc cgt tcc cct cgg ctt ccc cct ctc ttt 162
 Cys Ser Gly Pro Leu Ser Leu Arg Ser Pro Arg Leu Pro Pro Leu Phe
 -25 -20 -15
 tgc act ttt ctt tcc ctt tct ttg cat ccc tgg ggg ggt ttc ttt ttg 210
 Cys Thr Phe Leu Ser Leu Ser Leu His Pro Trp Gly Gly Phe Phe Leu
 -10 -5 1
 tgt gcc tgg att tct bkt ttc ctc ccg tgg gtg tgt gtg tgk gcg gg 257
 Cys Ala Trp Ile Ser Xaa Phe Leu Pro Trp Val Cys Val Xaa Ala
 5 10 15

<210> 620
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 <213> Homo sapiens

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 <222> 47..349
 <221> sig_peptide
 <222> 47..313
 <223> Von Heijne matrix
 score 3.90000009536743
 seq RLLVACCLADIFR/IY

<400> 620
 agcggagtak ygagtcggca acccggaggg tagaaatatt tctgtc atg gct cat 55
 Met Ala His
 tca aag act agg acc aat gat gga aaa att aca tat ccg cct ggg gtc 103
 Ser Lys Thr Arg Thr Asn Asp Gly Lys Ile Thr Tyr Pro Pro Gly Val
 -85 -80 -75
 aag gaa ata tca gat aaa ata tct aaa gag gag atg gtg aga cga tta 151
 Lys Glu Ile Ser Asp Lys Ile Ser Lys Glu Glu Met Val Arg Arg Leu
 -70 -65 -60 -55
 aag atg gtt gtg aaa act ttt atg gat atg gac cag gac tct gaa gaa 199
 Lys Met Val Val Lys Thr Phe Met Asp Met Asp Gln Asp Ser Glu Glu
 -50 -45 -40
 gaa aag gag ctt tat tta aac cta gct tta cat ctt gct tca gat ttt 247


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ggaaaagggtg cagaacagtg ta atg tgt cac tac ttg tgg aaa aaa tta tac      112
                        Met Cys His Tyr Leu Trp Lys Lys Leu Tyr
                        -25                    -20

tca aca ctt ttg tat ata ctc agc aga tct tct gga aga aga ggt aag      160
Ser Thr Leu Leu Tyr Ile Leu Ser Arg Ser Ser Gly Arg Arg Gly Lys
-15                    -10                    -5                    1
aat ctg ata act gca gtt gcc tcc agg gca ggg aat tta ggt gtc tgg      208
Asn Leu Ile Thr Ala Val Ala Ser Arg Ala Gly Asn Leu Gly Val Trp
                    5                    10                    15

aca gaa aag ggg g                                                    221
Thr Glu Lys Gly
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<210> 623
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<212> DNA
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<220>
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<222> 344..430

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<221> sig_peptide
<222> 344..424
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      score 3.90000009536743
      seq SRMVLLSSALLST/EN

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<221> misc_feature
<222> 348..349
<223> n=a, g, c or t
      Oligonucleotide

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<400> 623
gtttattgca ttttbcacaa ctcatataat ttaggcttat aagtagctgt atcctggttt      60
ggtttcactt gttttaatta ttttttgatg atttaagaca ctagccatat ggattcaagt      120
tttttagttt ttattttcct acaccatacc atagtagaac tattactgtt gttatttata      180
ttttttaaaa aattcacttg tttttctcga gaatttgtga ctgattttta tgttatactg      240
cataattcag taatttcaca cattaacaac atccagggtc atgtgaggat gagttttcta      300
gcttctgaaa tgttctgagg atgtaatttt ttaataagag gaa atg tnn tct cac      355
                        Met Xaa Ser His
                        -25

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aga cta ttt ggg tgt ttt cca agt gac ttg tca cga atg gtt ttg ctc      403
Arg Leu Phe Gly Cys Phe Pro Ser Asp Leu Ser Arg Met Val Leu Leu
-20                    -15                    -10

tct agt gca ctt ctg agt aca gaa aac ca                                432
Ser Ser Ala Leu Leu Ser Thr Glu Asn
-5                    1

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<210> 624
<211> 233
<212> DNA
<213> Homo sapiens

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<222> 91..153
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      seq YLCLHLCAFSTEG/WM

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agaggaaaga gaaaaacatg taacatgtaa caaattgttt tcctaaatga caactcagaa      60
caatagaagg cattagaaga gaccttccat atg cgc cca tca cat tct tca gcc      114
                               Met Arg Pro Ser His Ser Ser Ala
                               -20                               -15
tac cta tgt ctg cac ctt tgt gct ttc agt act gaa ggt tgg atg aac      162
Tyr Leu Cys Leu His Leu Cys Ala Phe Ser Thr Glu Gly Trp Met Asn
      -10                               -5                               1
cgt ctg tcc tct tct cta agg ctg gct cct cta cct ttg tac cct ttt      210
Arg Leu Ser Ser Ser Leu Arg Leu Ala Pro Leu Pro Leu Tyr Pro Phe
      5                               10                               15
tgc cta ccc agc aat tca ccc ca      233
Cys Leu Pro Ser Asn Ser Pro
20                               25

<210> 625
<211> 380
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 10..378

<221> sig_peptide
<222> 10..57
<223> Von Heijne matrix
      score 3.90000009536743
      seq RLVWLGLRAPLGG/RQ

<400> 625
aaggaagaa atg tgg tcg cgg ttg gtg tgg ctg ggm ctt cgg gcc cct ctg      51
      Met Trp Ser Arg Leu Val Trp Leu Gly Leu Arg Ala Pro Leu
      -15                               -10                               -5
ggt ggg cgc cag ggc ttc acc tcc aag gcg gat cct cag ggc agt ggc      99
Gly Gly Arg Gln Gly Phe Thr Ser Lys Ala Asp Pro Gln Gly Ser Gly
      1                               5                               10
cgg atc acg gct gcg gtg atc gag cac ctg gag cgt cta gcg ctt gtg      147
Arg Ile Thr Ala Ala Val Ile Glu His Leu Glu Arg Leu Ala Leu Val
15                               20                               25                               30
gac ttc ggc agc cgc gag gca gtg gcg cga ctg gag aaa gct atc gcc      195
Asp Phe Gly Ser Arg Glu Ala Val Ala Arg Leu Glu Lys Ala Ile Ala
      35                               40                               45
ttc gcc gac cgg cta cgc gcc gtg gac aca gac ggg gtg gag ccc atg      243

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<222> 174..413

<221> sig_peptide

<222> 174..353

<223> Von Heijne matrix
score 3.90000009536743
seq RLLVARLHMASLA/RR

<221> misc_feature

<222> 7

<223> n=a, g, c or t
Oligonucleotide

<400> 627

accggangtg	gagcctggga	gccttgacgt	taggaacgaa	gtctaacctg	gatctggagc	60
cgggtgagat	caaattggga	atgctttcat	aatgaacgtc	aaccagtcag	ttccacctgt	120
gccaccattt	gggcagcccc	agcccatcta	cccagggtat	catcagtcca	gct atg	176
					Met	
					-60	
gtg ggc aat cag ggt cca cag ccc ccg cca ttc cct atg gag cct aca	224					
Val Gly Asn Gln Gly Pro Gln Pro Pro Pro Phe Pro Met Glu Pro Thr						
	-55		-50		-45	
atg gcc cag tac cag gct atc agc aaa cac ctc ccc aag gta tgt caa	272					
Met Ala Gln Tyr Gln Ala Ile Ser Lys His Leu Pro Lys Val Cys Gln						
	-40		-35		-30	
gag ccc cac ctt cct cgg ggg cac ctc cag cct caa cag cac agg ctc	320					
Glu Pro His Leu Pro Arg Gly His Leu Gln Pro Gln Gln His Arg Leu						
	-25		-20		-15	
ctt gtg gcc agg ctg cat atg gcc agt ttg gca agg aga tgt aca gaa	368					
Leu Val Ala Arg Leu His Met Ala Ser Leu Ala Arg Arg Cys Thr Glu						
	-10		-5		1	5
tgg gcc aag ctc cac tgt tca gat gca agg ctg ccc tgg gtc tca gc	415					
Trp Ala Lys Leu His Cys Ser Asp Ala Arg Leu Pro Trp Val Ser						
	10		15		20	

<210> 628

<211> 318

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> 214..318

<221> sig_peptide

<222> 214..297

<223> Von Heijne matrix
score 3.90000009536743
seq GVAGVCFFRRSDA/SE

<221> misc_feature

<222> 8

<223> n=a, g, c or t
Oligonucleotide

<400> 628
amattgmknk hataractct taccatcatt ttaactggat aaaaagtga gttgtctaaag 60
atgtatatat ttsgcacgtt tgarttcaca agaggaagaa caawtttcta gccasgawac 120
catgahagga ttccaaacag agattaaact tgtcctttga ggataggtaa tgagtccaga 180
attggtgggt tcttggtttt gctgacttca aga atg aag cca cag acc ctc gca 234
Met Lys Pro Gln Thr Leu Ala

-25
gtg agt gtt aca gtt ctt aaa gat ggt gtg gct gga gtt tgt ttc ttc 282
Val Ser Val Thr Val Leu Lys Asp Gly Val Ala Gly Val Cys Phe Phe
-20 -15 -10
aga cgt tca gat gcg tct gaa gtt tct tcc ttc tgg 318
Arg Arg Ser Asp Ala Ser Glu Val Ser Ser Phe Trp
-5 1 5

<210> 629
<211> 170
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 29..169

<221> sig_peptide
<222> 29..157
<223> Von Heijne matrix
score 3.90000009536743
seq KCLFLSFAHFLMG/RT

<400> 629
cattttgact ggtgtaagat gatattctc atg gtg gtt ttg att tgc ctt tct 52
Met Val Val Leu Ile Cys Leu Ser
-40

ctc atg atc agt aat act gag ctt ttt ttc ata cgc ttc ttg act gca 100
Leu Met Ile Ser Asn Thr Glu Leu Phe Phe Ile Arg Phe Leu Thr Ala
-35 -30 -25 -20
tgt atg cct tct ttt gaa aag tgt ctg ttc tta tct ttt gcc cac ttc 148
Cys Met Pro Ser Phe Glu Lys Cys Leu Phe Leu Ser Phe Ala His Phe
-15 -10 -5
ttg atg gga aga acc cac cgt g 170
Leu Met Gly Arg Thr His Arg
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<210> 630
<211> 196
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 87..194

<221> sig_peptide

<222> 87..152
 <223> Von Heijne matrix
 score 3.90000009536743
 seq SLLSDILFANIFS/HS

<400> 630
 gccatttgta tatatttgav aaatatctat tcaaatacat tgcttgcttt aaaatactgt 60
 tattggctctt tttatcattg gattgt atg agt tct tta tat att ttg gat att 113
 Met Ser Ser Leu Tyr Ile Leu Asp Ile
 -20 -15
 agt ctc tta tca gat ata tta ttt gca aat att ttc tcc cat tct tgg 161
 Ser Leu Leu Ser Asp Ile Leu Phe Ala Asn Ile Phe Ser His Ser Trp
 -10 -5 1
 gac gtc ttt cca ctt tct ttt ctt ttc ttt tct tt 196
 Asp Val Phe Pro Leu Ser Phe Leu Phe Phe Ser
 5 10

<210> 631
 <211> 339
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 53..337
 <221> sig_peptide
 <222> 53..304
 <223> Von Heijne matrix
 score 3.90000009536743
 seq SLLIILLPNTQD/LR

<400> 631
 agttccgacg aaaaatggcg gggctctcctg agttgggtggt ccttgaccct cc atg gga 58
 Met Gly
 caa gga gct cgc ggc tgg cac aga gag cca ggc ctt ggt ctc cgc cac 106
 Gln Gly Ala Arg Gly Trp His Arg Glu Pro Gly Leu Gly Leu Arg His
 -80 -75 -70
 tcc ccg aga aga ctt tcg ggt gcg ctg cac ctc gaa gcg ggc tgt gac 154
 Ser Pro Arg Arg Leu Ser Gly Ala Leu His Leu Glu Ala Gly Cys Asp
 -65 -60 -55
 cga aat gct aca act gtg cgg ccg ctt cgt gca aaa shc ggg gac gct 202
 Arg Asn Ala Thr Thr Val Arg Pro Leu Arg Ala Lys Xaa Gly Asp Ala
 -50 -45 -40 -35
 ctg ccg gag gag att cgg gag ccc gct ctg cga gat gcg cag tgg gta 250
 Leu Pro Glu Glu Ile Arg Glu Pro Ala Leu Arg Asp Ala Gln Trp Val
 -30 -25 -20
 cgg gac cag tta gcc agt tct tta ctc atc atc ctc tta ccc aac acc 298
 Arg Asp Gln Leu Ala Ser Ser Leu Leu Ile Ile Leu Leu Pro Asn Thr
 -15 -10 -5
 cag gat ctt agg att cag aaa gat ccc aca cca ggc ccg gg 339
 Gln Asp Leu Arg Ile Gln Lys Asp Pro Thr Pro Gly Pro
 1 5 10

<210> 632
 <211> 433
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 171..431

<221> sig_peptide
 <222> 171..314
 <223> Von Heijne matrix
 score 3.79999995231628
 seq NSLLLLLCLYIYP/HS

<221> misc_feature
 <222> 376..377
 <223> n=a, g, c or t
 Oligonucleotide

<400> 632
 actctgaaag cagtcttcac agaaactttt cacagaagtc aaatagttaa agcaaattct 60
 agatacatgg tagagaccag gagaaaatat gaataacttt cttctaaaca aggagctcag 120
 tggataaacc atacctctag attccttgct tccattttcc cagaaacaag atg agg 176
 Met Arg
 aag aga aag atc agt gtg tgt caa caa act tgg gcc tta tta tgc aag 224
 Lys Arg Lys Ile Ser Val Cys Gln Gln Thr Trp Ala Leu Leu Cys Lys
 -45 -40 -35
 aac ttt ctt aaa aaa tgg aga atg aaa aga gag tcc tta atg gaa tgg 272
 Asn Phe Leu Lys Lys Trp Arg Met Lys Arg Glu Ser Leu Met Glu Trp
 -30 -25 -20 -15
 ctg aat tca ttg ctg cta cta ctt tgt ttg tat ata tat cct cat agt 320
 Leu Asn Ser Leu Leu Leu Leu Cys Leu Tyr Ile Tyr Pro His Ser
 -10 -5 1
 cat caa gta aat gaw tdd tct tca ctg ctt acc atg gac ctg gga cgg 368
 His Gln Val Asn Xaa Xaa Ser Ser Leu Leu Thr Met Asp Leu Gly Arg
 5 10 15
 gta gat rnn tkt aat gaa tcc aga ttt tct gtt gta tac aca cct gtc 416
 Val Asp Xaa Xaa Asn Glu Ser Arg Phe Ser Val Val Tyr Thr Pro Val
 20 25 30
 acc aac acg acc cct gg 433
 Thr Asn Thr Thr Pro
 35

<210> 633
 <211> 154
 <212> DNA
 <213> Homo sapiens

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 <221> CDS
 <222> 54..152

<221> sig_peptide

<222> 54..143
 <223> Von Heijne matrix
 score 3.79999995231628
 seq XFVFVCXLLKCMS/VP

<400> 633
 cagttaagtg tatctgtgtg tgagcaagtt tatatgtgta cacatgtttg ccc atg 56
 Met
 -30
 tgt act tgt ctt tgt gtg tgt ctg tat atg tay aat atg caa ttt tta 104
 Cys Thr Cys Leu Cys Val Cys Leu Tyr Met Tyr Asn Met Gln Phe Leu
 -25 -20 -15
 kyt ttt gtg ttt gtk tgc gww ttg cta aag tgt atg agt gtg cct ttg 152
 Xaa Phe Val Phe Val Cys Xaa Leu Leu Lys Cys Met Ser Val Pro Leu
 -10 -5 1
 tg 154

<210> 634
 <211> 390
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 34..390
 <221> sig_peptide
 <222> 34..126
 <223> Von Heijne matrix
 score 3.79999995231628
 seq PVCLLVLMAGSG/KT

<221> misc_feature
 <222> 224
 <223> n=a, g, c or t
 Oligonucleotide

<400> 634
 ctctatggtc ggggtgggtgg ggccaggagg aag atg gcg gcg tcc gca gct gcc 54
 Met Ala Ala Ser Ala Ala Ala
 -30 -25
 gct gag ctc cag gct tct ggg ggt ccg cgg cac cca gtg tgt ctg ttg 102
 Ala Glu Leu Gln Ala Ser Gly Gly Pro Arg His Pro Val Cys Leu Leu
 -20 -15 -10
 gtg ttg gga atg gcg gga tcc ggg aaa acc act ttt gta cag agg ctc 150
 Val Leu Gly Met Ala Gly Ser Gly Lys Thr Thr Phe Val Gln Arg Leu
 -5 1 5
 aca gga cac ctg cat gcc caa ggc act cca ccg tat gtg atc aac ctg 198
 Thr Gly His Leu His Ala Gln Gly Thr Pro Pro Tyr Val Ile Asn Leu
 10 15 20
 gat cca gca gta cat gaa gtt ccc tnt cct gcc aat att gat att cgt 246
 Asp Pro Ala Val His Glu Val Pro Xaa Pro Ala Asn Ile Asp Ile Arg
 25 30 35 40
 gat act gta aag tat aaa gaa gta atg aaa caa tat gga ctt gga ccc 294

Asp	Thr	Val	Lys	Tyr	Lys	Glu	Val	Met	Lys	Gln	Tyr	Gly	Leu	Gly	Pro	
			45						50					55		
aat	ggc	ggc	ata	gtg	acc	tca	ctc	aat	ctc	ttt	gst	acc	aga	ttt	gat	342
Asn	Gly	Gly	Ile	Val	Thr	Ser	Leu	Asn	Leu	Phe	Xaa	Thr	Arg	Phe	Asp	
			60					65					70			
cag	gtg	atg	aaa	tta	ttg	aga	agg	ccc	aga	aca	tgt	cca	aat	atg	tgt	390
Gln	Val	Met	Lys	Leu	Leu	Arg	Arg	Pro	Arg	Thr	Cys	Pro	Asn	Met	Cys	
		75					80					85				

<210> 635
 <211> 137
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 22..135
 <221> sig_peptide
 <222> 22..81
 <223> Von Heijne matrix
 score 3.79999995231628
 seq VLLTHGLIHYSFT/HH

<400> 635																
caacatgcag	gtttgttact	t	atg	tat	gca	tgt	gcc	atg	ttg	gtg	tta	tta				51
			Met	Tyr	Ala	Cys	Ala	Met	Leu	Val	Leu	Leu				
			-20				-15									
act	cat	gga	ctc	atc	cat	tac	tca	ttt	act	cat	cat	tta	cat	tac	gta	99
Thr	His	Gly	Leu	Ile	His	Tyr	Ser	Phe	Thr	His	His	Leu	His	Tyr	Val	
-10			-5					1				5				
ttt	atc	cta	att	ctt	ccc	ctc	cca	ccc	ccg	cca	cag	gg				137
Phe	Ile	Leu	Ile	Leu	Pro	Leu	Pro	Pro	Pro	Pro	Gln					
		10					15									

<210> 636
 <211> 172
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 38..172
 <221> sig_peptide
 <222> 38..109
 <223> Von Heijne matrix
 score 3.79999995231628
 seq SMCLLLDVSSXKS/TD

<400> 636																
catctt	gttag	aaaaa	agtta	caaatta	aaca	aaaaa	aga	atg	ggc	ttt	ctt	ggc	agc			55
								Met	Gly	Phe	Leu	Gly	Ser			
								-20								


```

ccc aga cag aga aac tca atg tgt ttg ctt tta gac gtc agc tct rcc      103
Pro Arg Gln Arg Asn Ser Met Cys Leu Leu Leu Asp Val Ser Ser Xaa
      -15                      -10                      -5
aag agc aca gat aat tth cya rtc gww wtt ttg att att tat tat ctg      151
Lys Ser Thr Asp Asn Xaa Xaa Xaa Xaa Xaa Leu Ile Ile Tyr Tyr Leu
      1                      5                      10
att acc aga aaa ggg cca ggg      172
Ile Thr Arg Lys Gly Pro Gly
15                      20

```

```

<210> 637
<211> 253
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> 100..252

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```

<221> sig_peptide
<222> 100..228
<223> Von Heijne matrix
      score 3.79999995231628
      seq FNIFLAAPSPVWQ/PQ

```

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<400> 637
acaagcactg caatgcagca accattgacc taactatgct tccttctcca ggtcatctca      60
agcagacccc tcactctgaa gcccccgat ccaagcagg atg agc tgc caa mct      114
                        Met Ser Cys Gln Xaa
                        -40

```

```

mag ctt gct cdg acc ttg act tgg ctc atg atc cgt gga aga cat ccc      162
Xaa Leu Ala Xaa Thr Leu Thr Trp Leu Met Ile Arg Gly Arg His Pro
      -35                      -30                      -25
tac ctg acc cgt cga tca gcc cga aac ttc aac atc ttt ttg gca gct      210
Tyr Leu Thr Arg Arg Ser Ala Arg Asn Phe Asn Ile Phe Leu Ala Ala
      -20                      -15                      -10
ccg tcc cca gtt tgg cag cct cag agg acc cgc cga ccc cag k      253
Pro Ser Pro Val Trp Gln Pro Gln Arg Thr Arg Arg Pro Gln
      -5                      1                      5

```

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<210> 638
<211> 185
<212> DNA
<213> Homo sapiens

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```

<220>
<221> CDS
<222> 32..184

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<221> sig_peptide
<222> 32..133
<223> Von Heijne matrix
      score 3.79999995231628
      seq FHQMALXPGTSRA/QA

```

<400> 638
acgcggcaca cagtcgccagt gctcagtcac c atg tgt cct gca tgg ctc cca 52
Met Cys Pro Ala Trp Leu Pro
-30
tgt tgg acg gca cag acg gaa cat ctc gat cgt tac agg aag ttc cac 100
Cys Trp Thr Ala Gln Thr Glu His Leu Asp Arg Tyr Arg Lys Phe His
-25 -20 -15
cag atg gcg ctg tyt cca ggg aca tct agg gca cag gcc tta ctt tat 148
Gln Met Ala Leu Xaa Pro Gly Thr Ser Arg Ala Gln Ala Leu Leu Tyr
-10 -5 1 5
aac gaa gtc cta gag aga ttt atg ttc acc cgg ctg c 185
Asn Glu Val Leu Glu Arg Phe Met Phe Thr Arg Leu
10 15

<210> 639
<211> 206
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 73..204

<221> sig_peptide
<222> 73..126
<223> Von Heijne matrix
score 3.79999995231628
seq RICTFLLPSHSTS/GP

<400> 639
ttggatgacc ttaatgcttc aggacttagt aagaaataag cccgagtact tgtgaaatgt 60
taggcttttgt tg atg aat gtc atg aag aga ata tgt acc ttt ctg ttg cct 111
Met Asn Val Met Lys Arg Ile Cys Thr Phe Leu Leu Pro
-15 -10
tca cac tct acc tct ggc cct ctg tgc tgt tca aat gcc cat ctt cct 159
Ser His Ser Thr Ser Gly Pro Leu Cys Cys Ser Asn Ala His Leu Pro
-5 1 5 10
gct acc tcc tct acc ttg aaa cat tgc agg gct tgg agg gaa gcg bv 206
Ala Thr Ser Ser Thr Leu Lys His Cys Arg Ala Trp Arg Glu Ala
15 20 25

<210> 640
<211> 507
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 21..506

<221> sig_peptide
<222> 21..383
<223> Von Heijne matrix

score 3.79999995231628
seq SLATLPFLSTVVT/DK

<221> misc_feature
<222> 495
<223> n=a, g, c or t
Oligonucleotide

<400> 640

aagtcacatg agccaccaaa atg gtg gtg ttc ggg tat gag gct ggg act aag 53
Met Val Val Phe Gly Tyr Glu Ala Gly Thr Lys
-120 -115
cca agg gat tca ggt gtg gtg ccg gtg gga act gag gaa gcg ccc aag 101
Pro Arg Asp Ser Gly Val Val Pro Val Gly Thr Glu Glu Ala Pro Lys
-110 -105 -100 -95
gtt ttc aag atg gca gca tct atg cat ggt cag ccc agt cct tct cta 149
Val Phe Lys Met Ala Ala Ser Met His Gly Gln Pro Ser Pro Ser Leu
-90 -85 -80
gaa gat gca aaa ctc aga aga cca atg gtc ata gaa atc ata gaa aaa 197
Glu Asp Ala Lys Leu Arg Arg Pro Met Val Ile Glu Ile Ile Glu Lys
-75 -70 -65
aat ttt gac tat ctt aga aaa gaa atg aca caa aat ata tat caa atg 245
Asn Phe Asp Tyr Leu Arg Lys Glu Met Thr Gln Asn Ile Tyr Gln Met
-60 -55 -50
gcg aca ttt gga aca aca gct ggt ttc tct gga ata ttc tca aac ttc 293
Ala Thr Phe Gly Thr Thr Ala Gly Phe Ser Gly Ile Phe Ser Asn Phe
-45 -40 -35
ctg ttc aga cgc tgc ttc aag gtt aaa cat gat gct ttg aag aca tat 341
Leu Phe Arg Arg Cys Phe Lys Val Lys His Asp Ala Leu Lys Thr Tyr
-30 -25 -20 -15
gca tca ttg gct aca ctt cca ttt ttg tct act gtt gtt act gac aag 389
Ala Ser Leu Ala Thr Leu Pro Phe Leu Ser Thr Val Val Thr Asp Lys
-10 -5 1
ctt ttt gta att gat gct ttg tat tca gat aat ata agc aag gaa aac 437
Leu Phe Val Ile Asp Ala Leu Tyr Ser Asp Asn Ile Ser Lys Glu Asn
5 10 15
tgt gtt ttc aga agc tca ctg att ggc ata gtt tgt ggw gtt ttc tat 485
Cys Val Phe Arg Ser Ser Leu Ile Gly Ile Val Cys Gly Val Phe Tyr
20 25 30
ccc agt tct ntg gct ttt act a 507
Pro Ser Ser Xaa Ala Phe Thr
35 40

<210> 641
<211> 483
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 295..483

<221> sig_peptide
<222> 295..408

<223> Von Heijne matrix
 score 3.79999995231628
 seq LVVCVSVTVFVWS/CC

<221> misc_feature
 <222> 54
 <223> n=a, g, c or t
 Oligonucleotide

<400> 641
 accattcgga agaggcggag tcttcttccg aggaccattc ggaagaaggc gganctacct 60
 ctcacatcagga ccagtctgac tgcacctgca tccttagctc agagcatccc cggagcatct 120
 taagagctga gcgcastgac aactaggggc cggaccgtcg caggaggcgt ccgctggata 180
 ccttccccct tccctgacct agagctctac agctgctgcc tcggtactga ccgagggttc 240
 ccagagctgt ctyaccattg caaaaacgtt atagcaacag cctctgatta cgac atg 297
 Met
 gct gag atc acc aat atc cga cct agc ttt gat gtg tca ccg gtg gtg 345
 Ala Glu Ile Thr Asn Ile Arg Pro Ser Phe Asp Val Ser Pro Val Val
 -35 -30 -25
 gcc ggc ctc atc ggg gcc tct gtg ctg gtg gtg tgt gtc tcg gtg acc 393
 Ala Gly Leu Ile Gly Ala Ser Val Leu Val Val Cys Val Ser Val Thr
 -20 -15 -10
 gtc ttt gtc tgg tca tgc tgc crc cag cag gca gag aag aag cac aag 441
 Val Phe Val Trp Ser Cys Cys Xaa Gln Gln Ala Glu Lys Lys His Lys
 -5 1 5 10
 aac cca cca tac aag ttt att cac atg ctc aaa ggc wtc agc 483
 Asn Pro Pro Tyr Lys Phe Ile His Met Leu Lys Gly Xaa Ser
 15 20 25

<210> 642
 <211> 309
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 235..309

<221> sig_peptide
 <222> 235..279
 <223> Von Heijne matrix
 score 3.79999995231628
 seq ILTMLILLIHEHG/IF

<400> 642
 attratctat gtgtctgttg ttatacgaat atcatgctgt tttggtttct atatccttgt 60
 aatatgtttt gaagtcaggt agtgtgatgc ctccagattt gttctttttg gtcaggattg 120
 ctttggtctgw tttgggttcw wttwtggttc catacaaatt ttaggattat tttttctatg 180
 tctgtgaaaa gtggcatggg tattacattc aatctgtaga ttgctttgga tagt atg 237
 Met
 -15
 gtc att tta act atg tta att ctt tta atc cat gag cat ggt att ttc 285
 Val Ile Leu Thr Met Leu Ile Leu Leu Ile His Glu His Gly Ile Phe
 -10 -5 1

ttt tca ctt gtt tgt gtc ctc ttc
Phe Ser Leu Val Cys Val Leu Phe
5 10

309

<210> 643
<211> 245
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 147..245

<221> sig_peptide
<222> 147..233
<223> Von Heijne matrix
score 3.79999995231628
seq LTHTHTCTPPSTA/HP

<221> misc_feature
<222> 61
<223> n=a, g, c or t
Oligonucleotide

<400> 643
aacagacccc acccggcaca acctgtcac atacacacac acaataacac acacccaatc 60
nyacgcaccc sactcagcat aacctgtca cacaatcaca cacacaatca cacacaccct 120
accagtaga gccactcag acacac atg ttc tca cac aat cac tca tac aca 173
Met Phe Ser His Asn His Ser Tyr Thr
-25
tac aca cca cag cac agc ccg ctc aca cac aca cac aca tgc acc cca 221
Tyr Thr Pro Gln His Ser Pro Leu Thr His Thr His Thr Cys Thr Pro
-20 -15 -10 -5
ccc agc aca gct cac cca cgc ggg 245
Pro Ser Thr Ala His Pro Arg Gly
1

<210> 644
<211> 211
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 144..209

<221> sig_peptide
<222> 144..188
<223> Von Heijne matrix
score 3.79999995231628
seq XMILLCFLAVSNF/NK

<400> 644
atactctttc tacattctgc tccgctttag ctgcgagagt ttaccaactc aaatctggcc 60

gaatttaata gggaagaaaag agacagtata actcaccagt gctgggtctc atcatcctgc 180
aatttcdgaa caactatgaa tacaaaaaga attttaaaat cccagtcctg cctagaaagg 240
ggaagtcatc tctaaat atg gtg gcc ctg ggg cag ctg gcc tdc ctg cca 290

Met Val Ala Leu Gly Gln Leu Ala Xaa Leu Pro
-15 -10

ggc nbc tdc cat ggg ggc ctt tct gca gtg act gtg gtt ctt ccc att 338
Gly Xaa Xaa His Gly Gly Leu Ser Ala Val Thr Val Val Leu Pro Ile

-5 1 5

tta ctc tgt 347
Leu Leu Cys

10

<210> 647
<211> 143
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 78..143

<221> sig_peptide
<222> 78..122
<223> Von Heijne matrix
score 3.79999995231628
seq VSFVCLLFERNVYS/NL

<400> 647
aaactggggt gagatgatat ctcaatgtag ttttcattta catctctaata gatcaataat 60
gttgagcaat ttttcat atg ccc gtt tca ttt gtc tgt ctt ctt ttc aga 110

Met Pro Val Ser Phe Val Cys Leu Leu Phe Arg
-15 -10 -5

aat gtt tat tca aat cta ttg cct tct ttt ttt 143
Asn Val Tyr Ser Asn Leu Leu Pro Ser Phe Phe

1 5

<210> 648
<211> 232
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 41..232

<221> sig_peptide
<222> 41..121
<223> Von Heijne matrix
score 3.79999995231628
seq LPLLLPAHHGRHG/SG

<400> 648
aaaaagtgtc cgggacaagg mcatagggct gagagtagcc atg ggc tct gga gga 55
Met Gly Ser Gly Gly


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<400> 650
ggagtggaca cggaggggcc tagaggaggg ccctagaggg gcggaggggc cgatggaaaag      60
ggaaaggtgg cctgtcctcc cctcccgaca ccaggggagg agccccagcc ccgcgacgag      120
gaggaagcgg actgragctg ctgaggcagt ttgacctggc ctggcagtac gggccctgca      180
ccgggatcac acggctgcag cgctggtgtc gggccaagca gatgggcttg gagcctcccc      240
cagaggtgtg gcaggtgctg aagaccacc ccggagaccc ccgcttccag tgcagtctct      300
ggcatctcta tcccc atg agg cac cac gta aga yct cct gcc ctt agc tct      352
          Met Arg His His Val Arg Xaa Pro Ala Leu Ser Ser
          -20          -15          -10
ctt gct cac cac cca aga acc tca gga cag aag cga gag ccc att gct      400
Leu Ala His His Pro Arg Thr Ser Gly Gln Lys Arg Glu Pro Ile Ala
          -5          1          5
cct gct cag ctc agc ccg g      419
Pro Ala Gln Leu Ser Pro
          10

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<210> 651
<211> 396
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> 52..396
<221> sig_peptide
<222> 52..270
<223> Von Heijne matrix
      score 3.79999995231628
      seq LAGNLALSPTGNA/KK

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<400> 651
ttggaagtgg tgtggagacg gaggacagga gcagtgccca agcagcgagg g atg ctg      57
          Met Leu
atc ttg aat ggc ttc cgg ggc cat gcc aca gat tcc gtg aag aac tcc      105
Ile Leu Asn Gly Phe Arg Gly His Ala Thr Asp Ser Val Lys Asn Ser
-70          -65          -60
atg gaa agc atg aac act gac atg gtg atc atc cca ggg ggt ctg acc      153
Met Glu Ser Met Asn Thr Asp Met Val Ile Ile Pro Gly Gly Leu Thr
-55          -50          -45          -40
tca cag ctt cag gtg ctg gat gtc gtg gtc tac aag cca ctg aat gac      201
Ser Gln Leu Gln Val Leu Asp Val Val Val Tyr Lys Pro Leu Asn Asp
          -35          -30          -25
agt gtg cgg gcc cag tac tcc aac tgg ctt ctg gct ggg aac ctg gcg      249
Ser Val Arg Ala Gln Tyr Ser Asn Trp Leu Leu Ala Gly Asn Leu Ala
          -20          -15          -10
ctg agc cca acc ggg aat gct aag aag cca ccc ctg ggc ctc ttt ctg      297
Leu Ser Pro Thr Gly Asn Ala Lys Lys Pro Pro Leu Gly Leu Phe Leu
          -5          1          5
gag tgg gtc atg gtc gcg tgg aat agc atc tca agt gag tcc atc gtc      345
Glu Trp Val Met Val Ala Trp Asn Ser Ile Ser Ser Glu Ser Ile Val
10          15          20          25
caa ggg whc aaa gaa gtg cca tat ctc crg caa ctt gga gga gga aga      393

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Gln Gly Xaa Lys Glu Val Pro Tyr Leu Xaa Gln Leu Gly Gly Gly Arg
30 35 40

cga 396
Arg

<210> 652
<211> 170
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 67..168

<221> sig_peptide
<222> 67..141
<223> Von Heijne matrix
score 3.79999995231628
seq YCLSNCLLXXSWG/LH

<400> 652
tgtatacaca taaccagata ttctcctaag tttttcaaaa taatagaaac agatattttg 60
ggattc atg atc tgt acc act gtt tat att acc atg gct cct tac tgt 108
Met Ile Cys Thr Thr Val Tyr Ile Thr Met Ala Pro Tyr Cys
-25 -20 -15
cta tca aac tgt tta ctt thw caw agt tgg ggc ctg cat ttg tat aga 156
Leu Ser Asn Cys Leu Leu Xaa Xaa Ser Trp Gly Leu His Leu Tyr Arg
-10 -5 1 5
ttt cta gcc ccc at 170
Phe Leu Ala Pro

<210> 653
<211> 178
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 131..178

<221> sig_peptide
<222> 131..172
<223> Von Heijne matrix
score 3.79999995231628
seq VSLCVAALFPLQA/YG

<400> 653
agagtacctg aaaaccttag agaaccctgg ggaaatattt atagccaggc ttcttgagaga 60
ctctgggaac aggaaagtca ggaaccctgc ctttcaggaa ctgctgtatc tcagtcggct 120
tcttcatttc atg gtt tct ctc tgt gta gct gct tta ttt cct ctt cag 169
Met Val Ser Leu Cys Val Ala Ala Leu Phe Pro Leu Gln
-10 -5
gct tac ggg 178
Ala Tyr Gly

1

<210> 654
<211> 121
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 36..119

<221> sig_peptide
<222> 36..107
<223> Von Heijne matrix
score 3.79999995231628
seq FVYLLLRNLXSYS/LP

<400> 654
tgtggttttg attggcattt ccctgatcat tactg atg ttg agc att ttt tca 53
Met Leu Ser Ile Phe Ser
-20
ttt ttt tgt agg cca ttt gta tat ctt ctt ttg aga aat ctc krt tca 101
Phe Phe Cys Arg Pro Phe Val Tyr Leu Leu Leu Arg Asn Leu Xaa Ser
-15 -10 -5
tat tct ttg ccc acc acg gg 121
Tyr Ser Leu Pro Thr Thr
1

<210> 655
<211> 370
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 89..370

<221> sig_peptide
<222> 89..319
<223> Von Heijne matrix
score 3.79999995231628
seq LGLQCDAVNLAFG/RR

<400> 655
acttcgccat tttcctccgg aagtgcggat cccagcggcg gtcgtgtagc tgagcagsgc 60
tggggcttgg ttctatgtcc ctgtggct atg ttt cca gtg tcc tct ggg tgt 112
Met Phe Pro Val Ser Ser Gly Cys
-75 -70
ttc caa gag caa caa gaa acg aat aaa tct ctg ccc cgc agc gcc tcc 160
Phe Gln Glu Gln Gln Glu Thr Asn Lys Ser Leu Pro Arg Ser Ala Ser
-65 -60 -55
acc cca gag acc cgg acc aag ttc aca cag gac aat ctg tgc cry gcc 208
Thr Pro Glu Thr Arg Thr Lys Phe Thr Gln Asp Asn Leu Cys Xaa Ala
-50 -45 -40

cag cgc gag cgc ctg gac tcg gcc aac ctg tgg gtc ctk gtg gac tgc	256
Gln Arg Glu Arg Leu Asp Ser Ala Asn Leu Trp Val Leu Val Asp Cys	
-35 -30 -25	
atc ctt cgc gac acc tcc gag gac ctg gga ctc cag tgt gac gcc gtg	304
Ile Leu Arg Asp Thr Ser Glu Asp Leu Gly Leu Gln Cys Asp Ala Val	
-20 -15 -10	
aac ctg gcc ttc ggg cgc cgc tgt gag gaa ctg gag gac gcg cgg cac	352
Asn Leu Ala Phe Gly Arg Arg Cys Glu Glu Leu Glu Asp Ala Arg His	
-5 1 5 10	
aag ctg cag yac cac ctg	370
Lys Leu Gln Xaa His Leu	
15	

<210> 656
 <211> 197
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 137..196

<221> sig_peptide
 <222> 137..181
 <223> Von Heijne matrix
 score 3.79999995231628
 seq LVHSFLWLSSILY/IY

<400> 656	
attgtatcgt tcttatgcct ttgcatcctc atagcttagc tcccacatat cagtgagaac	60
atacaatgtt tggttttcca ttcctgagtt acttcaactta gaataatagt ctccaatctc	120
atccaggtca ctgcaa atg cca ttg gtt cat tcc ttc tta tgg ctg agt agt	172
Met Pro Leu Val His Ser Phe Leu Trp Leu Ser Ser	
-15 -10 -5	
atc cta tat ata tac cac ctg cgg g	197
Ile Leu Tyr Ile Tyr His Leu Arg	
1 5	

<210> 657
 <211> 246
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 79..246

<221> sig_peptide
 <222> 79..150
 <223> Von Heijne matrix
 score 3.79999995231628
 seq XVFXFXFLXRXLX/XX

<400> 657

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tttttgacat cytattaata gccattctgg ctggtgtcag gtggtatctc attgtgggtt 60
cgattttgga tttctcta atg att agt aat ggt aag ttt ttt tgt ttt ttt 111
                Met Ile Ser Asn Gly Lys Phe Phe Cys Phe Phe
                        -20                                -15

ttk gtt ttt kgt ttt tkg ttt ttg ara cgg asy ttg cyc tkg ycg ccc 159
Xaa Val Phe Xaa Phe Xaa Phe Leu Xaa Arg Xaa Leu Xaa Xaa Xaa Pro
                -10                                -5                                1

agg ctg gag tgc aat ggm aar ayc tcg gcy cac tgm aac ctc cgc ctc 207
Arg Leu Glu Cys Asn Gly Lys Xaa Ser Ala His Xaa Asn Leu Arg Leu
                5                                10                                15

ctg agt yca agc aat tcy ctk gcc tca gcc ccc cga ggg 246
Leu Ser Xaa Ser Asn Ser Leu Ala Ser Ala Pro Arg Gly
20                25                30

```

<210> 658
<211> 335
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 31..333

<221> sig_peptide
<222> 31..300
<223> Von Heijne matrix
score 3.70000004768372
seq LRVRLTLPHSIRS/DS

<221> misc_feature
<222> 320
<223> n=a, g, c or t
Oligonucleotide

```

<400> 658
acacgcgcct cttcacgagg tggaaacaag atg gag gat tcg gcc tcg gcc tcg 54
                Met Glu Asp Ser Ala Ser Ala Ser
                        -90                                -85

ctg tct tct gca gcc gct act gga acc tcc acc tcg act cca gcg gcc 102
Leu Ser Ser Ala Ala Ala Thr Gly Thr Ser Thr Ser Thr Pro Ala Ala
                -80                                -75                                -70

ccg aca gca cgg aag cag ctg gat aaa gaa cag gtt aga aag gca gtg 150
Pro Thr Ala Arg Lys Gln Leu Asp Lys Glu Gln Val Arg Lys Ala Val
                -65                                -60                                -55

gac gct ctc ttg acg cat tgc aag tcc agg aaa aac aat tat ggg ttg 198
Asp Ala Leu Leu Thr His Cys Lys Ser Arg Lys Asn Asn Tyr Gly Leu
                -50                                -45                                -40                                -35

ctt ttg aat gag aat gaa agt tta ttt tta atg gtg gta tta tgg aaa 246
Leu Leu Asn Glu Asn Glu Ser Leu Phe Leu Met Val Val Leu Trp Lys
                -30                                -25                                -20

att cca agt aaa gaa ctg agg gtc aga ttg acc ttg cct cat agt att 294
Ile Pro Ser Lys Glu Leu Arg Val Arg Leu Thr Leu Pro His Ser Ile
                -15                                -10                                -5

cga tca gat tca gaa gat atc tgt tna ttt acg aag gat gg 335

```

Arg Ser Asp Ser Glu Asp Ile Cys Xaa Phe Thr Lys Asp
 1 5 10

<210> 659
 <211> 197
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 20..196

<221> sig_peptide
 <222> 20..106
 <223> Von Heijne matrix
 score 3.70000004768372
 seq LIELNLXSPVALQ/WP

<400> 659
 attcaacaag caatcaggt atg aat gca gaa ggg gct tcc cca gga aaa gaa 52
 Met Asn Ala Glu Gly Ala Ser Pro Gly Lys Glu
 -25 -20
 acg aac aca gga aca ttg ata gag cta aat ctg mcc agc cct gta gcc 100
 Thr Asn Thr Gly Thr Leu Ile Glu Leu Asn Leu Xaa Ser Pro Val Ala
 -15 -10 -5
 ctc cag tgg cca ctt tcc agc ccc tct tgc ctg agg atc ctc agc aac 148
 Leu Gln Trp Pro Leu Ser Ser Pro Ser Cys Leu Arg Ile Leu Ser Asn
 1 5 10
 aag gtg ccc agg aac ctg agg tgg cag aaa cac tac tcc acc cac cag g 197
 Lys Val Pro Arg Asn Leu Arg Trp Gln Lys His Tyr Ser Thr His Gln
 15 20 25 30

<210> 660
 <211> 272
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 28..270

<221> sig_peptide
 <222> 28..216
 <223> Von Heijne matrix
 score 3.70000004768372
 seq MAAAAALRAPAQSV

<400> 660
 attttggcct gtcaggtcca tccggcg atg ctg ggt ctg gac gag ctc ggg agg 54
 Met Leu Gly Leu Asp Glu Leu Gly Arg
 -60 -55
 agt ggt tgt ggc cat tgc aca cag gcg gat ctg agg ttc ggc gac gcc 102
 Ser Gly Cys Gly His Cys Thr Gln Ala Asp Leu Arg Phe Gly Asp Ala
 -50 -45 -40

gct ggy csc gaa ccc cgg gmc agg mca acg cac agg aac acc gcc gca	150
Ala Gly Xaa Glu Pro Arg Xaa Arg Xaa Thr His Arg Asn Thr Ala Ala	
-35 -30 -25	
gcc cgc gtt ccc ccc ccg ccc aga gtc atg gcg gca gca gcc gct ctg	198
Ala Arg Val Pro Pro Pro Pro Arg Val Met Ala Ala Ala Ala Ala Leu	
-20 -15 -10	
agg gcg cct gct cag agc agt gtg acc ttt gaa gat gtg gct gta aac	246
Arg Ala Pro Ala Gln Ser Ser Val Thr Phe Glu Asp Val Ala Val Asn	
-5 1 5 10	
ttt tcc ctg gag gaa tgg agt ctt ct	272
Phe Ser Leu Glu Glu Trp Ser Leu	
15	

<210> 661
 <211> 411
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 263..409

<221> sig_peptide
 <222> 263..340
 <223> Von Heijne matrix
 score 3.70000004768372
 seq WGNLSFHLQEAHG/SE

<400> 661	
tgaaaacaaa catctactaa tgttgtcaga tggtaggaa gcaagattct gcaactatag	60
agggtaagt tttctttggt tctgtgggtc ctctctaaaa ctctaagatc ttgaggggtg	120
catttcagaa agtgcagcgt gacccgcagt ttgtgggaag ccatggagct cggcactgcc	180
atcctaatac ttcttaaagc acaaaacccc agagacaatc tggggtcagg agagtgaag	240
gggcttgtct gccacactgg tg atg agt gcc ctg aaa gac ttc aga gaa ttt	292
Met Ser Ala Leu Lys Asp Phe Arg Glu Phe	
-25 -20	
ctg aac tgg tgg gga aac ctc tct ttt cat ctt cag gaa gct cat gga	340
Leu Asn Trp Trp Gly Asn Leu Ser Phe His Leu Gln Glu Ala His Gly	
-15 -10 -5	
agt gaa att gca gaa atg gga gct ggt att cta gag gaa aaa aat tat	388
Ser Glu Ile Ala Glu Met Gly Ala Gly Ile Leu Glu Glu Lys Asn Tyr	
1 5 10 15	
ggv caa caa wat cac tgt aac ta	411
Gly Gln Gln Xaa His Cys Asn	
20	

<210> 662
 <211> 146
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 38..145

<221> sig_peptide
 <222> 38..127
 <223> Von Heijne matrix
 score 3.70000004768372
 seq PPSLFLSLPPSL/PP

<400> 662
 awbwcccgcc cacacgtggc caacctttgc gttttta atg tct ctw ccc cct ttt 55
 Met Ser Leu Pro Pro Phe
 -30 -25
 ttc cac cct tct ccc gct ccc tct ctc gct ccc cct ccc tcc ctc ttt 103
 Phe His Pro Ser Pro Ala Pro Ser Leu Ala Pro Pro Pro Ser Leu Phe
 -20 -15 -10
 ctt tcc ctc cct ccc tct ctt tct ccc cct cta ccc gcc cgg g 146
 Leu Ser Leu Pro Pro Ser Leu Ser Pro Pro Leu Pro Ala Arg
 -5 1 5

<210> 663
 <211> 65
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 10..63
 <221> sig_peptide
 <222> 10..48
 <223> Von Heijne matrix
 score 3.70000004768372
 seq MFFLCGFLYLCFI/SF

<400> 663
 caatatgct atg ttt ttc ctt tgt ggt ttt ctg tat cta tgt ttt atc tca 51
 Met Phe Phe Leu Cys Gly Phe Leu Tyr Leu Cys Phe Ile Ser
 -10 -5 1
 ttt ttt ttt ttt tt 65
 Phe Phe Phe Phe
 5

<210> 664
 <211> 182
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 30..182

<221> sig_peptide
 <222> 30..155
 <223> Von Heijne matrix
 score 3.70000004768372

[illegible]

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<220>
<221> CDS
<222> 160..318

<221> sig_peptide
<222> 160..228
<223> Von Heijne matrix
      score 3.70000004768372
      seq  TNLLCLTFQRCQS/YN
```

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<210> 666
<211> 273
<212> DNA
<213> Homo sapiens
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<221> CDS
<222> 180..272

<221> sig_peptide
<222> 180..254
<223> Von Heijne matrix
score 3.70000004768372
seq QLLGCMVLYDCFS/FK

<400> 666
aagttgttgc atgtgtcaat gggtgttcct ttttatttct gagtaatggt ccatgatatg 60
aatgtaccac agtttggtta accattcacc cactgaagga cgtttggatt gtttctaagt 120
tttgactgtg gcaagtaaag atgctatgaa cattcatgta cacatgaatt tgtaggcat 179
atg ttt tta ttt tgc tgg gag aaa agc cca aga atg cag ttg ctg ggt 227
Met Phe Leu Phe Cys Trp Glu Lys Ser Pro Arg Met Gln Leu Leu Gly
-25 -20 -15 -10
tgt atg gta ttg tat gat tgt ttt tct ttt aag aaa ctg ccg ggg g 273
Cys Met Val Leu Tyr Asp Cys Phe Ser Phe Lys Lys Leu Pro Gly
-5 1 5

<210> 667
<211> 149
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 8..148

<221> sig_peptide
<222> 8..97
<223> Von Heijne matrix
score 3.70000004768372
seq FVCFHVFYCVFC/NV

<400> 667
atttttgt atg tct ttt ata tct gtt att ttt cct tta atc ctt tta aac 49
Met Ser Phe Ile Ser Val Ile Phe Pro Leu Ile Leu Leu Asn
-30 -25 -20
cgt ttt tca ttt gtt tgt ttc ttt cat gtc ttt tac tgt gtt ttc tgc 97
Arg Phe Ser Phe Val Cys Phe Phe His Val Phe Tyr Cys Val Phe Cys
-15 -10 -5
aac gtc tct tct ttg ttc tcc tat cag ttt ctt ctt cat ttc tgt gat 145
Asn Val Ser Ser Leu Phe Ser Tyr Gln Phe Leu Leu His Phe Cys Asp
1 5 10 15
gac t 149
Asp

<210> 668
<211> 122
<212> DNA
<213> Homo sapiens

<220>

<221> CDS
<222> 16..120

<221> sig_peptide
<222> 16..108
<223> Von Heijne matrix
score 3.70000004768372
seq LGMGMGFFSGVKS/WI

<400> 668
caaggaatta cagaa atg cat gaa tac tta cct aga aac ttt cat gac ttt 51
Met His Glu Tyr Leu Pro Arg Asn Phe His Asp Phe
-30 -25 -20
aat tct ccc aac tct aaa tta ggc atg gga atg ggc ttt ttc tca ggt 99
Asn Ser Pro Asn Ser Lys Leu Gly Met Gly Met Gly Phe Phe Ser Gly
-15 -10 -5
gtc aaa tct tgg att gga ggt ga 122
Val Lys Ser Trp Ile Gly Gly
1

<210> 669
<211> 288
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 38..286

<221> sig_peptide
<222> 38..145
<223> Von Heijne matrix
score 3.70000004768372
seq ILMRDFSPSGIFG/AF

<400> 669
tcgcgcggtc ccgcacagcg gacaccagga ctccaaa atg gcg tca rtt gta cca 55
Met Ala Ser Xaa Val Pro
-35
gtg aag gac aag aaa ctt ctg gag gtc aaa ctg ggg gag ctg cca agc 103
Val Lys Asp Lys Lys Leu Leu Glu Val Lys Leu Gly Glu Leu Pro Ser
-30 -25 -20 -15
tgg atc ttg atg cgg gac ttc agt cct agt ggc att ttc gga gcg ttt 151
Trp Ile Leu Met Arg Asp Phe Ser Pro Ser Gly Ile Phe Gly Ala Phe
-10 -5 1
caa aga ggt tac tac cgg tac tac aac aag tac atc aat gtg aag aag 199
Gln Arg Gly Tyr Tyr Arg Tyr Tyr Asn Lys Tyr Ile Asn Val Lys Lys
5 10 15
ggg agc atc tcg ggg att acc atg gtg ctg gca tgc tac gtg ctc ttt 247
Gly Ser Ile Ser Gly Ile Thr Met Val Leu Ala Cys Tyr Val Leu Phe
20 25 30
agc tac tcc ttt tcc tac aag cat ctc aag cac gag tcg gg 288
Ser Tyr Ser Phe Ser Tyr Lys His Leu Lys His Glu Ser
35 40 45

<210> 670
 <211> 160
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 89..160

<221> sig_peptide
 <222> 89..142
 <223> Von Heijne matrix
 score 3.70000004768372
 seq GALLWMAWDGQLS/RP

<400> 670
 cgtcaacatt cttttcattc tgggcctgag cgcgtggatc aagccgctgc ccttgcaact 60
 gctgagcctg aagctggact tgccggtg atg gtg ata tcg gcc ggg gca ctg 112
 Met Val Ile Ser Ala Gly Ala Leu
 -15
 ctg tgg atg gcg tgg gac ggc cag ctc agc cgc ccc gaa ggc gcc cgt 160
 Leu Trp Met Ala Trp Asp Gly Gln Leu Ser Arg Pro Glu Gly Ala Arg
 -10 -5 1 5

<210> 671
 <211> 137
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 44..136

<221> sig_peptide
 <222> 44..97
 <223> Von Heijne matrix
 score 3.70000004768372
 seq LELLGSSYNPISA/SP

<400> 671
 gaattttctt cttctgctca ggctggagta caatggcaca atc atg gtt cac tgt 55
 Met Val His Cys
 -15
 aat ctt gaa ctc ctg ggc tca agt tat aat ccc atc tca gcc tct cca 103
 Asn Leu Glu Leu Leu Gly Ser Ser Tyr Asn Pro Ile Ser Ala Ser Pro
 -10 -5 1
 gta gct agg act ata tca tgc ccc gct att gtg g 137
 Val Ala Arg Thr Ile Ser Cys Pro Ala Ile Val
 5 10

<210> 672
 <211> 493
 <212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 111..491

<221> sig_peptide

<222> 111..374

<223> Von Heijne matrix
score 3.70000004768372
seq CDLLLARFGLIQS/MK

<400> 672

gcccgcgctt gttgtgctga ggccgagggg gtcgccattt tggatggtga accctgaagt 60
cgggtgtctgc tgcgttcacg gcaggattcg gttaggagga acagcacagc atg ctg 116
Met Leu
ggc tct gga ttt aaa gct gag cgc tta aga gtg aat ttg aga tta gtc 164
Gly Ser Gly Phe Lys Ala Glu Arg Leu Arg Val Asn Leu Arg Leu Val
-85 -80 -75
ata aat cgc ctt aaa cta ttg gag aaa aag aaa acg gaa ctg gcc cag 212
Ile Asn Arg Leu Lys Leu Glu Lys Lys Lys Thr Glu Leu Ala Gln
-70 -65 -60 -55
aaa gca agg aag gag att gct gac tat ctg gct gct ggg aaa gat gaa 260
Lys Ala Arg Lys Glu Ile Ala Asp Tyr Leu Ala Ala Gly Lys Asp Glu
-50 -45 -40
cga gct cgg atc cgt gtg gag cac att atc cgg gaa gac tac ctc gtg 308
Arg Ala Arg Ile Arg Val Glu His Ile Ile Arg Glu Asp Tyr Leu Val
-35 -30 -25
gag gcc atg gag atc ctg gag ctg tac tgt gac ctg ctg ctg gct cgg 356
Glu Ala Met Glu Ile Leu Glu Leu Tyr Cys Asp Leu Leu Leu Ala Arg
-20 -15 -10
ttt ggc ctt atc cag tct atg aag gaa cta gat tct ggt ctg gct gaa 404
Phe Gly Leu Ile Gln Ser Met Lys Glu Leu Asp Ser Gly Leu Ala Glu
-5 1 5 10
tct gtg tct aca ttg atc tgg gct gct cct cga ctc cag tca gaa gtg 452
Ser Val Ser Thr Leu Ile Trp Ala Ala Pro Arg Leu Gln Ser Glu Val
15 20 25
gct gag ttg aaa ata gtt gct gat cag ctc tgt cca agt at 493
Ala Glu Leu Lys Ile Val Ala Asp Gln Leu Cys Pro Ser
30 35

<210> 673

<211> 263

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 102..263

<221> sig_peptide

<222> 102..230

<223> Von Heijne matrix
score 3.70000004768372

seq VWCLXLKLVPAIC/IS

<400> 673

tcccagcaga aggggyagcg cctggctgtc agcagcgtgt gcctcaggag ggatctgcgg 60
 tgacgggggtt gttacttcag taggatgagg aagagtcaca a atg cgg ggt tgg mmg 116
 Met Arg Gly Trp Xaa
 -40

gct cct gct tgg aga sgh ytg arc acy agg aga cta cca atg ggg agc 164
 Ala Pro Ala Trp Arg Xaa Leu Xaa Thr Arg Arg Leu Pro Met Gly Ser
 -35 -30 -25

agg cac ggt gcc agc ccg gcc tct gcc gtc tgg tgt ctg tmc ctc aag 212
 Arg His Gly Ala Ser Pro Ala Ser Ala Val Trp Cys Leu Xaa Leu Lys
 -20 -15 -10

tta gtc cca gct ttg tgc att agc ggg ctc acc ctc gga atc cag gga 260
 Leu Val Pro Ala Leu Cys Ile Ser Gly Leu Thr Leu Gly Ile Gln Gly
 -5 1 5 10

ttc 263
 Phe

<210> 674

<211> 263

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 115..261

<221> sig_peptide

<222> 115..216

<223> Von Heijne matrix
 score 3.70000004768372
 seq RLILXFHDNTWG/ST

<221> misc_feature

<222> 136,139..140

<223> n=a, g, c or t
 Oligonucleotide

<400> 674

gtcatttatg ccatattctg tccactagaa atgaattact aagtctggcc caaactcaag 60
 tggaggcgaa ttaagctgca tctcataagg gaaagagtat cgaagaactt ctgt atg 117
 Met

tat ttt aaa acc act aca nta nnb cat agt gca cat atg ctt ctg caa 165
 Tyr Phe Lys Thr Thr Thr Xaa Xaa His Ser Ala His Met Leu Leu Gln
 -30 -25 -20

att tgc ttt ttt cgc tta aca atc tta gkt ttc cat gac aat aca tgg 213
 Ile Cys Phe Phe Arg Leu Thr Ile Leu Xaa Phe His Asp Asn Thr Trp
 -15 -10 -5

ggg tca act tca ttc tct twa gtt gck gca atg cta ttc cac tac cgg 261
 Gly Ser Thr Ser Phe Ser Xaa Val Ala Ala Met Leu Phe His Tyr Arg
 1 5 10 15

gg 263

<210> 675
 <211> 107
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 30..107

<221> sig_peptide
 <222> 30..101
 <223> Von Heijne matrix
 score 3.70000004768372
 seq LLFLFFLFLFFFF/FF

<400> 675
 tgcactggca cacactcaca gctctgacc atg tca tca aac ata cag aga ctg 53
 Met Ser Ser Asn Ile Gln Arg Leu
 -20
 ggc ttc cct ctg ctt ttt ctt ttt ttt ctt ttt ctt ttt ttt ttt 101
 Gly Phe Pro Leu Leu Phe Leu Phe Phe Leu Phe Leu Phe Phe Phe
 -15 -10 -5
 ttt ttt 107
 Phe Phe
 1

<210> 676
 <211> 276
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 70..276

<221> sig_peptide
 <222> 70..270
 <223> Von Heijne matrix
 score 3.70000004768372
 seq LVLPLPMLPTS NR/KR

<400> 676
 gtcacagcac cctcctgaaa actgcagctt ccttctcacc ttgaagaata atcctagaaa 60
 actcacaaa atg tgt gat gct ttt gta ggt acc tgg aaa ctt gtc tcc agt 111
 Met Cys Asp Ala Phe Val Gly Thr Trp Lys Leu Val Ser Ser
 -65 -60 -55
 gaa aac ttt gat gat tat atg aaa gaa gta gga gtg ggc ttt gcc acc 159
 Glu Asn Phe Asp Asp Tyr Met Lys Glu Val Gly Val Gly Phe Ala Thr
 -50 -45 -40
 agg aaa gtg gct ggc atg gcc aaa cct aac atg atc atc agt gtg aat 207
 Arg Lys Val Ala Gly Met Ala Lys Pro Asn Met Ile Ile Ser Val Asn
 -35 -30 -25
 ggg gat gtg atc acc att ccc cac ctg gtc ctc ccc ctt ccc atg ctg 255
 Gly Asp Val Ile Thr Ile Pro His Leu Val Leu Pro Leu Pro Met Leu

276

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<210> 677
<211> 441
<212> DNA
<213> Homo sapiens
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<220>
<221> CDS
<222> 337..441
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<221> sig_peptide
<222> 337..399
<223> Von Heijne matrix
      score 3.59999990463257
      seq  GQLLSFLLGTYLG/RR
```

```

<400> 677
gggattcaag gaggcccatc atgtcagaat gctgtgggtt ggcaggaggc atcacaatga      60
aattttccat gttcccaaat ttgatattca cagtactaca tataatttct caggggaagat      120
aggggttgac acgatggaaa tattttggtg aaccattcgt tcccttgggt ttctttctca      180
tttggggagt gtggtttaca atgattggag caaaagtttc ctgaatcttt ttcttgtttc      240
cattttattg catggtaaaa cacaatttat ccactttctt gtcaatgagt atctagttag      300
attcctgttt tttggctaatt tcaaataaaa ctatga atg ttt ttg tac cgg tct      354
                               Met Phe Leu Tyr Arg Ser
                               -20

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[illegible]

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<210> 678
<211> 191
<212> DNA
<213> Homo sapiens
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<220>  
<221> CDS  
<222> 135..191
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<221> sig_peptide
<222> 135..182
<223> Von Heijne matrix
      score 3.59999990463257
      seq FFCLCAFNSFLLS/PE
```

```
<400> 678
aagtgtgtgt tgctgcgcca scacggaggc caaggacctc acgkwstaa aagatgacga      60
gactggcttc gggagaaaca ccatccagaa gagacctttc aaaaaacttc tagagactcc      120
```



```

ccaagacgta tgag atg ama ggc ttc ttc tgt ctg tgt gcg ttt aac tca      170
          Met Xaa Gly Phe Phe Cys Leu Cys Ala Phe Asn Ser
          -15                      -10                      -5

ttt ctc ctt agc ccc gag ggg      191
Phe Leu Leu Ser Pro Glu Gly
          1

```

```

<210> 679
<211> 235
<212> DNA
<213> Homo sapiens

```

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<220>
<221> CDS
<222> 31..234

```

```

<221> sig_peptide
<222> 31..228
<223> Von Heijne matrix
      score 3.59999990463257
      seq LTSFLSIXIFVNP/TR

```

```

<400> 679
atttttcacc actgcatagt gttacattgt atg att ttc cca cat tgc atg tac      54
                      Met Ile Phe Pro His Cys Met Tyr
                      -65                      -60

tgt tta gag tgt ata act aag aat gga ttg cta ggt tta aag gtg ctt      102
Cys Leu Glu Cys Ile Thr Lys Asn Gly Leu Leu Gly Leu Lys Val Leu
          -55                      -50                      -45

cca ctc tat ggg ata atg cta att ttt ttc cct aaa gtg gtt tat aac      150
Pro Leu Tyr Gly Ile Met Leu Ile Phe Phe Pro Lys Val Val Tyr Asn
          -40                      -35                      -30

aat caa ccc ttg cac tac aag tca gta atg gtg ttt cag ttg act tca      198
Asn Gln Pro Leu His Tyr Lys Ser Val Met Val Phe Gln Leu Thr Ser
          -25                      -20                      -15

ttc ttg tcg att tka att ttt gtc aac ccc act cgg g      235
Phe Leu Ser Ile Xaa Ile Phe Val Asn Pro Thr Arg
-10                      -5                      1

```

```

<210> 680
<211> 410
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> 173..409

```

```

<221> sig_peptide
<222> 173..334
<223> Von Heijne matrix
      score 3.59999990463257
      seq LMAXLLTVEVTHP/NS

```


Xaa	Xaa	Ser	Cys	Ser	Ser	Xaa	Ala	Pro	Ser	Ile	Lys	Ala	Arg	Thr	Leu	
				1				5					10			
tct	acg	acc	aca	tca	acg	agg	gga	agc	tgt	gga	aac	aca	tca	agc	aca	197
Ser	Thr	Thr	Thr	Ser	Thr	Arg	Gly	Ser	Cys	Gly	Asn	Thr	Ser	Ser	Thr	
		15					20					25				
agt	atg	aga	aca	agt	agt	tcc	ttg	gag	gcc	ccc	atc	cag	gcc	aga	agg	245
Ser	Met	Arg	Thr	Ser	Ser	Ser	Leu	Glu	Ala	Pro	Ile	Gln	Ala	Arg	Arg	
	30					35					40					
acc	agg	tcc	acc	cag	cag	ctg	ttt	gcc	cag	agc	tgg	agc	ctc	agc	dtg	293
Thr	Arg	Ser	Thr	Gln	Gln	Leu	Phe	Ala	Gln	Ser	Trp	Ser	Leu	Ser	Xaa	
45					50					55					60	
aag	atg	atg	c													303
Lys	Met	Met														

<210> 682
 <211> 328
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 79..327

<221> sig_peptide
 <222> 79..201
 <223> Von Heijne matrix
 score 3.59999990463257
 seq LHTSVTLFLLSYC/DC

<221> misc_feature
 <222> 258
 <223> n=a, g, c or t
 Oligonucleotide

<400>	682	
agatgattcc	ctgattctcc	agagagatta
acccaatgaa	agaagaaa	atg aaa gcc ata aag aaa agt ctt aca gaa gaa
	Met Lys Ala Ile Lys Lys	Ser Leu Thr Glu Glu
	-40	-35
gaa tac ctg tac ctg	gac ttt tct cac	caa aca gaa gga tgc atc ttt
Glu Tyr Leu Tyr Leu	Asp Phe Ser His	Gln Thr Glu Gly Cys Ile Phe
-30	-25	-20
cct ctt cat aca tct	gta act tta ttt	ctg tta tct tac tgt gac tgt
Pro Leu His Thr Ser	Val Thr Leu Phe	Leu Leu Ser Tyr Cys Asp Cys
	-10	-5
aaa atc ttt aaa att	tgc tta gtt gtc	acc aaa gag gtg agt aga gat
Lys Ile Phe Lys Ile	Cys Leu Val Val	Thr Lys Glu Val Ser Arg Asp
	5	10
avn tca cta cta aga	gat gac ctg atc	cag gat gtt gaa ata cag att
Xaa Ser Leu Leu Arg	Asp Asp Leu Ile	Gln Asp Val Glu Ile Gln Ile
	20	25
att tca agg cag gag	ctc cca cca a	
Ile Ser Arg Gln Glu	Leu Pro Pro	
35	40	328

<210> 683
 <211> 447
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 386..445

<221> sig_peptide
 <222> 386..427
 <223> Von Heijne matrix
 score 3.59999990463257
 seq FLCVCYFIRKSTS/FF

<221> misc_feature
 <222> 307
 <223> n=a, g, c or t
 Oligonucleotide

<400> 683
 ttaacatctt ccactgaaaa gaaaagataa tgatataaat aaagcaattt aaatcaagtc 60
 taaggtatag gaaggtatct aagaagaag caaacattct ctagatgttg ttatccaaaa 120
 tatattctct ttgtcagttt actgaaataa tttcttcagt gtgtgggaat ttcctttgca 180
 tccagcttta ctatagagat gacatcacac caacagtgac acgacttggt tacaagaggg 240
 tggataaac agcaaagtgt cttccttaaa acagatttct tgttgaactt caacagaaaa 300
 agaagcngta aatgtagaag gaagaacagg agatagtctt taacatgtag ggtaaaatct 360
 aaggtagagg agagagcagc tgata atg ttt tta tgt gtt tgc tac ttt att 412
 Met Phe Leu Cys Val Cys Tyr Phe Ile
 -10
 agg aag tct act tcc ttc ttt tcc ata tct agt ag 447
 Arg Lys Ser Thr Ser Phe Phe Ser Ile Ser Ser
 -5 1 5

<210> 684
 <211> 217
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 5..217

<221> sig_peptide
 <222> 5..139
 <223> Von Heijne matrix
 score 3.59999990463257
 seq AWWLLLPVWKLGG/QL

<400> 684
 tcaa atg ggg aag ccg aga ggt ggt gag atg ctt gag gtt gta aag act 49
 Met Gly Lys Pro Arg Gly Gly Glu Met Leu Glu Val Val Lys Thr
 -45 -40 -35

gtc tcc act ttc act ttg gga ggg tgg aaa ggg act gct cct gtg tcc	97
Val Ser Thr Phe Thr Leu Gly Gly Trp Lys Gly Thr Ala Pro Val Ser	
-30 -25 -20 -15	
tgc gcc tgg tgg ctg ctt ctc cca gtt tgg aag ctg gga ggg cag ctt	145
Cys Ala Trp Trp Leu Leu Leu Pro Val Trp Lys Leu Gly Gly Gln Leu	
-10 -5 1	
gag cgc agg aag aat cca aag gaa tac tgt ctt ggc tcc tgg gtg tgg	193
Glu Arg Arg Lys Asn Pro Lys Glu Tyr Cys Leu Gly Ser Trp Val Trp	
5 10 15	
ctc agt cct cag ctg gct cca agg	217
Leu Ser Pro Gln Leu Ala Pro Arg	
20 25	

<210> 685
 <211> 132
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 77..130

<221> sig_peptide
 <222> 77..124
 <223> Von Heijne matrix
 score 3.59999990463257
 seq FTFISTLLFVFLG/VV

<400> 685	
tgaaatccta gcttgaatat ttacattagt cttgtttctc aaacttgact ctttggtttg	60
atcgacattt tcccta atg ctg att ttc acc ttt att tct act ttg ctg ttt	112
Met Leu Ile Phe Thr Phe Ile Ser Thr Leu Leu Phe	
-15 -10 -5	
gta ttc ttg gga gtt gtg gg	132
Val Phe Leu Gly Val Val	
1	

<210> 686
 <211> 260
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 120..260

<221> sig_peptide
 <222> 120..230
 <223> Von Heijne matrix
 score 3.59999990463257
 seq PGSGLCMAAVQA/GN

<400> 686	
acatctcctt ggccccgcc cactcccgcg gggctattgt ccccggtaaa ctgcagtttc	60

tgggttcgaga ctccaatcct gtttcgaatt gctgcttgct gcccttggg ctggggata 119
 atg gaa gtt ctt tcb mtt ccc aac tct ttc cag acc caa gca ctc tgg 167
 Met Glu Val Leu Ser Xaa Pro Asn Ser Phe Gln Thr Gln Ala Leu Trp
 -35 -30 -25
 gac tca ctc cat agt cca gga gtt cca ggt tcc gga tta tgt tcc atg 215
 Asp Ser Leu His Ser Pro Gly Val Pro Gly Ser Gly Leu Cys Ser Met
 -20 -15 -10
 gca gca gtc caa gca gga aac caa gcc atc tac tct gcc tcg ggg 260
 Ala Ala Val Gln Ala Gly Asn Gln Ala Ile Tyr Ser Ala Ser Gly
 -5 1 5 10

<210> 687
 <211> 473
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 332..472

<221> sig_peptide
 <222> 332..457
 <223> Von Heijne matrix
 score 3.59999990463257
 seq LLTQAGFPRRGEA/AP

<400> 687
 tgtgtatgtg tgaaaatcag gaagagccag cggggagtgt gtgttgccat cgcgtctccg 60
 cctgcagggg cgggacccca ggaggaggga gaggacagag cactgcaga ggaccagact 120
 gggaaaacaa cgatatggca ggagccagtc ttggggccccg cttctaccgg cagatcaaaa 180
 gacatccggg gctgggacag aaagaacaac ccggagccct ggaaccgcct gagccccaat 240
 gaccaatata agttccttgc agtttccact gactataaga agctgaagaa ggaccggcca 300
 gacttctaag ccaggctggg ctgccagtgc c atg caa gcc aca gcc agc cag 352
 Met Gln Ala Thr Ala Ser Gln

 -40
 ccc atc cac ttc ttc crs tcc tcc ccg cag gcc cca agg cat cac tcc 400
 Pro Ile His Phe Phe Xaa Ser Ser Pro Gln Ala Pro Arg His His Ser
 -35 -30 -25 -20
 ggc cac cct gtc ccg cta ctg ctt aca cag gcc ggg ttc cca cgc aga 448
 Gly His Pro Val Pro Leu Leu Leu Thr Gln Ala Gly Phe Pro Arg Arg
 -15 -10 -5
 ggg gag gct gct cca ccc cta ctc c 473
 Gly Glu Ala Ala Pro Pro Leu Leu
 1 5

<210> 688
 <211> 107
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 5..106

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<221> sig_peptide
<222> 5..94
<223> Von Heijne matrix
      score 3.59999990463257
      seq LCTFTLNLTAVRT/IX

<400> 688
acac atg cga ggg tak aac tgh gtg ttc agg gtt ttc tct gaa agc ctg      49
      Met Arg Gly Xaa Asn Xaa Val Phe Arg Val Phe Ser Glu Ser Leu
      -30                      -25                      -20
aag gga ttg tgt acw ttt aca ttg aac ttg act gca gtt aga acc att      97
Lys Gly Leu Cys Thr Phe Thr Leu Asn Leu Thr Ala Val Arg Thr Ile
-15                      -10                      -5                      1
arc cta gat g.      107
Xaa Leu Asp

<210> 689
<211> 377
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 258..377

<221> sig_peptide
<222> 258..353
<223> Von Heijne matrix
      score 3.59999990463257
      seq RLTISTXLSTSXX/FM

<400> 689
aaacacaaca accagattcc tcctctaaag aagcccctgg gagcacagct catcaccatg      60
gactggacct ggaggttcct ctttttggtg acagcagcta cagatgtcca gtcccaggtc      120
cagctggtgc aagtctgggt actgaggtga agaggcctgg gtcctcgggtg aaggtctcct      180
gtaagacttc tggaggcacc ttcagtagta atgccatcac gtgggtgcga caggcccctg      240
gacaagggct tgagtgg atg ggr agg atc atc ccc atg gtt gaa aaa gcg      290
                        Met Gly Arg Ile Ile Pro Met Val Glu Lys Ala
                        -30                      -25
gac acc gca cag aag ttc cag ggc aga ctc act att agt aca dkv cta      338
Asp Thr Ala Gln Lys Phe Gln Gly Arg Leu Thr Ile Ser Thr Xaa Leu
-20                      -15                      -10
tcg acg agc asa gsc ttc atg gaa ctg agc agt ctg aga      377
Ser Thr Ser Xaa Xaa Phe Met Glu Leu Ser Ser Leu Arg
-5                      1                      5

<210> 690
<211> 388
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 53..388

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<221> sig_peptide
 <222> 53..253
 <223> Von Heijne matrix
 score 3.59999990463257
 seq IIMVFVFICFCYL/HY

<400> 690
 ataaattcag tagttacctt agtagacaaa tcatttgaac caagttgcgg ac atg aat 58
 Met Asn
 ctt gtt att tgt gtc cta ctt ttg tcc att tgg aaa aat aat tgc atg 106
 Leu Val Ile Cys Val Leu Leu Leu Ser Ile Trp Lys Asn Asn Cys Met
 -65 -60 -55 -50
 act aca aac caa acc aat gga tct tct act aca gga gat aaa cct gtt 154
 Thr Thr Asn Gln Thr Asn Gly Ser Ser Thr Thr Gly Asp Lys Pro Val
 -45 -40 -35
 gaa tca atg cag aca aaa ttg aac tac ctt aga aga aat cta ctc att 202
 Glu Ser Met Gln Thr Lys Leu Asn Tyr Leu Arg Arg Asn Leu Leu Ile
 -30 -25 -20
 tta gtt ggt att atc atc atg gtt ttt gtc ttt atc tgt ttt tgt tat 250
 Leu Val Gly Ile Ile Ile Met Val Phe Val Phe Ile Cys Phe Cys Tyr
 -15 -10 -5
 ctc cat tat aat tgt ctg agc gat gat gcg tcc aaa gca gga atg gtc 298
 Leu His Tyr Asn Cys Leu Ser Asp Asp Ala Ser Lys Ala Gly Met Val
 1 5 10 15
 aag aaa aaa ggc ata gca gcc aag tca tct aaa aca tca ttc agt gaa 346
 Lys Lys Lys Gly Ile Ala Ala Lys Ser Ser Lys Thr Ser Phe Ser Glu
 20 25 30
 gcc aag aca gcc tct caa tgc agt tca gaa aca caa acc ggg 388
 Ala Lys Thr Ala Ser Gln Cys Ser Ser Glu Thr Gln Thr Gly
 35 40 45

<210> 691
 <211> 408
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 304..408

<221> sig_peptide
 <222> 304..387
 <223> Von Heijne matrix
 score 3.59999990463257
 seq IFFSLTLGCKFS/KL

<400> 691
 cttgacttct gtgcactcac aggcttgatc aacaccacaa ggaagctgcc aaggccatcc 60
 tctgaaacca cagcccagac tctatgttgg ccccttttag ccatggctgg aatggctgag 120
 acacaggaca ccaagtccct aggctgtaca cagcactggg accctgggcc ctgcccattg 180
 aacaattttt tcttcctaaa tcttcaggcc tgtgatggga ggggctaccg caaaggtctc 240
 tgacatgccc cagatacatt ttccctattg tcttggggat taacatttgg ctctcgtta 300
 ctt atg caa att tct gca gcc agc ttg aat ttc tcc tca aaa aat gga 348

[illegible][illegible][illegible][illegible][illegible]

(The following are names of persons who have been convicted of crimes involving moral turpitude.)

[illegible][illegible]

<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 344..454

<221> sig_peptide
<222> 344..412
<223> Von Heijne matrix
score 3.59999990463257
seq LGCHFFSLALLNT/GP

<221> misc_feature
<222> 285,342..343
<223> n=a, g, c or t
Oligonucleotide

<400> 695
tggtatatgg gtctcttgaa gacaatatac agttgggtct ttcttcttta ttcaacttac 60
cactctgtgc cttttaagtg gggcatttag ctaakwtaca ttcaaggtta atattgatat 120
gtgcatatgt gatcctgtca tsatgttamc tggtcgttat tcagactaga ttgtgtagtt 180
tttttatagt gtgtcagtag ttacgttttg tggtagtcag tgacagtgat ttttttcccc 240
atgttttagca tccctttaag gacctattgt aaagcaggtc tagtngtaac aaatttcctt 300
ggcatttact tatcaggaaa ggatcttttt ttctcctttg cnn atg aag ctt agt 355
Met Lys Leu Ser
-20
ttg gct gga tat gaa att ctt ggt tgt cat ttc ttt tct tta gca ctg 403
Leu Ala Gly Tyr Glu Ile Leu Gly Cys His Phe Phe Ser Leu Ala Leu
-15 -10 -5
cta aat aca ggc ccc caa tat ctt ttg gct tat agg gtt tct gct gaa 451
Leu Asn Thr Gly Pro Gln Tyr Leu Leu Ala Tyr Arg Val Ser Ala Glu
1 5 10
agg t 455
Arg

<210> 696
<211> 153
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 8..151

<221> sig_peptide
<222> 8..127
<223> Von Heijne matrix
score 3.59999990463257
seq ITALSQSLQPLRK/LP

<400> 696
agacaag atg gcg acg tcc gtg ggg cac cga tgt ctg gga tta ctg cac 49
Met Ala Thr Ser Val Gly His Arg Cys Leu Gly Leu Leu His

	-40		-35		-30		
ggg gtc gcg ccg tgg cgg agc agc ctc cat ccc tgt gag atc act gcc							97
Gly Val Ala Pro Trp Arg Ser Ser Leu His Pro Cys Glu Ile Thr Ala							
	-25		-20		-15		
ctg agc caa tcc cta cag ccc tta cgg aag ctg cct ttt aga gcc tct							145
Leu Ser Gln Ser Leu Gln Pro Leu Arg Lys Leu Pro Phe Arg Ala Ser							
	-10		-5		1		5
ygc acg gg							153
Xaa Thr							

<210> 697
 <211> 493
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 116..493
 <221> sig_peptide
 <222> 116..262
 <223> Von Heijne matrix
 score 3.59999990463257
 seq YCLVTLVFFYSSA/SF

<400> 697	
aaaagctgac gacttcggtc tgcgccggaa gtgcatgagc tgccgatgtg gtgcttagtg	60
attgcggttt cggtcgctct cccgtgtttc ccgggctggg tattgcctc gcacc atg	118
	Met
gcg ccc aag ggc aaa gtg ggc acg aga ggg aag aag cag ata ttt gaa	166
Ala Pro Lys Gly Lys Val Gly Thr Arg Gly Lys Lys Gln Ile Phe Glu	
	-45
	-40
	-35
gag aac aga gag act ctg aag ttc tac ctg cgg atc ata ctg ggg gcc	214
Glu Asn Arg Glu Thr Leu Lys Phe Tyr Leu Arg Ile Ile Leu Gly Ala	
	-30
	-25
	-20
aat gcc att tac tgc ctt gtg acg ttg gtc ttc ttt tac tca tct gcc	262
Asn Ala Ile Tyr Cys Leu Val Thr Leu Val Phe Phe Tyr Ser Ser Ala	
	-15
	-10
	-5
tca ttt tgg gcc tgg ttg gcc ctg ggc ttt agt ctg gca gtg tat ggg	310
Ser Phe Trp Ala Trp Leu Ala Leu Gly Phe Ser Leu Ala Val Tyr Gly	
1	5
	10
	15
gcc agc tac cac tct atg agc tcg atg gca cga gca gcg ttc tct gag	358
Ala Ser Tyr His Ser Met Ser Ser Met Ala Arg Ala Ala Phe Ser Glu	
	20
	25
	30
gat ggg gcc ctg atg gat ggt ggc atg gac ctc aac atg gag cag ggc	406
Asp Gly Ala Leu Met Asp Gly Gly Met Asp Leu Asn Met Glu Gln Gly	
	35
	40
	45
atg gca gag cac ctt aag gat gtk atc cta ctg aca gcc atc gtg cag	454
Met Ala Glu His Leu Lys Asp Val Ile Leu Leu Thr Ala Ile Val Gln	
	50
	55
	60
gtg ctc agc tgc ttc tct ctc tat gtc tgg tcc ttc tgg	493
Val Leu Ser Cys Phe Ser Leu Tyr Val Trp Ser Phe Trp	
65	70
	75

<210> 698
 <211> 174
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 8..172

<221> sig_peptide
 <222> 8..94
 <223> Von Heijne matrix
 score 3.59999990463257
 seq AFNKAVWFTPCSC/QE

<400> 698
 aacaaag atg gcg gcg gtg act gtg acg gtg acg aag acg gcg gcg gcg 49
 Met Ala Ala Val Thr Val Thr Val Thr Lys Thr Ala Ala Ala
 -25 -20
 gcg acg gca ttt aac aag gcg gtg tgg ttt act cca tgc agt tgt cag 97
 Ala Thr Ala Phe Asn Lys Ala Val Trp Phe Thr Pro Cys Ser Cys Gln
 -15 -10 -5 1
 gag gta agt agc agg ctg ccg gct ccg acg gcg gcg acg ccg cag gac 145
 Glu Val Ser Ser Arg Leu Pro Ala Arg Thr Ala Ala Thr Arg Gln Asp
 5 10 15
 agg gcg gat aag aag gag ccg ccc tgt gg 174
 Arg Ala Asp Lys Lys Glu Arg Pro Cys
 20 25

<210> 699
 <211> 300
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 199..300

<221> sig_peptide
 <222> 199..255
 <223> Von Heijne matrix
 score 3.59999990463257
 seq PGSAICLWHSTLG/GX

<221> misc_feature
 <222> 261
 <223> n=a, g, c or t
 Oligonucleotide

<400> 699
 attttgtctc ggcagcgggtg gccgwagctc catcgcatTT tatgtttctg gcgagaaggg 60
 aacggagttt tcatcaggta gattggTTTT trtgccggccg tcctccaccg tttcctccag 120
 gacagcacct agtcgtggcc ggaggagtct catagctgtc agaaagaata agactgattt 180
 tatgggaaaa ttaagcag atg ctc cag ttt gag aaa cct gga tct gcg atc 231

	Met	Leu	Gln	Phe	Glu	Lys	Pro	Gly	Ser	Ala	Ile					
					-15					-10						
tgt	ttg	tg	cac	agc	act	ttg	gga	ggy	ymn	ggc	ggg	cgt	gag	att	gds	279
Cys	Leu	Trp	His	Ser	Thr	Leu	Gly	Gly	Xaa	Gly	Gly	Arg	Glu	Ile	Xaa	
			-5				1					5				
agt	ttg	aga	cca	gcc	tgc	ggg										300
Ser	Leu	Arg	Pro	Ala	Cys	Gly										
	10					15										

<210> 700
 <211> 159
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 86..157

<221> sig_peptide
 <222> 86..139
 <223> Von Heijne matrix
 score 3.59999990463257
 seq LAILLKWVSNSKS/FL

<400>	700	
ttttatagct	atcacaaatg	agattgcttt
cttaatTTTT	tttcagatta	atcatagtta
60		
acaaatagaa	actattgatt	ttygt atg
ttg att	tcg tat	ctt gca
att tta		
112		
	Met	Leu
	Ile	Ser
	Tyr	Leu
	Ala	Ile
	Leu	
	-15	-10
cta aaa	tggtt	agc aat
tct aag	agt ttt	ttg gtg
aag gca	tcg gg	
159		
Leu Lys	Trp Val	Ser Asn
Ser Lys	Ser Phe	Leu Val
Lys Ala	Ser	
	-5	1
		5

<210> 701
 <211> 274
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 46..273

<221> sig_peptide
 <222> 46..90
 <223> Von Heijne matrix
 score 3.59999990463257
 seq LQTLAFWSAYVPC/QT

<400>	701	
agtgtgtccg	gaattggtgg	gttcttggtc
tactgagtt	ctaga atg	aag ctg
cag		
57		
	Met	Lys
	Leu	Gln
	-15	
acc ctc	gca ttc	tggtca
gcc tat	gtg cca	tgc cag
acc cag	gac cgg	
105		
Thr Leu	Ala Phe	Trp Ser
Ala Tyr	Val Pro	Cys Gln
Thr Gln	Asp Arg	

-10		-5		1		5	
gat gcc ccg cgc ctc acc ctg gag cag att gac ctc ata cgc cgc atg	153						
Asp Ala Pro Arg Leu Thr Leu Glu Gln Ile Asp Leu Ile Arg Arg Met							
10	15	20					
tgt gcc tcc tat tct gag ctg gag ctt gtg acc tcg gct aaa gct ctg	201						
Cys Ala Ser Tyr Ser Glu Leu Glu Leu Val Thr Ser Ala Lys Ala Leu							
25	30	35					
aac gac act cag aaa ttg gcc tgc ctc atc ggt gta gag ggt ggc cac	249						
Asn Asp Thr Gln Lys Leu Ala Cys Leu Ile Gly Val Glu Gly Gly His							
40	45	50					
tcg ctg gac aat agc ctc tcc agg g	274						
Ser Leu Asp Asn Ser Leu Ser Arg							
55	60						

<210> 702
 <211> 175
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 107..175

<221> sig_peptide
 <222> 107..148
 <223> Von Heijne matrix
 score 3.5
 seq PACLSSFVIPSSL/SP

<400> 702			
ttgcttttcta agacacttac tttcatcggc actttcagat ttttgaatta tacttttctca	60		
atttgatttt tcaagtgagt tattaggata taggtggggag tggaga atg cct gcc	115		
	Met Pro Ala		
tgc ctt tct tcc ttt gtc att ccc tct ctc ctt tct ccc tcc tcc cct	163		
Cys Leu Ser Ser Phe Val Ile Pro Ser Leu Leu Ser Pro Ser Ser Pro			
-10	-5	1	5
ccc tcc ata ggg	175		
Pro Ser Ile Gly			

<210> 703
 <211> 298
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 197..298

<221> sig_peptide
 <222> 197..244
 <223> Von Heijne matrix
 score 3.5
 seq SFAGSCTILGASS/HS

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<400> 703
ttttcatgtg tctgttggt gcataaatgt cttcttctga gaagtgtctg ttcataatcct    60
tcgcccactt gttgatgagg ttgttttttt cttgttaaatt tgtttgtgtt cattgtaagt    120
tctggatatt agccctttgt cagatgagta gattgtaaaa attttctccc attctacagg    180
ttgcctgttc actctg atg gta gtt tct ttt gct ggt tct tgc aca att cta    232
                Met Val Val Ser Phe Ala Gly Ser Cys Thr Ile Leu
                -15                -10                -5
ggc gcc agt agc cat tca ttc ccc att gaa gtc agc ctg ttc cca gtg    280
Gly Ala Ser Ser His Ser Phe Pro Ile Glu Val Ser Leu Phe Pro Val
                1                5                10
gac tgt ggc ttc ctc ttg    298
Asp Cys Gly Phe Leu Leu
                15

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<210> 704
<211> 136
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 41..136

<221> sig_peptide
<222> 41..100
<223> Von Heijne matrix
        score 3.5
        seq AVSQSWLAAPSTS/WV

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```

<400> 704
ttcttattaa agatttattt ttgtagagac agatgtctca atg tgt tgc cca ggc    55
                Met Cys Cys Pro Gly
                -20
tgg aac gca gtg tgc caa tct tgg ctc gct gca cct tcc acc tcc tgg    103
Trp Asn Ala Val Ser Gln Ser Trp Leu Ala Ala Pro Ser Thr Ser Trp
-15                -10                -5                1
gtt caa gag att ctc gta ctt cag cct cca ggg    136
Val Gln Glu Ile Leu Val Leu Gln Pro Pro Gly
                5                10

```

```

<210> 705
<211> 433
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 225..431

<221> sig_peptide
<222> 225..386
<223> Von Heijne matrix
        score 3.5
        seq IRCPLIFLXXVSG/TX

```



```

<400> 705
agaggactay gcgagagcgt ctacggttgt gccaaaggaa aaaaaatggt cctaagaaaa      60
gagtatacaa agttgtgttc atcaaagtct ggaacccaaa ggtgtccctc caaagctgta      120
cacgacagag aaaacgcgaa ctgaaagaag aagcaggtcc caaggggccca ggcgcctcct      180
ccacctctctc ctctctctag gattaacctc catttcagct aatc atg gga gag att      236
                               Met Gly Glu Ile
aaa gtc tct cct gat tat aac tgg ttt aga ggt aca gtt ccc ctt aaa      284
Lys Val Ser Pro Asp Tyr Asn Trp Phe Arg Gly Thr Val Pro Leu Lys
-50                               -45                               -40                               -35
aab dtw atk gtg gat gat gat gac agt aag ata tgg tcg chc tat gac      332
Xaa Xaa Xaa Val Asp Asp Asp Asp Ser Lys Ile Trp Ser Xaa Tyr Asp
                               -30                               -25                               -20
gcg ggc ccc cga agt atc agg tgt cct ctc ata ttc ctg cyc yct gtc      380
Ala Gly Pro Arg Ser Ile Arg Cys Pro Leu Ile Phe Leu Xaa Xaa Val
                               -15                               -10                               -5
agt gga act gha gat gtc ttt ttc cgg cag att ttg gct ctg act gga      428
Ser Gly Thr Xaa Asp Val Phe Arg Gln Ile Leu Ala Leu Thr Gly
      1                               5                               10
tgg gg      433
Trp
15

```

```

<210> 706
<211> 419
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> 284..418

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```

<221> sig_peptide
<222> 284..331
<223> Von Heijne matrix
      score 3.5
      seq SHSHLSLVGHSRA/CG

```

```

<400> 706
attgaaaatc attaaaaatc ttagcaattg ttttaaatta tctaattttt ttctccaaat      60
aatatctatt ttagcagcca aatcaccaca aatcattggt ttttatcttt agttgtgggt      120
gcacagcggg tgcgtgtatt ttggggcatg tgaggtgtct tgatgcgttc atgcagtgtg      180
taacagtcac atcagggtaa atgggacatc tttcacctca agcatttatc cttcgtgtta      240
tggacaccct cagctggaaa ggggggctgc gtcgtgagta tga atg gat gca agt      295
                               Met Asp Ala Ser
                               -15
cat agc cac ctg agc ctg gtg ggg cac agc agg gcc tgt gga gtc aca      343
His Ser His Leu Ser Leu Val Gly His Ser Arg Ala Cys Gly Val Thr
                               -10                               -5                               1
tcc cgg cct cat gct cgg cat agg gga cgc tgc tta ggt cca tgc agt      391
Ser Arg Pro His Ala Arg His Arg Gly Arg Cys Leu Gly Pro Cys Ser
      5                               10                               15                               20
cgc tca ggg ccc agg ctg tgc agc gcc a      419
Arg Ser Gly Pro Arg Leu Cys Ser Ala

```

<210> 707
 <211> 382
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 200..382

<221> sig_peptide
 <222> 200..301
 <223> Von Heijne matrix
 score 3.5
 seq LISHDPWPRGAFA/LS

<221> misc_feature
 <222> 365
 <223> n=a, g, c or t
 Oligonucleotide

<400> 707
 gttacttatg gttgagagag aatatttttc agattttatt ggacattgat atttgtaaatt 60
 tggttcattcc ttttgcccag ttttctattg agtggttcat agtttctcat gggatccaa 120
 gagttctgga tatgtagagg tggagggtca atctcatcay ttccttggtt taaaaatctt 180
 ccatggtttt gtcactcat atg ggc tca aac gcc gtg gtg tgg cat aca aag 232
 Met Gly Ser Asn Ala Val Val Trp His Thr Lys
 -30 -25
 ccc tca ctt ctg aac cac cct gct tcc agc ctc atc tcc cat gat ccc 280
 Pro Ser Leu Leu Asn His Pro Ala Ser Ser Leu Ile Ser His Asp Pro
 -20 -15 -10
 tgg cca cgc ggt gcg ttt gcg ctt tca tgt cca agt gct tcc ttc atg 328
 Trp Pro Arg Gly Ala Phe Ala Leu Ser Cys Pro Ser Ala Ser Phe Met
 -5 1 5
 ttg ttt tct tcc tta caa tgc cct ttc cct tat tgd naa aca gag tgc 376
 Leu Phe Ser Ser Leu Gln Cys Pro Phe Pro Tyr Xaa Xaa Thr Glu Cys
 10 15 20 25
 aac gwg 382
 Asn Xaa

<210> 708
 <211> 384
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 215..382

<221> sig_peptide
 <222> 215..268
 <223> Von Heijne matrix
 score 3.5

<220>
 <221> CDS
 <222> 15..167

<221> sig_peptide
 <222> 15..155
 <223> Von Heijne matrix
 score 3.5
 seq CLXFGILASEVYS/WN

<400> 710
 atattttcatg gcga atg tac cac aat tta ttt gct ctg ttg ttg ata gac 50
 Met Tyr His Asn Leu Phe Ala Leu Leu Leu Ile Asp
 -45 -40
 att cat gtt gtt cta gtt ttt tac tgc ctg gat ctc tta atg att cat 98
 Ile His Val Val Leu Val Phe Tyr Cys Leu Asp Leu Leu Met Ile His
 -35 -30 -25 -20
 att ttc tat tgt aaa tac tgc ctt gka ttt ggk att tta gca agt gaa 146
 Ile Phe Tyr Cys Lys Tyr Cys Leu Xaa Phe Gly Ile Leu Ala Ser Glu
 -15 -10 -5
 gtc tat tct tgg aac att tac 167
 Val Tyr Ser Trp Asn Ile Tyr
 1

<210> 711
 <211> 215
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 84..215

<221> sig_peptide
 <222> 84..170
 <223> Von Heijne matrix
 score 3.5
 seq SPLCSXSSGYCXA/FP

<400> 711
 ccgctttttg ctgcatcagc cggggattgc cggcgccagg tgctgggggc gactcggaca 60
 gcgggagcgt ggggtggagt agg atg gag tct ccc tcc cga gct ggg ggt gtr 113
 Met Glu Ser Pro Ser Arg Ala Gly Gly Val
 -25 -20
 grc ctm vga aag gct gct tcg ccg ctg tgt tcg gmv agc tct gga tac 161
 Xaa Leu Xaa Lys Ala Ala Ser Pro Leu Cys Ser Xaa Ser Ser Gly Tyr
 -15 -10 -5
 tgc rgg gct ttt ccg cgg agg agc gcc cgc cgg cat ctg cat ccg gga 209
 Cys Xaa Ala Phe Pro Arg Arg Ser Ala Arg Arg His Leu His Pro Gly
 1 5 10
 cac ggg 215
 His Gly
 15

<210> 712
 <211> 241
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 59..241

<221> sig_peptide
 <222> 59..133
 <223> Von Heijne matrix
 score 3.5
 seq LISLSVLMPVQHS/PD

<400> 712
 actatccttt cctcattgaa ttgctgtgat acctttgttg caaatcagct gtctgcag 58
 atg tgg agg tat gtt tct aga ctt tct tct gtt cca ttg atc agc ttg 106
 Met Trp Arg Tyr Val Ser Arg Leu Ser Ser Val Pro Leu Ile Ser Leu
 -25 -20 -15 -10
 tct gtc ttg atg cca gta cag cac tcc cct gat ttt tgt agc ttt att 154
 Ser Val Leu Met Pro Val Gln His Ser Pro Asp Phe Cys Ser Phe Ile
 -5 1 5
 gta agt aca gtt atc cct tgg ttt cct tgg gga att ggt tcc agg acc 202
 Val Ser Thr Val Ile Pro Trp Phe Pro Trp Gly Ile Gly Ser Arg Thr
 10 15 20
 ctc atg gat ata aaa atc ctg gga tgc tcg agt cca ggg 241
 Leu Met Asp Ile Lys Ile Leu Gly Cys Ser Ser Pro Gly
 25 30 35

<210> 713
 <211> 376
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 276..374

<221> sig_peptide
 <222> 276..365
 <223> Von Heijne matrix
 score 3.5
 seq NLLKLSSHPTCA/CK

<221> misc_feature
 <222> 154,217
 <223> n=a, g, c or t
 Oligonucleotide

<400> 713
 tatgtacatt tgtcaaaact cagaaaatgt atatataata tgtgtgcata tgattttaag 60
 tagttttaca taaaaagata agcaaatatt ggatgctggt taacactaag catgctgaaa 120

tatttagagg gaagagtatt attgtctaca atyngcttta aagacaccaa aaataaggtg	180
grttaattwa wkggsywwgg grmdwtggat aaatggnkag awatgtgata aagcaagtct	240
aatagaattt tgtggcagaa tctaattggcg gctat atg gat gtt agc tgt aaa	293
Met Asp Val Ser Cys Lys	
-30 -25	
att ctt tac aat gtg att gaa aaa ttt tgc aat aat ctg ttg aag ctt	341
Ile Leu Tyr Asn Val Ile Glu Lys Phe Cys Asn Asn Leu Leu Lys Leu	
-20 -15 -10	
tct tcc cat tcc cct act tgt gct tgc aaa cta aa	376
Ser Ser His Ser Pro Thr Cys Ala Cys Lys Leu	
-5 1	

<210> 714
 <211> 304
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 216..302

<221> sig_peptide
 <222> 216..275
 <223> Von Heijne matrix
 score 3.5
 seq SHLSGSSLQLCVA/QF

<400> 714	
gtatgtgtga ttgattttta ttgtcccttt gaactatgac ccaatactcc ccaaacctgt	60
tattcagttt ttgccagag ttattatatc tggggaataa acagaggaca cacaccaga	120
ggctgccagt agcaaaaatc actgtaattc aaaaagcatg aactacggt agtgaaatta	180
tcacactttt ctttgcatag agcagttttac ttgtg atg att ttc aaa gat gtg	233
Met Ile Phe Lys Asp Val	
-20 -15	
ttc tcc cac ttg tca ggt tca tct ctt caa ctg tgt gtc gca caa ttt	281
Phe Ser His Leu Ser Gly Ser Ser Leu Gln Leu Cys Val Ala Gln Phe	
-10 -5 1	
ctc gaw ctc agt gct gtt gac at	304
Leu Xaa Leu Ser Ala Val Asp	
5	

<210> 715
 <211> 242
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 91..240

<221> sig_peptide
 <222> 91..222
 <223> Von Heijne matrix
 score 3.5

seq SFSFLFFFFLSFF/FF

<400> 715

```
gtttgtgatt aagtgatttc ctctagtggt atgctttgac tcctcttttag cttttgtgta      60
aatactatag gtttttgctt tgtgggttaac atg aag ctt aca aaa aat atc tta      114
                               Met Lys Leu Thr Lys Asn Ile Leu
                               -40
twa gta ata ata ggc tgt ttt aag ctg ata gcc tac aaa aac tct gta      162
Xaa Val Ile Ile Gly Cys Phe Lys Leu Ile Ala Tyr Lys Asn Ser Val
-35                               -30                               -25
ctg tac ttt tac tct aac ttc tca ttt tct ttt ctt ttc ttt ttt ttc      210
Leu Tyr Phe Tyr Ser Asn Phe Ser Phe Ser Phe Leu Phe Phe Phe Phe
-20                               -15                               -10                               -5
ctt tct ttc ttt ttt ttc ttt ttt ttt ttt tt      242
Leu Ser Phe Phe Phe Phe Phe Phe Phe Phe
                               1                               5
```

<210> 716

<211> 375

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 100..375

<221> sig_peptide

<222> 100..360

<223> Von Heijne matrix

score 3.5

seq VAGXMLAPGGTLA/DD

<400> 716

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ctggcgtyag ttccggtcgc agaggagaca ccgccgcagt tgccggtaca tcggggattt      60
ctggctcttt cctcttcgcc ttaaattcgg gtgtctttt atg aat aat caa aag      114
                               Met Asn Asn Gln Lys
                               -85
cag caw rag cca acg cta tca ggc cag cgt ttt aaa act aga aaa aga      162
Gln Xaa Xaa Pro Thr Leu Ser Gly Gln Arg Phe Lys Thr Arg Lys Arg
-80                               -75                               -70
gat gaa aaa gag agg ttt gac cct act cag ttt caa gac tgt att att      210
Asp Glu Lys Glu Arg Phe Asp Pro Thr Gln Phe Gln Asp Cys Ile Ile
-65                               -60                               -55
caa ggc tta act gaa acc ggt act gat ttg gaa gca gta gct aag ttt      258
Gln Gly Leu Thr Glu Thr Gly Thr Asp Leu Glu Ala Val Ala Lys Phe
-50                               -45                               -40                               -35
ctt gat gct tct gga gca aaa ctt gat tac cgt cga tat gca gaa aca      306
Leu Asp Ala Ser Gly Ala Lys Leu Asp Tyr Arg Arg Tyr Ala Glu Thr
-30                               -25                               -20
ctc ttt gac att ctg gtg gct ggt kga atg ctg gcc cca ggt ggt aca      354
Leu Phe Asp Ile Leu Val Ala Gly Xaa Met Leu Ala Pro Gly Gly Thr
-15                               -10                               -5
ctg gca gat gac atg atg cvg      375
Leu Ala Asp Asp Met Met Xaa
```

1 5

<210> 717
 <211> 429
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 324..428

<221> sig_peptide
 <222> 324..374
 <223> Von Heijne matrix
 score 3.5
 seq LEIKLPFLPFAQQ/ID

<400> 717
 aacagtctat ttctgtttgt aaatattagt atttctgtgg attctgtact tgttccttgt 60
 tatcctttca ttctcttagg ttcatttggt ctgatggatt caggtaccat tgaaattctg 120
 atagtttcaa aatcttttat ctccagggtt gatctctctt gtgaactctg gaactgtatt 180
 cccaattgtc aattggacat ccctacgtat gggacctcag atatttcaaa catgatgtgt 240
 ccaagtctgt atcacttctg gccatcatat tgttctttta tttttccaaa tttcacatca 300
 ccagtaacaa actagctgtg atc atg gca gat agc ctg gaa ata aaa ctc ccc 353
 Met Ala Asp Ser Leu Glu Ile Lys Leu Pro
 -15 -10
 ttt tta ccc ttt gca cag caa att gac atc aaa tcc tgt ttc tac ttt 401
 Phe Leu Pro Phe Ala Gln Gln Ile Asp Ile Lys Ser Cys Phe Tyr Phe
 -5 1 5
 ttt ttt ttw aac wat kgc ttc cct agg g 429
 Phe Phe Xaa Asn Xaa Xaa Phe Pro Arg
 10 15

<210> 718
 <211> 350
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 4..348

<221> sig_peptide
 <222> 4..108
 <223> Von Heijne matrix
 score 3.5
 seq ATAAATAASATTG/AS

<221> misc_feature
 <222> 155
 <223> n=a, g, c or t
 Oligonucleotide

<400> 718


```

tga atg gac aga aaa tgg acc tgg aag aga ggg caa agg tca cat ctg      48
  Met Asp Arg Lys Trp Thr Trp Lys Arg Gly Gln Arg Ser His Leu
    -35                -30                -25

gag tca ggc cag gct gcc ccg gcc act gca gca gct acg gca gca tct      96
Glu Ser Gly Gln Ala Ala Pro Ala Thr Ala Ala Ala Thr Ala Ala Ser
-20                -15                -10                -5

gcc aca acg ggg gca agt gtg tgg aga agc aca atg ggc wac ctg tgt      144
Ala Thr Thr Gly Ala Ser Val Trp Arg Ser Thr Met Gly Xaa Leu Cys
              1              5              10

gat tgc acc anb dca cct tat gaa ggg ccc ttt tgc aaa aaa gag gtt      192
Asp Cys Thr Xaa Xaa Pro Tyr Glu Gly Pro Phe Cys Lys Lys Glu Val
              15              20              25

tct gct gtt ttt gag gct ggc acg tcg gtt act tac atg ttt caa gaa      240
Ser Ala Val Phe Glu Ala Gly Thr Ser Val Thr Tyr Met Phe Gln Glu
    30              35              40

ccc tat cct gtg acc aag aat ata agc ctc tca tcc tca gct att tac      288
Pro Tyr Pro Val Thr Lys Asn Ile Ser Leu Ser Ser Ser Ala Ile Tyr
    45              50              55              60

aca gat tca gct cca tcc aag gaa aac att gca ctt agc ttt gtg aca      336
Thr Asp Ser Ala Pro Ser Lys Glu Asn Ile Ala Leu Ser Phe Val Thr
              65              70              75

acc caa gca ccg gg
Thr Gln Ala Pro
              80

<210> 719
<211> 305
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 84..305

<221> sig_peptide
<222> 84..212
<223> Von Heijne matrix
      score 3.5
      seq VLSIKHLPPQLRA/FQ

<400> 719
gttttttccct ttctatttca gcctgactgc cggaatcaga gccgcgggtg agatccccag      60
ccctgtgagc ctgtaggagt aga atg gct ccc caa atg tat gag ttc cat ctg      113
              Met Ala Pro Gln Met Tyr Glu Phe His Leu
                  -40                  -35

cca tta tcc cca gag gag ttg ttg aaa agt gga ggg gtg aat cag tat      161
Pro Leu Ser Pro Glu Glu Leu Leu Lys Ser Gly Gly Val Asn Gln Tyr
              -30              -25              -20

gtt gtg caa gag gta ctg tcc atc aaa cat ctt cca cca cag ctt aga      209
Val Val Gln Glu Val Leu Ser Ile Lys His Leu Pro Pro Gln Leu Arg
              -15              -10              -5

gct ttt cag gct gcc ttt cga gct cag ggg ccc ctg gct atg ctg cag      257
Ala Phe Gln Ala Ala Phe Arg Ala Gln Gly Pro Leu Ala Met Leu Gln
    1              5              10              15

```

cac ttt gat act atc tac agc att ttg cat cac ttt cga agt ata gat 305
 His Phe Asp Thr Ile Tyr Ser Ile Leu His His Phe Arg Ser Ile Asp
 20 25 30

<210> 720
 <211> 257
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 6..257

<221> sig_peptide
 <222> 6..50
 <223> Von Heijne matrix
 score 3.5
 seq AVQVVGSWPSVQP/RE

<400> 720
 aaaag atg gct gct gtg caa gtt gtc ggt tcg tgg cct tcc gtg cag ccg 50
 Met Ala Ala Val Gln Val Val Gly Ser Trp Pro Ser Val Gln Pro
 -15 -10 -5
 cgg gag gca ccg cgg gaa gca atc cct gag cga ggc aat ggg ttt cgc 98
 Arg Glu Ala Pro Arg Glu Ala Ile Pro Glu Arg Gly Asn Gly Phe Arg
 1 5 10 15
 ctc ttg tct gcc agg ctc tgc gcc ctg cgc ccg gat gac agc agc tcc 146
 Leu Leu Ser Ala Arg Leu Cys Ala Leu Arg Pro Asp Asp Ser Ser Ser
 20 25 30
 gcc cgm acc gag atc cac ctg mtc ttc gat cag ctc atc tcc gag aac 194
 Ala Arg Thr Glu Ile His Leu Xaa Phe Asp Gln Leu Ile Ser Glu Asn
 35 40 45
 tac agc gag ggc agt ggc gtg gcc ccg gag gac gtw agt gct ctt ctt 242
 Tyr Ser Glu Gly Ser Gly Val Ala Pro Glu Asp Val Ser Ala Leu Leu
 50 55 60
 gtc cag gct tgc ggg 257
 Val Gln Ala Cys Gly
 65

<210> 721
 <211> 360
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 217..360

<221> sig_peptide
 <222> 217..306
 <223> Von Heijne matrix
 score 3.5
 seq FLFFLQFSFPLY/ LF

<221> misc_feature
 <222> 316,319
 <223> n=a, g, c or t
 Oligonucleotide

<400> 721
 ggcatgttta tatactcatt ccctggtgat tgtattttgc atacttgatt tttacctaag 60
 catttatctt ttttccttta ttttctgttg ctttgtcttt ttgtaatgcc tcctggggca 120
 atttctttga tttttatctt gcagttcttc tattgagttt tgcattgttg ctatcatgtt 180
 ttaaattttc atttttcata gtattctgtc ctatgg atg ttt cat ggc tgt cat 234
 Met Phe His Gly Cys His
 -30 -25
 att tta tct ttt ctg agg ata tca act aga ggt ttt ctt ttt ttt ctt 282
 Ile Leu Ser Phe Leu Arg Ile Ser Thr Arg Gly Phe Leu Phe Phe Leu
 -20 -15 -10
 caa ttt tcc ttt cct ctg tat tat ctc ttt cgg ngg ntt ttc cct cag 330
 Gln Phe Ser Phe Pro Leu Tyr Tyr Leu Phe Arg Xaa Xaa Phe Pro Gln
 -5 1 5
 tct ttc atg ttg gag gca ttt gtc aga tgt 360
 Ser Phe Met Leu Glu Ala Phe Val Arg Cys
 10 15

<210> 722
 <211> 191
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 64..189

<221> sig_peptide
 <222> 64..141
 <223> Von Heijne matrix
 score 3.5
 seq LVLYPWPPLLL/AF

<400> 722
 ttctcctctt gtgaaggcag ctctcagat ccagggagta tctgcacgga cctcatttat 60
 gtt atg tat aga cat tcc aaa cag cgt aat aat gtc cca tgc ctt gta 108
 Met Tyr Arg His Ser Lys Gln Arg Asn Asn Val Pro Cys Leu Val
 -25 -20 -15
 ctc tac gcc cct tgg gtc cct ccc ctc ctc cta gct ttc tgg ggc tgg 156
 Leu Tyr Ala Pro Trp Val Pro Pro Leu Leu Leu Ala Phe Trp Gly Trp
 -10 -5 1 5
 tgg ctc ctg gag cag ggt ctt ttt ttt ttt ttt tt 191
 Trp Leu Leu Glu Gln Gly Leu Phe Phe Phe Phe
 10 15

<210> 723
 <211> 473
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 63..473

<221> sig_peptide
 <222> 63..212
 <223> Von Heijne matrix
 score 3.5
 seq ITYGVFLCIDCSG/SH

<400> 723
 ttttttttttc gtcgactctt accggttggc tgggccagct gcgccgcggc tcacagctga 60
 cg atg ggg gac ccc agc aag cag gac atc ttg acc atc ttc aag cgc 107
 Met Gly Asp Pro Ser Lys Gln Asp Ile Leu Thr Ile Phe Lys Arg
 -50 -45 -40
 ctc cgc tcg gtg ccc act aac aag gtg tgt ttt gat tgt ggt gcc aaa 155
 Leu Arg Ser Val Pro Thr Asn Lys Val Cys Phe Asp Cys Gly Ala Lys
 -35 -30 -25 -20
 aat ccc agc tgg gca agc ata acc tat gga gtg ttc ctt tgc att gat 203
 Asn Pro Ser Trp Ala Ser Ile Thr Tyr Gly Val Phe Leu Cys Ile Asp
 -15 -10 -5
 tgc tca ggg tcc cac cgg tca ctt ggt gtt cac ttg agt ttt att cga 251
 Cys Ser Gly Ser His Arg Ser Leu Gly Val His Leu Ser Phe Ile Arg
 1 5 10
 tct aca gag ttg gat tcc aac tgg tca tgg ttt cag ttg cga tgc atg 299
 Ser Thr Glu Leu Asp Ser Asn Trp Ser Trp Phe Gln Leu Arg Cys Met
 15 20 25
 caa gtc gga gga aac gct agt gca tct tcc ttt ttt cat caa cat ggg 347
 Gln Val Gly Gly Asn Ala Ser Ala Ser Ser Phe Phe His Gln His Gly
 30 35 40 45
 tgt tcc acc aat gac acc aat gcc aag tac aac agt cgt gct gct cag 395
 Cys Ser Thr Asn Asp Thr Asn Ala Lys Tyr Asn Ser Arg Ala Ala Gln
 50 55 60
 ctc tat agg gag aaa atc aaa tcg ctc gcc tct caa gca aca cgg aag 443
 Leu Tyr Arg Glu Lys Ile Lys Ser Leu Ala Ser Gln Ala Thr Arg Lys
 65 70 75
 cat ggc act gat ctg tgg ctt gat agt tgt 473
 His Gly Thr Asp Leu Trp Leu Asp Ser Cys
 80 85

<210> 724
 <211> 139
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 60..137

<221> sig_peptide
 <222> 60..125
 <223> Von Heijne matrix
 score 3.5
 seq LLLHLVHFQRTLI/SL

<400> 724
 ttttagcattc aagccgtgat tagtgctttc tcttctcccc agcctgcctt tcagaacag 59
 atg cct ctg cct ccc aat cag tcc cct cta ctg ctg cac ctg gtg ttt 107
 Met Pro Leu Pro Pro Asn Gln Ser Pro Leu Leu Leu His Leu Val Phe
 -20 -15 -10
 cat caa agg acc ctg att tcc ctg ccg ccg cc 139
 His Gln Arg Thr Leu Ile Ser Leu Pro Pro
 -5 1

<210> 725
 <211> 187
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 125..187
 <221> sig_peptide
 <222> 125..163
 <223> Von Heijne matrix
 score 3.5
 seq MFLTFFFCTQVHG/PS

<400> 725
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 tctttttttg gcctacttag atctgttttc ctttcttgcc ttaaattggga attgctagag 120
 gmat atg ttt cta act ttt ttt ttc tgc aca caa gtt cat ggt cct tct 169
 Met Phe Leu Thr Phe Phe Phe Cys Thr Gln Val His Gly Pro Ser
 -10 -5 1
 ata ctt gat agc cca gct 187
 Ile Leu Asp Ser Pro Ala
 5

<210> 726
 <211> 207
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 39..206
 <221> sig_peptide
 <222> 39..80
 <223> Von Heijne matrix
 score 3.5
 seq VTLWIFQFFLCLT/CK

<221> misc_feature
 <222> 154
 <223> n=a, g, c or t
 Oligonucleotide

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<400> 726
aatataaata ccaaatacat aaatagtttt ggtgtag atg gtc act tta tgg att      56
                                   Met Val Thr Leu Trp Ile
                                   -10
ttt caa ttt ttc ttg tgt ttg act tgt aaa gct tat aat tta aga aac      104
Phe Gln Phe Phe Leu Cys Leu Thr Cys Lys Ala Tyr Asn Leu Arg Asn
               -5                      1                      5
tgt aat gat ggg aag ggh wga gsm tca gwg gtg ctt gga ttg gaa caa      152
Cys Asn Asp Gly Lys Gly Xaa Xaa Ser Xaa Val Leu Gly Leu Glu Gln
               10                      15                      20
mnr cta cct gaa tct gct ggt atg gta caw ttt tta ggt ttg aaa cac      200
Xaa Leu Pro Glu Ser Ala Gly Met Val Xaa Phe Leu Gly Leu Lys His
               25                      30                      35                      40
agg tgg g      207
Arg Trp

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<210> 727
<211> 164
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> 54..164

<221> sig_peptide
<222> 54..95
<223> Von Heijne matrix
      score 3.5
      seq VLWAGPXVPLLCA/AX

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<400> 727
agacaatggg gmmaatgtca cacatcacag accaagaggc ctaggaggav aag atg      56
                                   Met
ggt ttg tgg gct ggg ccc akc gtc ccc ctg ctg tgt gca gcc tas gga      104
Val Leu Trp Ala Gly Pro Xaa Val Pro Leu Leu Cys Ala Ala Xaa Gly
               -10                      -5                      1
ctt ggt gcc ctg cat ccc aga tgc tct agt caa ggc ttg agg ctt gcr      152
Leu Gly Ala Leu His Pro Arg Cys Ser Ser Gln Gly Leu Arg Leu Ala
               5                      10                      15
sct tct gaa gcc      164
Xaa Ser Glu Ala
20

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<210> 728
<211> 321
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> 139..321

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<221> sig_peptide
 <222> 139..261
 <223> Von Heijne matrix
 score 3.5
 seq FNIGLLWVPXXXG/AV

<400> 728
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 gccattagca tcataaacca ggtgattggc tggatctact ttgtggcctg gtccatctcc 120
 ttctaccctc aggtgmtc atg aat tgg agg cgg aaa agt gtc att ggt ctg 171
 Met Asn Trp Arg Arg Lys Ser Val Ile Gly Leu
 -40 -35
 agc ttc gac ttc gtg gct ctg aac ctg acg ggc ttc gtg gcc tac agt 219
 Ser Phe Asp Phe Val Ala Leu Asn Leu Thr Gly Phe Val Ala Tyr Ser
 -30 -25 -20 -15
 gta ttc aac atc ggc ctc ctc tgg gtg ccc twc wtc daa gga gca gtt 267
 Val Phe Asn Ile Gly Leu Leu Trp Val Pro Xaa Xaa Xaa Gly Ala Val
 -10 -5 1
 tct cct caa ata ccc caa cgg agt gaa ccc cgt gaa cag caa cga cgt 315
 Ser Pro Gln Ile Pro Gln Arg Ser Glu Pro Arg Glu Gln Gln Arg Arg
 5 10 15
 ctt ctt 321
 Leu Leu
 20

<210> 729
 <211> 472
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 25..471

<400> 729
 gacttcctc tagaatcctc caac atg gag cct ctt gca gct tac ccg cta 51
 Met Glu Pro Leu Ala Ala Tyr Pro Leu
 1 5
 aaa tgt tcc ggg ccc aga gca aag gta ttt gca gtt ttg ctg tct ata 99
 Lys Cys Ser Gly Pro Arg Ala Lys Val Phe Ala Val Leu Leu Ser Ile
 10 15 20 25
 gtt cta tgc aca gta acg cta ttt ctt cta caa cta aaa wtc ctc aaa 147
 Val Leu Cys Thr Val Thr Leu Phe Leu Leu Gln Leu Lys Xaa Leu Lys
 30 35 40
 cct aaa atc aac agc ttt tat gcc ttt gaa gtg aag gat gca aaa gga 195
 Pro Lys Ile Asn Ser Phe Tyr Ala Phe Glu Val Lys Asp Ala Lys Gly
 45 50 55
 aga act gtt tct ctg gaa aag tat aaa ggc aaa gtt tca cta gtt gta 243
 Arg Thr Val Ser Leu Glu Lys Tyr Lys Gly Lys Val Ser Leu Val Val
 60 65 70
 aac gtg gcc agt gac tgc caa ctc aca gac aga aat tac tta ggg ctg 291
 Asn Val Ala Ser Asp Cys Gln Leu Thr Asp Arg Asn Tyr Leu Gly Leu
 75 80 85
 aag gaa ctg cac aaa gag ttt gga cca tcc cac ttc agc gtg ttg gct 339

Lys	Glu	Leu	His	Lys	Glu	Phe	Gly	Pro	Ser	His	Phe	Ser	Val	Leu	Ala		
90					95					100					105		
ttt	ccc	tgc	aat	cag	ttt	gga	gaa	tcg	gag	ccc	cgc	cca	agc	aag	gaa		387
Phe	Pro	Cys	Asn	Gln	Phe	Gly	Glu	Ser	Glu	Pro	Arg	Pro	Ser	Lys	Glu		
				110					115					120			
gta	gaa	tct	ttt	gca	aga	aaa	aac	tac	gga	gta	act	ttc	ccc	atc	ttc		435
Val	Glu	Ser	Phe	Ala	Arg	Lys	Asn	Tyr	Gly	Val	Thr	Phe	Pro	Ile	Phe		
			125					130					135				
cac	aag	att	aag	att	cta	gga	tct	gaa	gga	gaa	ctg	c					472
His	Lys	Ile	Lys	Ile	Leu	Gly	Ser	Glu	Gly	Glu	Leu						
		140					145										

<210> 730
 <211> 465
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 70..465

<400>	730																
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gcccggtttt	atg aat gaa gct atg gct aca gat tcc cca aga aga ccc agt															111	
	Met Asn Glu Ala Met Ala Thr Asp Ser Pro Arg Arg Pro Ser																
	1		5		10												
cgt tgt act ggt gga gtt gtg gtt cgc ccc cag gct gtc aca gag cag																159	
Arg Cys Thr Gly Gly Val Val Val Arg Pro Gln Ala Val Thr Glu Gln																	
15		20		25		30											
tcc tac atg gaa agt gtt gtg act ttt ctg cag gat gtt gtg cca cag																207	
Ser Tyr Met Glu Ser Val Val Thr Phe Leu Gln Asp Val Val Pro Gln																	
	35		40		45												
gct tac agt gga aca cct cta aca gaa gaa aag gag aaa ata gtc tgg																255	
Ala Tyr Ser Gly Thr Pro Leu Thr Glu Glu Lys Glu Lys Ile Val Trp																	
	50		55		60												
gtc aga ttt gaa aat gca gat tta aat gat aca tca aga aat ctg gaa																303	
Val Arg Phe Glu Asn Ala Asp Leu Asn Asp Thr Ser Arg Asn Leu Glu																	
	65		70		75												
ttt cat gaa ata cat agt act ggg agt gaa ccg cct ttg ttg att atg																351	
Phe His Glu Ile His Ser Thr Gly Ser Glu Pro Pro Leu Leu Ile Met																	
	80		85		90												
att ggc tac agt gat gga atg cag gtc tgg agc atc cct atc akt ggc																399	
Ile Gly Tyr Ser Asp Gly Met Gln Val Trp Ser Ile Pro Ile Xaa Gly																	
	95		100		105											110	
gaa sac aag agc tct tct ctg ttc gac atg gcc caa ttc gag cgg cta																447	
Glu Xaa Lys Ser Ser Ser Leu Phe Asp Met Ala Gln Phe Glu Arg Leu																	
	115		120		125												
gaa tct tgc ctg ctc cac																465	
Glu Ser Cys Leu Leu His																	
	130																

<210> 731
 <211> 345
 <212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 207..344

<400> 731

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aagccggcgg gaccgagtgc tttaggccgc tygaaagaaa gttgctccga cccgggaaaa      120
ggagaagatg aaggaagcca aggatgcccg ctataccaat gggcacctct tcaccaccat      180
ttcagtttca ggcataacca tgtgct atg cct gta aca aga gca tca cag cca      233
                               Met Pro Val Thr Arg Ala Ser Gln Pro
                               1             5
agg aag ccc tca tct gcc caa caa cag aaa gcg gcc ctg ctg aak aac      281
Arg Lys Pro Ser Ser Ala Gln Gln Gln Lys Ala Ala Leu Leu Xaa Asn
10             15             20             25
aac acc gcc ttg cag tcc gtt tct ctt cga agt aag aca acc atc cgg      329
Asn Thr Ala Leu Gln Ser Val Ser Leu Arg Ser Lys Thr Thr Ile Arg
30             35             40
gag cgg cca agc tcg g      345
Glu Arg Pro Ser Ser
45
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<210> 732

<211> 398

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 274..396

<400> 732

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agcaaccaag tcgcacctgg agctgtccta gcgcctagtt ctctcccggc cgcagagctg      60
gccgcccgagg gggagtcgca gagtttgga gattctctta acacctctcg gccaaactca      120
gaagtgtata agatcagctt tatctttcca aatggagaca agtatgatgg tgactgtaca      180
agaacatctt ctggaatcta cgagagaaat ggaataggta ttcataccac tcctaattgg      240
attgtctaca caggaagctg gaaagatgac aag atg aat ggt ttt gga aga ctt      294
                               Met Asn Gly Phe Gly Arg Leu
                               1             5
gag cat ttt tca gga gca gta tat gaa gga caa ttt aag gat aat atg      342
Glu His Phe Ser Gly Ala Val Tyr Glu Gly Gln Phe Lys Asp Asn Met
10             15             20
ttt cat gga ctg ggg act tac aca ttc cca aat ggg gca aag tat act      390
Phe His Gly Leu Gly Thr Tyr Thr Phe Pro Asn Gly Ala Lys Tyr Thr
25             30             35
gga att tc      398
Gly Ile
40
```

<210> 733

<211> 443

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 49..441

<400> 733

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ggaagttctt gggagcgcca gttccgtctg tgtgttcgag tggacaaa atg gcg aag      57
                                   Met Ala Lys
                                   1
atc gcc aag act cac gaa gat att gaa gca cag att cga gaa att caa      105
Ile Ala Lys Thr His Glu Asp Ile Glu Ala Gln Ile Arg Glu Ile Gln
   5              10              15
ggc aag aag gca gct ctt gat gaa gct caa gga gtg ggc ctc gat tct      153
Gly Lys Lys Ala Ala Leu Asp Glu Ala Gln Gly Val Gly Leu Asp Ser
  20              25              30              35
aca ggt tat tat gac cag gaa att tat ggt gga agt gac agc aga ttt      201
Thr Gly Tyr Tyr Asp Gln Glu Ile Tyr Gly Gly Ser Asp Ser Arg Phe
   40              45              50
gct gga tac gtg aca tca att gct gca act gaa ctt gaa gat gat gac      249
Ala Gly Tyr Val Thr Ser Ile Ala Ala Thr Glu Leu Glu Asp Asp Asp
   55              60              65
gat gac tat tca tca tct acg agt ttg ctt ggt cag aag aag cca gga      297
Asp Asp Tyr Ser Ser Ser Thr Ser Leu Leu Gly Gln Lys Lys Pro Gly
   70              75              80
tat cat gcc cct gtg gca ttg ctt aat gat ata cca cag tca aca gaa      345
Tyr His Ala Pro Val Ala Leu Leu Asn Asp Ile Pro Gln Ser Thr Glu
   85              90              95
cag tat gat cca ttt gct gag cac aga cct cca aag att gca gac cgg      393
Gln Tyr Asp Pro Phe Ala Glu His Arg Pro Pro Lys Ile Ala Asp Arg
  100              105              110              115
gaa gat gaa tac aaa aag cat agg cgg acc atg ata att tcc cag agc      441
Glu Asp Glu Tyr Lys Lys His Arg Arg Thr Met Ile Ile Ser Gln Ser
   120              125              130
gt
443
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<210> 734

<211> 373

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 128..373

<400> 734

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gagaagccgc agtctcgaga gcgtaacga ggtgtttcgg tagtctctgg ccataccttc      60
tgcgcacccg gtgtcgctgg gctgcacccc gggcggggac gtccgccggg cacgggaggg      120
ggccaag atg ccg atc aat aaa tca gag aag cca gaa agc tgc gat aat      169
      Met Pro Ile Asn Lys Ser Glu Lys Pro Glu Ser Cys Asp Asn
      1              5              10
gtg aag gtt gtt gtt agg tgc cgg ccc ctc aat gag aga gag aaa tca      217
Val Lys Val Val Val Arg Cys Arg Pro Leu Asn Glu Arg Glu Lys Ser
  15              20              25              30
atg tgc tac aaa cag gct gtc agt gtg gat gag atg agg gga act atc      265
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Met	Cys	Tyr	Lys	Gln	Ala	Val	Ser	Val	Asp	Glu	Met	Arg	Gly	Thr	Ile	
				35					40					45		
act	gta	cat	aag	act	gat	tct	tcc	aat	gaa	cct	cca	aag	aca	ttt	act	313
Thr	Val	His	Lys	Thr	Asp	Ser	Ser	Asn	Glu	Pro	Pro	Lys	Thr	Phe	Thr	
			50					55					60			
ttt	gat	act	gtt	ttt	gga	cca	gag	agt	aaa	caa	ctt	gat	gtt	tat	aac	361
Phe	Asp	Thr	Val	Phe	Gly	Pro	Glu	Ser	Lys	Gln	Leu	Asp	Val	Tyr	Asn	
			65				70					75				
tta	act	gca	aga													373
Leu	Thr	Ala	Arg													
			80													

<210> 735
 <211> 322
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 202..321

<400> 735																
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gaagattgga	ttcatcttac	gcagtttgct	ggtggtggga	agcttctctg	ggctagtggg											120
cctctggtct	tcctgaccc	cgcgccgga	cgacccaagc	ccgctgagca	ggatgaggga											180
agacagagat	gtcatgaccc	c atg	ccc aac	cga ggc	ggc aat	gga cta	gct									231
		Met	Pro	Asn	Arg	Gly	Gly	Asn	Gly	Leu	Ala					
		1				5					10					
cct	ggg	gag	gac	aga	ttc	aaa	cct	gtg	gta	cca	tgg	cct	cat	gtt	gaa	279
Pro	Gly	Glu	Asp	Arg	Phe	Lys	Pro	Val	Val	Pro	Trp	Pro	His	Val	Glu	
			15					20						25		
gga	gta	gaa	gtg	gac	tta	gag	tct	att	aga	aga	ata	aac	aag	g		322
Gly	Val	Glu	Val	Asp	Leu	Glu	Ser	Ile	Arg	Arg	Ile	Asn	Lys			
			30				35						40			

<210> 736
 <211> 181
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 75..179

<400> 736																
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tggggcttgg	ttct	atg	tcc	ctg	tgg	cta	tgt	ttc	cag	tgt	cct	ctg	ggt			110
		Met	Ser	Leu	Trp	Leu	Cys	Phe	Gln	Cys	Pro	Leu	Gly			
		1				5					10					
gtt	tcc	aag	agc	aac	aag	aaa	cga	ata	aat	ctc	tgt	aat	ggt	ttc	tgg	158
Val	Ser	Lys	Ser	Asn	Lys	Lys	Arg	Ile	Asn	Leu	Cys	Asn	Gly	Phe	Trp	
		15				20					25					
aat	gaa	aaa	ata	aaa	aac	agg	ag									181
Asn	Glu	Lys	Ile	Lys	Asn	Arg										

35

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<220>  
<221> CDS  
<222> 18..158
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[illegible]

<220>
<221> CDS
<222> 66..233

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<210> 739
<211> 589
<212> DNA
<213> Homo sapiens
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<220>
 <221> CDS
 <222> 424..588

<400> 739
 atcaaaagaa ctcttatata caggagccca ggcaccatac tgtcttttcg aggtaggagt 60
 cgactcctgt gaggtatggt gctgggtgca gatgcagtgt ggctctggat agcaccttat 120
 ggacagttgt gtccccaagg aaggatgaga atagctactg aagtcctaaa gagcaagcct 180
 aactcaagcc attggcacac aggcattaga cagaaagctg gaagttgaaa tgggtggagtc 240
 caacttgcct ggaccagctt aatggttctg ctctgtgtaa cgtttttatc catggatgac 300
 ttgcttgggt atggagagtc ggcttgacta cactgtgtgg agcaagtttt aaagaagcaa 360
 aggactcaga attcatgatt gaagaaatgc aggcagacct gttatcctaa actagggttt 420
 tta atg acc aca aca agc aag cat gca gct tac tgc ttg aaa ggg tct 468
 Met Thr Thr Thr Ser Lys His Ala Ala Tyr Cys Leu Lys Gly Ser
 1 5 10 15
 tgc ctc amc caa gct aga gtg cag tgg cct ttg aag cwt act aca gcc 516
 Cys Leu Xaa Gln Ala Arg Val Gln Trp Pro Leu Lys Xaa Thr Thr Ala
 20 25 30
 tca aac ttc tgg gct caa gtg atc ctc agc ctc cca gtg gtc ttt gta 564
 Ser Asn Phe Trp Ala Gln Val Ile Leu Ser Leu Pro Val Val Phe Val
 35 40 45
 gac tgc ctg atg gag tmt cat ggc a 589
 Asp Cys Leu Met Glu Xaa His Gly
 50 55

<210> 740
 <211> 388
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 26..388

<400> 740
 aaaaaacgct gttggaaatc tcgctg atg gag gga gga gga ggt ata ccc cta 52
 Met Glu Gly Gly Gly Gly Ile Pro Leu
 1 5
 gaa aca ctt aaa gaa gaa agt cag tca aga cat gtt cta cct gca agt 100
 Glu Thr Leu Lys Glu Glu Ser Gln Ser Arg His Val Leu Pro Ala Ser
 10 15 20 25
 ttt gaa gtc aac agt ttg cag aaa agc aac tgg ggg ttc tta ctt act 148
 Phe Glu Val Asn Ser Leu Gln Lys Ser Asn Trp Gly Phe Leu Leu Thr
 30 35 40
 ggg ctt gtg ggt ggc acc ctg gtg gct gtg tac gct gta gcc acg ccg 196
 Gly Leu Val Gly Gly Thr Leu Val Ala Val Tyr Ala Val Ala Thr Pro
 45 50 55
 ttt gta acg cca gcc ctt cga aaa gtc tgt ttg cca ttt gta cct gca 244
 Phe Val Thr Pro Ala Leu Arg Lys Val Cys Leu Pro Phe Val Pro Ala
 60 65 70
 act atg aag cag att gaa aat gtt gtg aaa atg ttg cga tgc cga aga 292
 Thr Met Lys Gln Ile Glu Asn Val Val Lys Met Leu Arg Cys Arg Arg
 75 80 85
 gga tcc ctt gtg gac atc ggt agt ggg gac gga cgc att gtc ata gcg 340

Gly	Ser	Leu	Val	Asp	Ile	Gly	Ser	Gly	Asp	Gly	Arg	Ile	Val	Ile	Ala	
90					95					100					105	
gct	gcg	aag	aaa	ggg	ttc	ama	gca	gtt	ggg	tat	gaa	tta	aac	cca	tg	388
Ala	Ala	Lys	Lys	Gly	Phe	Xaa	Ala	Val	Gly	Tyr	Glu	Leu	Asn	Pro	Trp	
				110					115					120		

<210> 741
 <211> 478
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 15..476

<400> 741																
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		Met	Ala	Thr	Pro	Leu	Ala	Val	Asn	Ser	Ala	Ala	Ser			
		1				5					10					
cta	tg	gg	cct	tac	aaa	gac	att	tg	cat	aaa	gtg	gga	aat	gct	ctt	98
Leu	Trp	Gly	Pro	Tyr	Lys	Asp	Ile	Trp	His	Lys	Val	Gly	Asn	Ala	Leu	
	15					20					25					
tg	aga	aga	caa	cct	gaa	gct	gtt	cam	ctt	ctt	gat	aag	att	ttg	aag	146
Trp	Arg	Arg	Gln	Pro	Glu	Ala	Val	Xaa	Leu	Leu	Asp	Lys	Ile	Leu	Lys	
	30				35						40					
aaa	cac	aaa	cct	gac	ttc	atc	tca	ttg	ttc	aaa	aat	ccg	cca	aaa	aat	194
Lys	His	Lys	Pro	Asp	Phe	Ile	Ser	Leu	Phe	Lys	Asn	Pro	Pro	Lys	Asn	
45				50					55					60		
gtt	caa	cag	cat	gag	aag	gtt	cag	aaa	gcc	agt	aca	gag	gga	gtc	gcc	242
Val	Gln	Gln	His	Glu	Lys	Val	Gln	Lys	Ala	Ser	Thr	Glu	Gly	Val	Ala	
			65					70					75			
att	cag	ggt	caa	cag	gga	act	cga	ctt	ctt	cct	gaa	cag	ctc	att	aaa	290
Ile	Gln	Gly	Gln	Gln	Gly	Thr	Arg	Leu	Leu	Pro	Glu	Gln	Leu	Ile	Lys	
	80					85						90				
gaa	gcc	ttt	att	ctc	agt	gac	ctt	ttt	gat	att	gga	gaa	ttg	gca	gct	338
Glu	Ala	Phe	Ile	Leu	Ser	Asp	Leu	Phe	Asp	Ile	Gly	Glu	Leu	Ala	Ala	
	95					100					105					
gtt	gag	ctt	ctt	ctt	gct	gga	gag	cat	caa	cag	cca	cat	ttt	cct	ggc	386
Val	Glu	Leu	Leu	Leu	Ala	Gly	Glu	His	Gln	Gln	Pro	His	Phe	Pro	Gly	
	110				115						120					
ctt	acc	aga	gga	tta	gta	gct	gtt	ctt	ctg	tac	tg	gat	gga	aag	cga	434
Leu	Thr	Arg	Gly	Leu	Val	Ala	Val	Leu	Leu	Tyr	Trp	Asp	Gly	Lys	Arg	
	125			130					135					140		
tg	att	gcg	aat	tcc	ttg	aaa	gcc	ttg	ata	cag	tct	aga	cgg	gg		478
Cys	Ile	Ala	Asn	Ser	Leu	Lys	Ala	Leu	Ile	Gln	Ser	Arg	Arg			
				145				150								

<210> 742
 <211> 752
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS

<222> 377..751

<400> 742

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atttcctgcc gtaagtatac agtgcctccg ggtcgcggtc attttgagcc cctgtctgga    60
tgacttcttg cggctgttct acccctcccc ctcccccggt cggcctgmct gctgtcgtcg    120
ggaggtgggt gaggtgacgc aaacagcccc gttgttgccc tccgcgtatc ccctcaccac    180
ctttgcggcc atccacgact ttccgacatt ccgccatttt cctgcctgtg aggggtggaca    240
gatcgcgctc ggggtctcggc ctccctgagt ccgggtgact cgggaggcga cggagtgttt    300
ctgggggtgt gagctgggga agttcgtggg cacggatgcg tgtgggggtg ctgctcagtc    360
tgtaacggca ggaaag atg aat ggg agg gct gat ttt cga gag ccg aat gca    412
```

Met Asn Gly Arg Ala Asp Phe Arg Glu Pro Asn Ala
1 5 10

```
gag gtt cca aga cca att ccc cac ata ggg cct gat tac att cca aca    460
Glu Val Pro Arg Pro Ile Pro His Ile Gly Pro Asp Tyr Ile Pro Thr
15 20 25
```

```
gag gaa gaa agg aga gtc ttc gca gaa tgc aat gat gaa agc ttc tgg    508
Glu Glu Glu Arg Arg Val Phe Ala Glu Cys Asn Asp Glu Ser Phe Trp
30 35 40
```

```
ttc aga tct gtg cct ttg gct gca aca agt atg ttg att act caa gga    556
Phe Arg Ser Val Pro Leu Ala Ala Thr Ser Met Leu Ile Thr Gln Gly
45 50 55 60
```

```
tta att agt aaa gga ata ctt tca agt cat ccc aaa tat ggt tcc atc    604
Leu Ile Ser Lys Gly Ile Leu Ser Ser His Pro Lys Tyr Gly Ser Ile
65 70 75
```

```
cct aaa ctt ata ctt gct tgt atc atg gga tac ttt gct gga aaa ctt    652
Pro Lys Leu Ile Leu Ala Cys Ile Met Gly Tyr Phe Ala Gly Lys Leu
80 85 90
```

```
tct tat gtg aaa act tgc caa gag aaa ttc aag aaa ctt gaa aat tcc    700
Ser Tyr Val Lys Thr Cys Gln Glu Lys Phe Lys Lys Leu Glu Asn Ser
95 100 105
```

```
ccc ctt gga gaa gct tta cga tca gga caa gca cga cga tct tca cca    748
Pro Leu Gly Glu Ala Leu Arg Ser Gly Gln Ala Arg Arg Ser Ser Pro
110 115 120
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cct g    752
Pro
125
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<210> 743

<211> 459

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 353..457

<221> misc_feature

<222> 438

<223> n=a, g, c or t
Oligonucleotide

<400> 743

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tcaaagtgat gctggtgtga caatataaca ttngaagctg ctccaaacaa ctttgactgt    120
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aagaaaatgg ccaagagaat acaagaggct ctaaccaagg actctgactt cactaagcca	180
ctgaaacatt cctggcacta cctacctcct gccttttcgt tatgggagga aaccctattg	240
gttaggtcac tggtttaaaa cacgtccttt aaattgcaga ggaagaaaag gcttggaggt	300
gataaaggaa tayagttcat tcccttsmtt atgggtgatgg tttcataggc at atg cat	358
	Met His
	1
atg tcc aaa ctc atc aac ttg tat aca tca rat atg tgc aat tta ctg	406
Met Ser Lys Leu Ile Asn Leu Tyr Thr Ser Xaa Met Cys Asn Leu Leu	
5 10 15	
tmt atc cac cty mtc tym ata agc tgt tta ant aat aat aar rta aca	454
Xaa Ile His Leu Xaa Xaa Ile Ser Cys Leu Xaa Asn Asn Lys Xaa Thr	
20 25 30	
tta cg	459
Leu	
35	

<210> 744
 <211> 411
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 79..411

<400> 744	
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gctgctctcg gcacaagc atg tac ggc aaa ggc aag agt aac agc agc gcc	111
Met Tyr Gly Lys Gly Lys Ser Asn Ser Ser Ala	
1 5 10	
gtc ccg tcc gac agc cag gcc cgg gag aag tta gca ctc tac gta tat	159
Val Pro Ser Asp Ser Gln Ala Arg Glu Lys Leu Ala Leu Tyr Val Tyr	
15 20 25	
gaa tat ctg ctc cat gta gga gct cag aaa tca gct caa aca ttt tta	207
Glu Tyr Leu Leu His Val Gly Ala Gln Lys Ser Ala Gln Thr Phe Leu	
30 35 40	
tca gag ata aga tgg gaa aaa aac atc aca ttg ggg gaa cca cca gga	255
Ser Glu Ile Arg Trp Glu Lys Asn Ile Thr Leu Gly Glu Pro Pro Gly	
45 50 55	
ttc tta cat tct tgg tgg tgt gta ttt tgg gat ctc tac tgt gca gct	303
Phe Leu His Ser Trp Trp Cys Val Phe Trp Asp Leu Tyr Cys Ala Ala	
60 65 70 75	
cca gag aga cgt gaa aca tgt gaa cac tca agt gaa gca aaa gcc ttc	351
Pro Glu Arg Arg Glu Thr Cys Glu His Ser Ser Glu Ala Lys Ala Phe	
80 85 90	
cat gat tac agt gct gca gca gct ccc agt cca gtg cta gga aac att	399
His Asp Tyr Ser Ala Ala Ala Ala Pro Ser Pro Val Leu Gly Asn Ile	
95 100 105	
ccc cca gga gat	411
Pro Pro Gly Asp	
110	

<210> 745
 <211> 404

<212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 83..403

<400> 745
 ctctggggcg gasggccacc atcttggaac gggaggcgga sagagtcgac tgggagcgac 60
 cgagcggggcc gccgccgccg cc atg aac ccc gaa tat gac tac ctg ttt aag 112
 Met Asn Pro Glu Tyr Asp Tyr Leu Phe Lys
 1 5 10
 ctg ctt ttg att ggc gac tca ggc gtg ggc aag tca tgc ctg ctc ctg 160
 Leu Leu Leu Ile Gly Asp Ser Gly Val Gly Lys Ser Cys Leu Leu Leu
 15 20 25
 cgg ttt gct gat gac acg tac aca gag agc tac atc agc acc atc ggg 208
 Arg Phe Ala Asp Asp Thr Tyr Thr Glu Ser Tyr Ile Ser Thr Ile Gly
 30 35 40
 gtg gac ttc aag atc cga acc atc gag ctg gat ggc aaa act atc aaa 256
 Val Asp Phe Lys Ile Arg Thr Ile Glu Leu Asp Gly Lys Thr Ile Lys
 45 50 55
 ctt cag atc tgg gac aca gcg ggc cag gaa cgg ttc cgg acc atc act 304
 Leu Gln Ile Trp Asp Thr Ala Gly Gln Glu Arg Phe Arg Thr Ile Thr
 60 65 70
 tcc agc tac tac cgg ggg gct cat ggc atc atc gtg gtg tat gac gtc 352
 Ser Ser Tyr Tyr Arg Gly Ala His Gly Ile Ile Val Val Tyr Asp Val
 75 80 85 90
 act gac cag gaa tcc tac gcc ary gtg aag cag tgg ctg cag gag att 400
 Thr Asp Gln Glu Ser Tyr Ala Xaa Val Lys Gln Trp Leu Gln Glu Ile
 95 100 105
 gac c 404
 Asp

<210> 746
 <211> 429
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 336..428

<221> misc_feature
 <222> 393
 <223> n=a, g, c or t
 Oligonucleotide

<400> 746
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 cgccgctatt accactgaac ccggaccccc taccaggtc cagggccagc cgccatgacg 120
 aacgtgtact ccttgatgg gattctggtg tttggtttgc tctttgtttg cacctgtgcc 180
 tacttcaaga aagtacctcg tctcaaaacc tggctgctat cagagaagaa ggggtgtttg 240
 ggtgtgtttt acaaagccgs tgtgattgga accaggctgc atgctgctgt ggcaattgct 300
 tgtgttgtaa tgggctttta cgtcctgttt ataaa atg aat tcc aaa gca scc 353

									Met	Asn	Ser	Lys	Ala	Xaa	
									1				5		
aag	tca	tca	act	gcc	aac	caa	ggg	gac	ggg	gat	gaa	gaa	nct	gtt	ggg
Lys	Ser	Ser	Thr	Ala	Asn	Gln	Gly	Asp	Gly	Asp	Glu	Glu	Xaa	Val	Gly
			10				15						20		
mga	mct	gaa	scc	agt	gta	gga	gag	ttc	a						
Arg	Xaa	Glu	Xaa	Ser	Val	Gly	Glu	Phe							
		25				30									

<210> 747
 <211> 179
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 35..178

<221> misc_feature
 <222> 140
 <223> n=a, g, c or t
 Oligonucleotide

<400> 747	
gaaatataca ataccttatg ttgtatatta catt atg ttg tat agt acg ttg aaa	55
	Met Leu Tyr Ser Thr Leu Lys
	1 5
cat aca cta caa tac gtt atc att aat tgt ggt cac cat gct gtg caa	103
His Thr Leu Gln Tyr Val Ile Ile Asn Cys Gly His His Ala Val Gln	
	10 15 20
aag atc tct aaa acg tat tcc tcc tgt ctg act gaa nyt ttg tat cct	151
Lys Ile Ser Lys Thr Tyr Ser Ser Cys Leu Thr Glu Xaa Leu Tyr Pro	
	25 30 35
ttg cct aat atc tcc cca atc cct cca c	179
Leu Pro Asn Ile Ser Pro Ile Pro Pro	
	40 45

<210> 748
 <211> 383
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 101..382

<400> 748	
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ctttggcgct ggttctctgtg ggcaacttgg acacgactcc atg aat gat gag gtt	115
	Met Asn Asp Glu Val
	1 5
aac cct aga aga gtt cta gag ctg atg ggt agt gaa gta act caa att	163
Asn Pro Arg Arg Val Leu Glu Leu Met Gly Ser Glu Val Thr Gln Ile	
	10 15 20

gct tgt ggc aga caa cat acc cta gsm ttc gtg cct tct tct gga ctc	211
Ala Cys Gly Arg Gln His Thr Leu Xaa Phe Val Pro Ser Ser Gly Leu	
25 30 35	
atc tat gca ttt ggt tgt gga gca aga ggt caa tta gga act ggg cac	259
Ile Tyr Ala Phe Gly Cys Gly Ala Arg Gly Gln Leu Gly Thr Gly His	
40 45 50	
act tgt aat gtt aag tgc cca tct cct gtc aag ggt tac tgg gct gcc	307
Thr Cys Asn Val Lys Cys Pro Ser Pro Val Lys Gly Tyr Trp Ala Ala	
55 60 65	
cac agt ggc cag ctt tca gcc cga gct gat cgc ttt aaa tat cat atc	355
His Ser Gly Gln Leu Ser Ala Arg Ala Asp Arg Phe Lys Tyr His Ile	
70 75 80 85	
gtt aag cag atc ttc tct gga gga gac c	383
Val Lys Gln Ile Phe Ser Gly Gly Asp	
90	

<210> 749
 <211> 446
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 381..446

<400> 749	
aacaatcaca gctccgggca ttgggggaac cssagccggc tgcgccgggg gaatccgtgc	60
gggcgccttc cgtcccggtc ccattcctcgc cgcgctccag cacctctgaa gttttgcagc	120
gccagaaaag gaggcgagga aggcaggag tgtgtgagag gagggagcaa aaagctcacc	180
ctaaaacatt tatttcaagg agaaaagaaa aagggggggc gcaaaaatgg ctggggcaat	240
tatagaaaac atgagcacca agaagctgtg cattgttggg gggattctgc tcgtgttcca	300
aatcatcgcc tttctggtgg gaggcttgat tgctccagg sccacaacgg cagtgtccta	360
catgtcgggtg aaatgtgtgg atg ccc gta aga acc atc aca aga caa aat ggt	413
Met Pro Val Arg Thr Ile Thr Arg Gln Asn Gly	
1 5 10	
tcg gtg cct tgg gga ccc aat cat tgt gac aag	446
Ser Val Pro Trp Gly Pro Asn His Cys Asp Lys	
15 20	

<210> 750
 <211> 410
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 129..410

<400> 750	
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agaaataact tgctggcttg tctggagtca catggtgaca atttacagaa agtcattctt	120
gcagcttg atg ggc gac aac cct ttt caa cca aaa agt aat tca aaa atg	170
Met Gly Asp Asn Pro Phe Gln Pro Lys Ser Asn Ser Lys Met	
1 5 10	

gca gaa ctg ttt atg gaa tgt gaa gaa gag gag ctg gaa cca tgg cag	218
Ala Glu Leu Phe Met Glu Cys Glu Glu Glu Glu Leu Glu Pro Trp Gln	
15 20 25 30	
aag aaa gta aaa gaa gtt gag gat gac gat gat gat gag cca atc ttt	266
Lys Lys Val Lys Glu Val Glu Asp Asp Asp Asp Asp Glu Pro Ile Phe	
35 40 45	
gtt ggc gag ata tca agt tca aaa cca gca att tca aat att ttg aac	314
Val Gly Glu Ile Ser Ser Ser Lys Pro Ala Ile Ser Asn Ile Leu Asn	
50 55 60	
aga gtt aac ccc agc tca tat tca agg gga cta aag aat ggt gca ctc	362
Arg Val Asn Pro Ser Ser Tyr Ser Arg Gly Leu Lys Asn Gly Ala Leu	
65 70 75	
agt cga ggt att act gct gca ttc aag cct aca agt caa cac tac acg	410
Ser Arg Gly Ile Thr Ala Ala Phe Lys Pro Thr Ser Gln His Tyr Thr	
80 85 90	

<210> 751
 <211> 536
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 334..534

<221> misc_feature
 <222> 148
 <223> n=a, g, c or t
 Oligonucleotide

<400> 751	
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tctcccaagg cagaggagat cgttgggttt caaggccccg cgggcatttc tcgccggccc	120
tgccggagaga gttcttcact accacaancm arggagggat atgataggcg gccagtggat	180
ataactcctt tagaaciaaag gaaattaact ttgtataccc atgcatttgt tcaggacttg	240
gaaactcatg gatttgacaa aacacaagca gaaacaattg tatcagcgtt aactgcttta	300
tcaaattgtca gcctggatac tatctataaa gag atg gtc act caa gct caa cag	354
Met Val Thr Gln Ala Gln Gln	
1 5	
gaa ata aca gta caa cag cta atg gct cat ttg gat gct atc agg aaa	402
Glu Ile Thr Val Gln Gln Leu Met Ala His Leu Asp Ala Ile Arg Lys	
10 15 20	
gac atg gtc atc cta gag aaa agt gaa ttt gca aat ctg aga gca gag	450
Asp Met Val Ile Leu Glu Lys Ser Glu Phe Ala Asn Leu Arg Ala Glu	
25 30 35	
aat gag aaa atg aaa att gaa tta gac caa gtt aag caa caa cta atg	498
Asn Glu Lys Met Lys Ile Glu Leu Asp Gln Val Lys Gln Gln Leu Met	
40 45 50 55	
cat gaa acc agt yga atc aga gca gat aat aaa ctg ga	536
His Glu Thr Ser Xaa Ile Arg Ala Asp Asn Lys Leu	
60 65	

<210> 752
 <211> 139

<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 25..138

<400> 752
cttgatctt tgggtgttacc ttaa atg aaa ttt gga aat gtt agg atg tya 51
Met Lys Phe Gly Asn Val Arg Met Xaa
1 5
tct att caa ata ttt att gtg tcc atc tgg agc ttc ttc ctt ttc tat 99
Ser Ile Gln Ile Phe Ile Val Ser Ile Trp Ser Phe Phe Leu Phe Tyr
10 15 20 25
ggc aag tat aca tat att aga ctg atc ttg tcc caa ggc c 139
Gly Lys Tyr Thr Tyr Ile Arg Leu Ile Leu Ser Gln Gly
30 35

<210> 753
<211> 193
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 87..191

<400> 753
tattacagag tttgcagact gaaagagagt ctagctaagg cttgctcctc ataccagga 60
tttgatctaa tccaacaagc ctttgt atg acc ttt gac ctc agt gtg ttc agt 113
Met Thr Phe Asp Leu Ser Val Phe Ser
1 5
act ttg tca gat cac ttt tac tca tca tca ttg tcc aat act gca agg 161
Thr Leu Ser Asp His Phe Tyr Ser Ser Ser Leu Ser Asn Thr Ala Arg
10 15 20 25
aat ctg tat att tgt tta ttt cat atc aca ca 193
Asn Leu Tyr Ile Cys Leu Phe His Ile Thr
30 35

<210> 754
<211> 395
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 310..393

<400> 754
cggcctcgca cttccggtgg ggagattccg gcctggagct cccagggccg agcagacctt 60
gggacctgtg agcgctgcat ccaattaacc atgggaaggg tcagcaccag ccaccagccc 120
cttaggtgag gactctgcct ggggctctgc tgatggttcc gaatcatgga gctgcagaga 180
gctcctccag cctggagacg ttcttggtga aagctgtggt ctaactccac cggctcttcc 240
tgcacattgt attcaagagg ggtgcctgcc cccgctgact caggagctcc ggtgctgcag 300

<400> 756
aagcctgact tcagcgctcc cactctcggc cgacaccct c atg gcc aac cgt tac 56
Met Ala Asn Arg Tyr
1 5
acc atg gat ctg act gcc atc tac gag agc ctc ctg tcg ctg agc cct 104
Thr Met Asp Leu Thr Ala Ile Tyr Glu Ser Leu Leu Ser Leu Ser Pro
10 15 20
gac gts acc ctc acc cac ttc gcc cac tgc aac ctc ca 142
Asp Val Thr Leu Thr His Phe Ala His Cys Asn Leu
25 30

<210> 757
<211> 362
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 158..361

<400> 757
atcttgtagg cggggacacg ccgaggtaac ttccagggtg cgccttcggt gtcttctcca 60
agctgtagtt ctacgtcccg acctccctat cataccacac tcttcagcga ccacgcaggc 120
actttcccg tccccagtat accataattg aagaaaa atg atg gaa gag agt gga 175
Met Met Glu Glu Ser Gly
1 5
ata gag aca aca cca cct ggg act cct cca cca aat cct gca ggg ctg 223
Ile Glu Thr Thr Pro Pro Gly Thr Pro Pro Pro Asn Pro Ala Gly Leu
10 15 20
gct gct act gct atg tct tct acc cct gtt cca tta gcg gca acc agt 271
Ala Ala Thr Ala Met Ser Ser Thr Pro Val Pro Leu Ala Ala Thr Ser
25 30 35
tct ttt tct tct cca aat gta tcc tcc atg gag tcc ttc cca cca ctc 319
Ser Phe Ser Ser Pro Asn Val Ser Ser Met Glu Ser Phe Pro Pro Leu
40 45 50
gca tac tct act cct cag ccg ccc ctt cct cct gtg agg cct t 362
Ala Tyr Ser Thr Pro Gln Pro Pro Leu Pro Pro Val Arg Pro
55 60 65

<210> 758
<211> 368
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 219..368

<221> misc_feature
<222> 317
<223> n=a, g, c or t
Oligonucleotide

<400> 758

gaagaaggct cttacagcat ggccgcccggg actgcagctg ccttagcgtt tttgagtcag 60
gagagccgaa cgcgggccgg gggtgtcggg ggcctacggg tcccggcccc ggtcactatg 120
gacagttttt tcttcggctg tgagctctcc ggccacaccc gctccttcac ctttaaggta 180
gaggaagagg atgatgcgga sacgtgctgg cactaacc atg ctc tgc ctc acc gag 236
Met Leu Cys Leu Thr Glu

1 5
gga gcc aaa gac gag tgt aat gtg gta gaa gtt gtg gcc cgg aac cat 284
Gly Ala Lys Asp Glu Cys Asn Val Val Glu Val Val Ala Arg Asn His
10 15 20

gac cat cag gag atc gca gtc cct gtg gcc aan ctc aag ctg tcc tgc 332
Asp His Gln Glu Ile Ala Val Pro Val Ala Xaa Leu Lys Leu Ser Cys
25 30 35

caa ccc atg ctc agt ctg gat gac ttc cag ctc caa 368
Gln Pro Met Leu Ser Leu Asp Asp Phe Gln Leu Gln
40 45 50

<210> 759

<211> 452

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 36..452

<400> 759

agctcgctgc gcaggcgcag tgagttcgac acacc atg ccg act gtc agc gtg 53
Met Pro Thr Val Ser Val
1 5

aag cgt gat ctg ctc ttc caa gcc ctg ggc cgc acc tac act gac gaa 101
Lys Arg Asp Leu Leu Phe Gln Ala Leu Gly Arg Thr Tyr Thr Asp Glu
10 15 20

gaa ttt gat gaa cta tgt ttt gaa ttt ggt ctg gag ctt gat gaa att 149
Glu Phe Asp Glu Leu Cys Phe Glu Phe Gly Leu Glu Leu Asp Glu Ile
25 30 35

aca tct gag aag gaa ata ata agt aaa gaa caa ggt aat gta aag gca 197
Thr Ser Glu Lys Glu Ile Ile Ser Lys Glu Gln Gly Asn Val Lys Ala
40 45 50

gca gga gcc tct gat gtt gtt ctt tac aaa att gac gtc cct gcc aat 245
Ala Gly Ala Ser Asp Val Val Leu Tyr Lys Ile Asp Val Pro Ala Asn
55 60 65 70

aga tat gat ctc ctg tgt ctg gaa gga ttg gtt cga gga ctt cag gtc 293
Arg Tyr Asp Leu Leu Cys Leu Glu Gly Leu Val Arg Gly Leu Gln Val
75 80 85

ttc aaa gaa agg ata aag gct cca gtg tat aaa ccg gta atg cct gat 341
Phe Lys Glu Arg Ile Lys Ala Pro Val Tyr Lys Arg Val Met Pro Asp
90 95 100

gga aaa atc cag aaa ttg att atc aca gaa gag aca gct aag ata cgt 389
Gly Lys Ile Gln Lys Leu Ile Ile Thr Glu Glu Thr Ala Lys Ile Arg
105 110 115

cct ttt gcg gta gca gca gtt ctc cgt aat ata aag ttt act aaa gat 437
Pro Phe Ala Val Ala Ala Val Leu Arg Asn Ile Lys Phe Thr Lys Asp
120 125 130

cga tat gac agc ttc
Arg Tyr Asp Ser Phe
135

452

<210> 760
<211> 295
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 83..295

<400> 760
aagctgctggt tcgaaaatss tgacagcaca gggcttcctg ggctctgcag agcaaactgg 60
aaagagctgg gatccaggca ct atg ttc tct gaa gaa ctg tgg ctg gaa aat 112
Met Phe Ser Glu Glu Leu Trp Leu Glu Asn
1 5 10
gag aaa aag tgt gct gtg gtt cgg aag tct aag cag ggc agg aaa cgc 160
Glu Lys Lys Cys Ala Val Val Arg Lys Ser Lys Gln Gly Arg Lys Arg
15 20 25
caa gaa ctg ctg gcc gta gcc ttc ggg gtg aag gtc cac acg ttc cga 208
Gln Glu Leu Leu Ala Val Ala Phe Gly Val Lys Val His Thr Phe Arg
30 35 40
ggc cca cac tgg tgt gaa tat tgt gcc aat ttc atg tgg ggg ctc atc 256
Gly Pro His Trp Cys Glu Tyr Cys Ala Asn Phe Met Trp Gly Leu Ile
45 50 55
gcc caa ggg gtc cgg tgc tca gac tgt gga ttg aac gta 295
Ala Gln Gly Val Arg Cys Ser Asp Cys Gly Leu Asn Val
60 65 70

<210> 761
<211> 212
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 124..210

<400> 761
ttggccattt tattcctttg gctttgattt gtgaactata tccaagactc attggagtaa 60
tagttaactg attgcagtgg atttcgaggt gtggcaacta gtggcaatgc tcatgcgaca 120
gtg atg gtg gtt ttc atg aca tat gta act tta ccc ttt ttt ttt tct 168
Met Val Val Phe Met Thr Tyr Val Thr Leu Pro Phe Phe Phe Ser
1 5 10 15
ttc atc tct tcc ctt ctt tca ttt ttt ttt ctt ttt cta ctc tc 212
Phe Ile Ser Ser Leu Leu Ser Phe Phe Phe Leu Phe Leu Leu
20 25

<210> 762
<211> 623
<212> DNA
<213> Homo sapiens

<220>
 <221> CDS
 <222> 474..623

<400> 762
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 gatgactttt aagctttcat atgccgttat ttaataacctg tcacttccaa atgagagatg 120
 taagggcaac ggccgttagc gttctgwttt ggatcaggct ctggagtgga cgcccctagc 180
 ttaggggtcc ttctaggcag ccagaaacct gcggaaaatg gtagcgatgg cggctgggcc 240
 gagtgggtgt ctggtgccgg cgtttgggct acggttggtg ttggcgactg tgcttcaagc 300
 ggtgtctgct tttggggcag agttttcatc ggaggcatgc agagagttrg gcttttctag 360
 caacttgctt tgcagctctt gtgatcttct cggacagttc aacctgcttc agctggatcc 420
 tgattgcaga ggatgstgtc aggaggaagc acaatttgaa accaaaaagc tgt atg 476
 Met
 1
 cag gag cta ttc ttg aag ttt gtg gat gaa aat tgg gaa ggt tcc ctc 524
 Gln Glu Leu Phe Leu Lys Phe Val Asp Glu Asn Trp Glu Gly Ser Leu
 5 10 15
 aag tcc aag tat gtc cgt ggt tca gac cct gta tta aag ctt ttg gac 572
 Lys Ser Lys Tyr Val Arg Gly Ser Asp Pro Val Leu Lys Leu Leu Asp
 20 25 30
 gac aat ggg aac att gct gaa gaa ctg agc att ctc aaa tgg aca cag 620
 Asp Asn Gly Asn Ile Ala Glu Glu Leu Ser Ile Leu Lys Trp Thr Gln
 35 40 45
 aca 623
 Thr
 50

<210> 763
 <211> 261
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 58..261

<400> 763
 gacatccacg gggcgcgagt gacacgcggg agggagagca gtgttctgct ggagccg 57
 atg cca aaa acc atg cat ttc tta ttc aga ttc att gtt ttc ttt tat 105
 Met Pro Lys Thr Met His Phe Leu Phe Arg Phe Ile Val Phe Phe Tyr
 1 5 10 15
 ctg tgg ggc ctt ttt act gct cag aga caa aag aaa gag gag agc acc 153
 Leu Trp Gly Leu Phe Thr Ala Gln Arg Gln Lys Lys Glu Glu Ser Thr
 20 25 30
 gaa gaa gtg aaa ata gaa gtt ttg cat cgt cca gaa aac tgc tct aag 201
 Glu Glu Val Lys Ile Glu Val Leu His Arg Pro Glu Asn Cys Ser Lys
 35 40 45
 aca agc aag aag gga gac cta cta aat gcc cat tat gac ggc tac ctg 249
 Thr Ser Lys Lys Gly Asp Leu Leu Asn Ala His Tyr Asp Gly Tyr Leu
 50 55 60
 gct aaa gac ggc 261
 Ala Lys Asp Gly

65

<210> 764
<211> 160
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 4..159

<400> 764
agt atg ctt gag gaa ttg aaa gct ggc cag gag ttg gag gaa cag acc 48
Met Leu Glu Glu Leu Lys Ala Gly Gln Glu Leu Glu Glu Gln Thr
1 5 10 15
att agc cac ggc ttt gca cgt ggt gtg agg agg ggt gtg gct att gtg 96
Ile Ser His Gly Phe Ala Arg Gly Val Arg Arg Gly Val Ala Ile Val
20 25 30
ggc aag ggt ctg gaa tgg cat ggg tgt tgg tgg atg tgc cac gga tac 144
Gly Lys Gly Leu Glu Trp His Gly Cys Trp Trp Met Cys His Gly Tyr
35 40 45
agg att cta gcc ggg a 160
Arg Ile Leu Ala Gly
50

<210> 765
<211> 516
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 404..514

<400> 765
aagaaagaga gaggcaagcg aaattcctga atggatagac agatgctacg tcatcggagc 60
tgcatcctcc actccacaag aggctaggag ctggggggag agaggcagtc cagccgcagg 120
gccacccgaa cagtctctcc tcctcacaga agcctggagc tgggcatcca agaagaagca 180
gcctcatttg ttttctggtg tcatcgtagg tggccaccta tggcttttgg gcttctcacc 240
tggggcgggg gggttctgca ccacctccc accctccttc ctccgtgtgg acgatagagc 300
cacatccagc accacggaca gctcccgggc gaccaaagag aagaatgtac ttcattctgt 360
tgggctggat tccctctgat aagccttccc agttgactga aag atg agg cta ggc 415
Met Arg Leu Gly
1
tct agc aag ttg aag tca aac cag ctc ctt caa gaa gct ttg agc aga 463
Ser Ser Lys Leu Lys Ser Asn Gln Leu Leu Gln Glu Ala Leu Ser Arg
5 10 15 20
atg aag tgg gga gga ccc agc ttc cag ccc agg aag ccc act gta cct 511
Met Lys Trp Gly Gly Pro Ser Phe Gln Pro Arg Lys Pro Thr Val Pro
25 30 35
gga gc 516
Gly

<210> 766

<211> 626
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 68..238

<221> sig_peptide
 <222> 68..106
 <223> Von Heijne matrix
 score 15
 seq MLLLLLLLPLALG/DK

<221> misc_feature
 <222> 529
 <223> n=a, g, c or t
 Oligonucleotide

<400> 766
 agtttctgag agaagaaccc tgaggaacag acgttccttg gcggccctgg cgccttcaaa 60
 cccagac atg ctg ctg ctg ctg ctg ctg ctg ccc ctt gct ctg ggg gac 109
 Met Leu Leu Leu Leu Leu Leu Leu Pro Leu Ala Leu Gly Asp ,
 -10 -5 1
 aaa ggg gat gga ggg aga cag aca ata tgg gga tgg tta ctt gct gca 157
 Lys Gly Asp Gly Gly Arg Gln Thr Ile Trp Gly Trp Leu Leu Ala Ala
 5 10 15
 agt gca gga gct ggt gac ggt gca gga ggg cct gtg tgt cca tgt gcc 205
 Ser Ala Gly Ala Gly Asp Gly Ala Gly Gly Pro Val Cys Pro Cys Ala
 20 25 30
 ctg ctc ctt ctc cta ccc cca gga tgg ctg gac tgactctgac ccagttcatg 258
 Leu Leu Leu Leu Leu Pro Pro Gly Trp Leu Asp
 35 40
 gctactggtt ccgggcaggg aatgatataa gctggaaggc tccagtggcc acaaacaacc 318
 cagcttgggc agtgcaggag gaaactcggg accgattcca mctycyttgg ggaccacacag 378
 accaaaaatt gcactctgag catcagagat gccagaatga gtgatgcggg gagatacttc 438
 tttcgtatgg agaaaggaaa tataaaatgg aattataaat atgaccagct ctctgtgaac 498
 gtgayagcct tgaccacacag gcccaacats nktatccccg gtaccctgga gtctggctgc 558
 ttccagaatc tgacctgctc tgtgccctgg gcctgtgagc aggggacgcc ccctatgatc 618
 tcctggat 626

<210> 767
 <211> 473
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 60..344

<221> sig_peptide
 <222> 60..113
 <223> Von Heijne matrix
 score 10.3000001907349

seq VLMLAALLLHCYA/DS

<400> 767

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acagcaactt ccttgatccc tgccacgcac gactgaacac agacagcagc cgcctcgcc      59
atg aag ctg ctg atg gtc ctc atg ctg gcg gcc ctc ctc ctg cac tgc      107
Met Lys Leu Leu Met Val Leu Met Leu Ala Ala Leu Leu Leu His Cys
          -15          -10          -5
tat gca gat tct ggc tgc aaa ctc ctg gag gac atg gtt gaa aag acc      155
Tyr Ala Asp Ser Gly Cys Lys Leu Leu Glu Asp Met Val Glu Lys Thr
          1          5          10
atc aat tcc gac ata tct ata cct gaa tac aaa gag ctt ctt caa gag      203
Ile Asn Ser Asp Ile Ser Ile Pro Glu Tyr Lys Glu Leu Leu Gln Glu
15          20          25          30
ttc ata gac agt gat gcc gct gca gag gct atg ggg aaa ttc aag cag      251
Phe Ile Asp Ser Asp Ala Ala Ala Glu Ala Met Gly Lys Phe Lys Gln
          35          40          45
tgt ttc ctc aac cag tca cat aga act ctg aaa aac ttt gga ctg atg      299
Cys Phe Leu Asn Gln Ser His Arg Thr Leu Lys Asn Phe Gly Leu Met
          50          55          60
atg cat aca gtg tac gac agc att tgg tgt aat atg aag agt aat      344
Met His Thr Val Tyr Asp Ser Ile Trp Cys Asn Met Lys Ser Asn
          65          70          75
taactttacc caaggcgttt ggctcagagg gctacagact atggccagaa ctcatctgtt      404
gattgctaga aaccactttt ctttcttggt ttgtctkttt atgwggaam tgctagacaa      464
ctgttgaaa      473

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<210> 768

<211> 673

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 218..502

<221> sig_peptide

<222> 218..310

<223> Von Heijne matrix

score 9.19999980926514

seq RLLLATVQLQAVSA/FG

<400> 768

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agtggggagt ttaggcaagt gcctgatttg ggtaatcgaa agcaccagc gattgtattt      60
gatgactttt aagctttcat atgccgttat ttaataacctg tcacttccaa atgagagatg      120
taagggaac ggccgtagc gttctgwttt ggatcaggct ctggagtga cgcccctagc      180
ttaggggtcc ttctaggcag ccagaaacct gcggaaa atg gta gcg atg gcg gct      235
          Met Val Ala Met Ala Ala
          -30
ggg ccg agt ggg tgt ctg gtg ccg gcg ttt ggg cta ccg ttg ttg ttg      283
Gly Pro Ser Gly Cys Leu Val Pro Ala Phe Gly Leu Arg Leu Leu Leu
-25          -20          -15          -10
gcg act gtg ctt caa gcg gtg tct gct ttt ggg gca gag ttt tca tcg      331
Ala Thr Val Leu Gln Ala Val Ser Ala Phe Gly Ala Glu Phe Ser Ser
          -5          1          5

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gag gca tgc aga gag tta ggc ttt tct agc aac ttg ctt tgc agc tct	379
Glu Ala Cys Arg Glu Leu Gly Phe Ser Ser Asn Leu Leu Cys Ser Ser	
10 15 20	
tgt gat ctt ctc gga cag ttc aac ctg ctt cag ctg gat cct gat tgc	427
Cys Asp Leu Leu Gly Gln Phe Asn Leu Leu Gln Leu Asp Pro Asp Cys	
25 30 35	
aga gga tgc tgt cag gag gaa gca caa ttt gaa acc aaa aag ctg tat	475
Arg Gly Cys Cys Gln Glu Glu Ala Gln Phe Glu Thr Lys Lys Leu Tyr	
40 45 50 55	
gca gga gct att ctt gaa gtt tgt gga tgaaaattgg gaaggttccc	522
Ala Gly Ala Ile Leu Glu Val Cys Gly	
60	
tcaagtccaa gcttttgtta ggagtgataa acccaaactg ttcagaggac tgcaaatcaa	582
gtatgtccgt ggttcagacc ctgtattaaa gcttttggac gacaatggga acattgctga	642
agaactgagc atttctcaaat ggacacagac a	673

<210> 769

<211> 539

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 190..492

<221> sig_peptide

<222> 190..285

<223> Von Heijne matrix
score 8.80000019073486
seq VPMLLLIVGGSFG/LR

<221> misc_feature

<222> 500..501

<223> n=a, g, c or t
Oligonucleotide

<400> 769

acaagtatgt tacgatggct cgattgcttt tgcctagcgg aaaccattca ctaaggaccg	60
agcaccaaat aaccaaggaa aaggaagtga gttaaggacg tactcgtctt ggtgagagcg	120
tgagctgctg agatttggga gtctgcgcta ggcccgttg gagttctgag ccgatggaag	180
agttcactc atg ttt gca ccc gcg gtg atg cgt gct ttt cgc aag aac aag	231
Met Phe Ala Pro Ala Val Met Arg Ala Phe Arg Lys Asn Lys	
-30 -25 -20	
act ctc ggc tat gga gtc ccc atg ttg ttg ctg att gtt gga ggt tct	279
Thr Leu Gly Tyr Gly Val Pro Met Leu Leu Leu Ile Val Gly Gly Ser	
-15 -10 -5	
ttt ggt ctt cgt gag ttt tct caa atc cga tat gat gct gtg aag agt	327
Phe Gly Leu Arg Glu Phe Ser Gln Ile Arg Tyr Asp Ala Val Lys Ser	
1 5 10	
aaa atg gat cct gag ctt gaa aaa aaa ctg aaa gag aat aaa ata tct	375
Lys Met Asp Pro Glu Leu Glu Lys Lys Leu Lys Glu Asn Lys Ile Ser	
15 20 25 30	
tta gag tcg gaa tat gag aaa atc aaa gac tcc aag ttt gat gac tgg	423
Leu Glu Ser Glu Tyr Glu Lys Ile Lys Asp Ser Lys Phe Asp Asp Trp	

	35	40	45	
aag aat att cga gga ccc agg cct tgg gaa gat cct gac ctc ctc caa				471
Lys Asn Ile Arg Gly Pro Arg Pro Trp Glu Asp Pro Asp Leu Leu Gln				
	50	55	60	
gga aag aaa tcc aga aag cct taagacannng acaacttgac tctgctgatt				522
Gly Lys Lys Ser Arg Lys Pro				
	65			
cttttttcct ttttttt				539

<210> 770
 <211> 479
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 124..468

<221> sig_peptide
 <222> 124..276
 <223> Von Heijne matrix
 score 8.10000038146973
 seq VCLCGTFCFPCLG/CQ

<400> 770	
aagttacctc tcccctttca cgtarttttc atttgtgggtg agattctctc ccaggccaca	60
agacatttcc tgctcggaac ctgttttact aatttccact gcttttaagg ccctgcactg	120
aaa atg caa gct cag gcg ccg gtg gtc gtt gtg acc caa cct gga gtc	168
Met Gln Ala Gln Ala Pro Val Val Val Val Thr Gln Pro Gly Val	
-50 -45 -40	
ggt ccc ggt ccg gcc ccc cag aac tcc aac tgg cag aca ggc atg tgt	216
Gly Pro Gly Pro Ala Pro Gln Asn Ser Asn Trp Gln Thr Gly Met Cys	
-35 -30 -25	
gac tgt ttc agc gac tgc gga gtc tgt ctc tgt ggc aca ttt tgt ttc	264
Asp Cys Phe Ser Asp Cys Gly Val Cys Leu Cys Gly Thr Phe Cys Phe	
-20 -15 -10 -5	
ccg tgc ctt ggg tgt caa gtt gca gct gat atg aat gaa tgc tgt ctg	312
Pro Cys Leu Gly Cys Gln Val Ala Ala Asp Met Asn Glu Cys Cys Leu	
1 5 10	
tgt gga aca agc gtc gca atg agg act ctc tac agg acc cga tat ggc	360
Cys Gly Thr Ser Val Ala Met Arg Thr Leu Tyr Arg Thr Arg Tyr Gly	
15 20 25	
atc cct gga tct att tgt gat gac tat atg gca act ctt tgc tgt cct	408
Ile Pro Gly Ser Ile Cys Asp Asp Tyr Met Ala Thr Leu Cys Cys Pro	
30 35 40	
cat tgt act ctt tgc caa atc aag aga gat atc aac aga agg aga gcc	456
His Cys Thr Leu Cys Gln Ile Lys Arg Asp Ile Asn Arg Arg Arg Ala	
45 50 55 60	
atg cgt act ttc taaaaactga t	479
Met Arg Thr Phe	

<210> 771
 <211> 492
 <212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 25..402

<221> sig_peptide

<222> 25..96

<223> Von Heijne matrix

score 7

seq LLCCFRALSGSLS/MR

<221> misc_feature

<222> 371

<223> n=a, g, c or t

Oligonucleotide

<400> 771

agsgctggccc tccctctttc caaa atg gac aag tcc ctc ttg ctg gaa ctc 51
Met Asp Lys Ser Leu Leu Leu Glu Leu

-20

ccc atc ctg ctc tgc tgc ttt agg gca tta tct gga tca ctt tca atg 99
Pro Ile Leu Leu Cys Cys Phe Arg Ala Leu Ser Gly Ser Leu Ser Met
-15 -10 -5 1

aga aat gat gca gtc aat gaa ata gtt gct gtg aaa aac aat ttt cct 147
Arg Asn Asp Ala Val Asn Glu Ile Val Ala Val Lys Asn Asn Phe Pro
5 10 15

gtg ata gaa att gtt cgg tgt agg atg tgc cac ctc cag ttc cca gga 195
Val Ile Glu Ile Val Arg Cys Arg Met Cys His Leu Gln Phe Pro Gly
20 25 30

gaa aag tgc tcc aga gga aga gga ata tgc aca gca aca aca gaa gag 243
Glu Lys Cys Ser Arg Gly Arg Gly Ile Cys Thr Ala Thr Thr Glu Glu
35 40 45

gcc tgc atg gtt gga agg atg ttc aaa agg gat ggt aat ccc tgg tta 291
Ala Cys Met Val Gly Arg Met Phe Lys Arg Asp Gly Asn Pro Trp Leu
50 55 60 65

acc ttc atg ggc tgc cta aag aac tgt gct gat gtg aaa ggc ata agg 339
Thr Phe Met Gly Cys Leu Lys Asn Cys Ala Asp Val Lys Gly Ile Arg
70 75 80

tgg agt gtc tat ttg gtg aac ttc agg tgc tnm agg agc cat gac ctg 387
Trp Ser Val Tyr Leu Val Asn Phe Arg Cys Xaa Arg Ser His Asp Leu
85 90 95

tgc aat gaa gac ctt tagaagttaa tgggtcttct gtgactccaa tttctgggtg 442
Cys Asn Glu Asp Leu
100

aggttggtgc ctcagcctct tcacaatgac tttctaaaaa aatcacacac 492

<210> 772

<211> 396

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 7..312

<221> sig_peptide

<222> 7..54

<223> Von Heijne matrix

score 6.80000019073486

seq LWILPSLWLLLLG/GP

<400> 772

agcaag atg gat cta ctg tgg atc ctg ccc tcc ctg tgg ctt ctc ctg 48
Met Asp Leu Leu Trp Ile Leu Pro Ser Leu Trp Leu Leu Leu
-15 -10 -5
ctt ggg ggg cct gcc tgc ctg aag acc cag gaa cac ccc agc tgc cca 96
Leu Gly Gly Pro Ala Cys Leu Lys Thr Gln Glu His Pro Ser Cys Pro
1 5 10
gga ccc agg gaa ctg gaa gcc agc aaa gtt gtc ctc ctg ccc agt tgt 144
Gly Pro Arg Glu Leu Glu Ala Ser Lys Val Val Leu Leu Pro Ser Cys
15 20 25 30
ccc gga gct cca gga agt cct ggg gag aag gga gcc cca ggt cct caa 192
Pro Gly Ala Pro Gly Ser Pro Gly Glu Lys Gly Ala Pro Gly Pro Gln
35 40 45
ggg cca cct gga cca cca ggc aag atg ggc ccc aag ggt gag cca gga 240
Gly Pro Pro Gly Pro Pro Gly Lys Met Gly Pro Lys Gly Glu Pro Gly
50 55 60
gat cca gtg aac ctg ctc cgg tgc cag gaa ggc ccc aga aac tgc cgg 288
Asp Pro Val Asn Leu Leu Arg Cys Gln Glu Gly Pro Arg Asn Cys Arg
65 70 75
gag ctg ttg agc agg gcg cca cct tgagcggctg gtamcatctg tgcctacctg 342
Glu Leu Leu Ser Arg Ala Pro Pro
80 85
agggcagggc ctcccagtct tttgtgacat ggacaccgag gggggcggct ggct 396

<210> 773

<211> 417

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 50..229

<221> sig_peptide

<222> 50..106

<223> Von Heijne matrix

score 6.59999990463257

seq SAVVLPSTPQASA/NP

<221> misc_feature

<222> 206,354

<223> n=a, g, c or t

Oligonucleotide

<400> 773

acaggatcga tttacggycg cagagaaaaa ccaagatttc actttcaag atg gaa agt 58

40	45	50	55	
tac aag ggc cga gtt act ctg aga gca ata ccc acg caa gaa tct gtt				413
Tyr Lys Gly Arg Val Thr Leu Arg Ala Ile Pro Thr Gln Glu Ser Val				
	60	65	70	
cct agt gga ggt aac aca gct gac aga aag tgacagcgga g				454
Pro Ser Gly Gly Asn Thr Ala Asp Arg Lys				
	75	80		

<210> 775
 <211> 531
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 8..253

<221> sig_peptide
 <222> 8..109
 <223> Von Heijne matrix
 score 6.19999980926514
 seq MAVLAPLIALVYS/XP

<400> 775	
agtcgtt atg gtg ggg gag gcg ggg cga gac cta cga cgc cgg cga gca	49
Met Val Gly Glu Ala Gly Arg Asp Leu Arg Arg Arg Arg Ala	
	-30 -25
gtg gcc gtt acg gcc gaa aag atg gcg gtc ttg gca cct cta att gct	97
Val Ala Val Thr Ala Glu Lys Met Ala Val Leu Ala Pro Leu Ile Ala	
	-20 -15 -10 -5
ctc gtg tat tcg gys ccg cga ctt tca cga tgg ctc gcc caa cct tac	145
Leu Val Tyr Ser Xaa Pro Arg Leu Ser Arg Trp Leu Ala Gln Pro Tyr	
	1 5 10
tac ctt ctg tcg scc ctg ctc tct gmt gcc ttc cta ctc gtg agg maa	193
Tyr Leu Leu Ser Xaa Leu Leu Ser Xaa Ala Phe Leu Leu Val Arg Xaa	
	15 20 25
ctg ccg ccg ctc tgc cac ggt ctg ccc acc caa cgc gaa smc ggt aac	241
Leu Pro Pro Leu Cys His Gly Leu Pro Thr Gln Arg Glu Xaa Gly Asn	
	30 35 40
ccg tcr wsa ytt tgactgggtg agcctccgc gtgtagtac cccgcgacsk	293
Pro Ser Xaa Xaa	
45	
tgactgtscg tgcccttgca ggtgtatctg ggaaccctgg ggtttacctc tctgaggaca	353
cctgaggttc cgagcctgta gcggacttag agactattaw ktgcagggtc cgaaccatca	413
tcgagtctaa actttgtgtt taagatggga aaacggaaca tgtagtcgt agcccatgca	473
caacggccca acagcttttg actgttgagt ccaggtttct ttctgtttca ccattgag	531

<210> 776
 <211> 368
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS

<222> 220..363

<221> sig_peptide

<222> 220..270

<223> Von Heijne matrix
score 6
seq WLSCFLLPALVVS/VA

<221> misc_feature

<222> 201

<223> n=a, g, c or t
Oligonucleotide

<400> 776

agagggtgcc	cacctgtgtg	ccagcgccctg	tccggcgccct	gcctgccgcc	tccgtggcga	60
aggggacaca	gaaatactca	ctgagcctac	actgggctca	gcctgtgctt	ggtcctgggg	120
tcacaaaggt	gcatcagacg	cagaccttgc	cctcacatct	cttctggcct	ggtagggagag	180
gctcatctgc	aaagagataa	ngaggtcctt	gcggatgtg	atg gcc cag	cta tgg	234
				Met Ala Gln	Leu Trp	
				-15		
ctg tcc tgc	ttc ctc ctt	cct gcc ctc	gtg gtg tct	gtg gca gcc	aac	282
Leu Ser Cys	Phe Leu Leu	Pro Ala Leu	Val Val Ser	Val Ala Ala	Asn	
	-10	-5	1			
gtg gcc cck	wag ttc cta	gcc aac atg	acg tca gtg	atc ctg cct	gag	330
Val Ala Pro	Xaa Phe Leu	Ala Asn Met	Thr Ser Val	Ile Leu Pro	Glu	
5	10	15	20			
gac tgc ctg	tgg gtg ccc	agg cct tct	ggg tgg tagcg			368
Asp Cys Leu	Trp Val Pro	Arg Pro Ser	Gly Trp			
	25	30				

<210> 777

<211> 469

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 8..322

<221> sig_peptide

<222> 8..109

<223> Von Heijne matrix
score 5.90000009536743
seq MAVLAPLIALVYS/VP

<221> misc_feature

<222> 233,352

<223> n=a, g, c or t
Oligonucleotide

<400> 777

agtcggtt	atg gtg ggg	gag gcg ggg	cga gac cta	cga cgc cgg	cga gca	49
	Met Val Gly	Glu Ala Gly	Arg Asp Leu	Arg Arg Arg	Ala	
	-30	-25				

gtg gcc gtt acg gcc gaa aag atg gcg gtc ttg gca cct cta att gct	97
Val Ala Val Thr Ala Glu Lys Met Ala Val Leu Ala Pro Leu Ile Ala	
-20 -15 -10 -5	
ctc gtg tat tcg gtg ccg cga ctt tca cga tgg ctc gcc caa cct tac	145
Leu Val Tyr Ser Val Pro Arg Leu Ser Arg Trp Leu Ala Gln Pro Tyr	
1 5 10	
tac ctt ctg tcg gcc ctg ctc tct gct gcc ttc cta ctc gtg agg aaa	193
Tyr Leu Leu Ser Ala Leu Leu Ser Ala Ala Phe Leu Leu Val Arg Lys	
15 20 25	
ctg ccg ccg ctc tgc cac ggt ctg ccc acc caa cgc gar nac ggt aac	241
Leu Pro Pro Leu Cys His Gly Leu Pro Thr Gln Arg Glu Xaa Gly Asn	
30 35 40	
ccg tgt gac ttt gac tgg aga gaa gtg gag atc ctg atg ttt ctc agt	289
Pro Cys Asp Phe Asp Trp Arg Glu Val Glu Ile Leu Met Phe Leu Ser	
45 50 55 60	
gcc att gtg atg atg aag aac cgc aga tcc agc tgaatttgaa cttggacttc	342
Ala Ile Val Met Met Lys Asn Arg Arg Ser Ser	
65 70	
tatcccytmn gwgctctccta tttcaaagt ccccatgaag agggacaaaag aatgggatat	402
aggagtgcac agcccagcct gacctgtgac atctctgtgt ttcagtcact gtggagcaac	462
atatagg	469

<210> 778
 <211> 468
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 77..340

<221> sig_peptide
 <222> 77..133
 <223> Von Heijne matrix
 score 5.90000009536743
 seq AFLVCLAFSLATL/VQ

<400> 778	
agctcckcct cggcctcccc ttcgggagct ctgcgcgctaa ctgtgctcct ccggggccct	60
ccgcctgctc ccagcc atg gtg gcc tgg cgc tcg gcg ttc ctt gtc tgc ctc	112
Met Val Ala Trp Arg Ser Ala Phe Leu Val Cys Leu	
-15 -10	
gct ttc tcc ttg gcc acc ctg gtc cag cga gga tct ggg gac ttt gat	160
Ala Phe Ser Leu Ala Thr Leu Val Gln Arg Gly Ser Gly Asp Phe Asp	
-5 1 5	
gat ttt aac ctg gag gat gca gtg aaa gaa act tcc tca gta aag cag	208
Asp Phe Asn Leu Glu Asp Ala Val Lys Glu Thr Ser Ser Val Lys Gln	
10 15 20 25	
cca tgg gac cac acc acc acc acc aca acc aat agg cca gga acc acc	256
Pro Trp Asp His Thr Thr Thr Thr Thr Thr Asn Arg Pro Gly Thr Thr	
30 35 40	
aga gct ccg gca aaa cct cca ggt agt gga ttg gac ttg gct gat gct	304
Arg Ala Pro Ala Lys Pro Pro Gly Ser Gly Leu Asp Leu Ala Asp Ala	
45 50 55	

ttg gat gat caa gat gat ggc cgc aga aac cgg gta taggaggaag 350
 Leu Asp Asp Gln Asp Asp Gly Arg Arg Asn Arg Val
 60 65

agagagatgg aaccatgtaa ccaccacgac caagaggcca gtaaccacca gagctccagc 410
 aaatacttta ggaaatgatt ttgacttggc tgatgcctgg atgatcgaaa tgatcgag 468

<210> 779
 <211> 479
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 73..429

<221> sig_peptide
 <222> 73..231
 <223> Von Heijne matrix
 score 5.80000019073486
 seq ILSLQVLLTTVTS/TV

<400> 779
 gctctctcgc ggaastgggg aggaggcggg tgccggttagt ggaccggggac cggtaggggt 60
 gctgttgcca tc atg gct gac ccc gac ccc cgg tac cct cgc tcc tcg atc 111
 Met Ala Asp Pro Asp Pro Arg Tyr Pro Arg Ser Ser Ile
 -50 -45

gag gac gac ttc aac tat ggc agc agc gtg gcc tcc gcc acc gtg cac 159
 Glu Asp Asp Phe Asn Tyr Gly Ser Ser Val Ala Ser Ala Thr Val His
 -40 -35 -30 -25

atc cga atg gcc ttt ctg aga aaa gtc tac agc att ctt tct ctg cag 207
 Ile Arg Met Ala Phe Leu Arg Lys Val Tyr Ser Ile Leu Ser Leu Gln
 -20 -15 -10

gtt ctc tta act aca gtg act tca aca gtt ttt tta tac ttt gag tct 255
 Val Leu Leu Thr Thr Val Thr Ser Thr Val Phe Leu Tyr Phe Glu Ser
 -5 1 5

gta cgg aca ttt gta cat gag agt cct gcc tta att ttg ctg ttt gcc 303
 Val Arg Thr Phe Val His Glu Ser Pro Ala Leu Ile Leu Leu Phe Ala
 10 15 20

ctc gga tct ctg ggt ttg att ttt gcg ttg ayt tta aac aga cat aag 351
 Leu Gly Ser Leu Gly Leu Ile Phe Ala Leu Xaa Leu Asn Arg His Lys
 25 30 35 40

tat ccc ctt aac ctg tac cta ctt ttt gga ttt acg ctg ttg gaa gct 399
 Tyr Pro Leu Asn Leu Tyr Leu Leu Phe Gly Phe Thr Leu Leu Glu Ala
 45 50 55

ctg act gtg gca gtt gtc gtt act gtt cta tgatgtatat attattctgc 449
 Leu Thr Val Ala Val Val Val Thr Val Leu
 60 65

aagctttcat actgactact acagtatttt 479

<210> 780
 <211> 504
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 112..423

<221> sig_peptide
 <222> 112..276
 <223> Von Heijne matrix
 score 5.59999990463257
 seq ELCCLFCCPPCPG/KI

<400> 780
 agtttcttcc gggtcattga cagaagcgtc aattcctggg agtagttcgt tggttttctt 60
 tccccctcatc cttttgcctg ctcccggcga ggggtggcct tgatttcggc g atg agc 117
 Met Ser
 -55
 tcc cag aaa ggc aac gtg gct cgt tcc aga cct cag aag cac cag aat 165
 Ser Gln Lys Gly Asn Val Ala Arg Ser Arg Pro Gln Lys His Gln Asn
 -50 -45 -40
 acg ttt agc ttc aaa aat gac aag ttc gat aaa agt gtg cag acc aag 213
 Thr Phe Ser Phe Lys Asn Asp Lys Phe Asp Lys Ser Val Gln Thr Lys
 -35 -30 -25
 agc atg aat aat ctt tca ttt agt gag cta tgt tgc ctc ttc tgc tgt 261
 Ser Met Asn Asn Leu Ser Phe Ser Glu Leu Cys Cys Leu Phe Cys Cys
 -20 -15 -10
 cca cct tgt cca ggg aag att gct tca aaa tta gcg ttt ttg cca cct 309
 Pro Pro Cys Pro Gly Lys Ile Ala Ser Lys Leu Ala Phe Leu Pro Pro
 -5 1 5 10
 gat cca act tac aca ctg atg tgt gat gaa agc gga agc gtt gga ctt 357
 Asp Pro Thr Tyr Thr Leu Met Cys Asp Glu Ser Gly Ser Val Gly Leu
 15 20 25
 tac atc tgt ctg aac gag cag act ggc agt att ctt cta gag aaa aag 405
 Tyr Ile Cys Leu Asn Glu Gln Thr Gly Ser Ile Leu Leu Glu Lys Lys
 30 35 40
 atg cta ttg agt gtt tca tgactagaac cagtaaaggc aacagaattg 453
 Met Leu Leu Ser Val Ser
 45
 cttgtatgtt tgtacgttgt tcacccaatg cgaaatacac tttactcttc t 504

<210> 781
 <211> 544
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 102..479
 <221> sig_peptide
 <222> 102..287
 <223> Von Heijne matrix
 score 5.59999990463257
 seq VIYLILLTAGAGL/LV

<221> misc_feature

<222> 521

<223> n=a, g, c or t
Oligonucleotide

<400> 781

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agctgcagtg gttcgatggg aaggatcttt ctccaagtgg ttcctcttga ggggagcatt    60
tctgctggct ccaggacttt ggccatctat aaagcttggc a atg aga aat aag aaa    116
                               Met Arg Asn Lys Lys
                               -60
```

```
att ctc aag gag gac gag ctc ttg agt gag acc caa caa gct gct ttt    164
Ile Leu Lys Glu Asp Glu Leu Leu Ser Glu Thr Gln Gln Ala Ala Phe
      -55                    -50                    -45
```

```
cac caa att gca atg gag cct ttc gaa atc aat gtt cca aag ccc aag    212
His Gln Ile Ala Met Glu Pro Phe Glu Ile Asn Val Pro Lys Pro Lys
      -40                    -35                    -30
```

```
agg aga aat ggg gtg aac ttc tcc cta gct gtg gtg gtc atc tac ctg    260
Arg Arg Asn Gly Val Asn Phe Ser Leu Ala Val Val Val Ile Tyr Leu
      -25                    -20                    -15                    -10
```

```
atc ctg ctc acc gct ggc gct ggg ctg ctg gtg gtc caa gtt ctg aat    308
Ile Leu Leu Thr Ala Gly Ala Gly Leu Leu Val Val Gln Val Leu Asn
      -5                    1                    5
```

```
ctg cag gcg cgg ctc cgg gtc ctg gag atg tat ttc ctc aat gac act    356
Leu Gln Ala Arg Leu Arg Val Leu Glu Met Tyr Phe Leu Asn Asp Thr
      10                    15                    20
```

```
ctg gcg gct gag gac agc ccg tcc ttc tcc ttg ctg cag tca gca cac    404
Leu Ala Ala Glu Asp Ser Pro Ser Phe Ser Leu Leu Gln Ser Ala His
      25                    30                    35
```

```
cct gga gaa cac ctg gct cag ggt gca tcg agg ctg cag tcc tgc agg    452
Pro Gly Glu His Leu Ala Gln Gly Ala Ser Arg Leu Gln Ser Cys Arg
      40                    45                    50                    55
```

```
ccc aac tca cct ggg tcc gcg tca sca tgagcacttg ctgcagcggg    499
Pro Asn Ser Pro Gly Ser Ala Ser Xaa
      60
```

```
tagacaactt cactcagaak cnacggatgt tcagaatcaa aaggt    544
```

<210> 782

<211> 455

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 27..428

<221> sig_peptide

<222> 27..194

<223> Von Heijne matrix
score 5.30000019073486
seq LAKLLPLPAITS/QL

<400> 782

```
aagagaggaa aaaaaatagc aggaag atg gcg ccc acc aag ccc agc ttt cag    53
                               Met Ala Pro Thr Lys Pro Ser Phe Gln
                               -55                    -50
```



```

cag gat cct tcc agg cga gaa cgt tta caa gca ttg aga aag gag aaa      101
Gln Asp Pro Ser Arg Arg Glu Arg Leu Gln Ala Leu Arg Lys Glu Lys
      -45                      -40                      -35

tcc cga gat gct gct cgc tcc cgc cgg gga aaa gaa aac ttt gag ttc      149
Ser Arg Asp Ala Ala Arg Ser Arg Arg Gly Lys Glu Asn Phe Glu Phe
      -30                      -25                      -20

tat gaa ttg gcc aag ttg ttg cct ctt cct gca gcc att acc agc cag      197
Tyr Glu Leu Ala Lys Leu Leu Pro Leu Pro Ala Ala Ile Thr Ser Gln
      -15                      -10                      -5                      1

ctc gac aag gca tcc atc att cga ctt aca att agc tat ctg aaa atg      245
Leu Asp Lys Ala Ser Ile Ile Arg Leu Thr Ile Ser Tyr Leu Lys Met
                        5                      10                      15

agg gac ttt gct aac cag ggg gac cct ccg tgg aac ttg cga atg gaa      293
Arg Asp Phe Ala Asn Gln Gly Asp Pro Pro Trp Asn Leu Arg Met Glu
                        20                      25                      30

ggc cct cca cct aac aca tca gta aaa gtt ata ggt gca cag cga agg      341
Gly Pro Pro Pro Asn Thr Ser Val Lys Val Ile Gly Ala Gln Arg Arg
                        35                      40                      45

aga agc ccc agt gca cta gcc att gaa gta ttt gaa gca cat ttg gga      389
Arg Ser Pro Ser Ala Leu Ala Ile Glu Val Phe Glu Ala His Leu Gly
50                      55                      60                      65

agc cac att ttg cag tcc tgg atg gct ttg tat ttg cac taaatcagga      438
Ser His Ile Leu Gln Ser Trp Met Ala Leu Tyr Leu His
                        70                      75

aggaaaattt ttgtaca      455

<210> 783
<211> 453
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 85..168

<221> sig_peptide
<222> 85..144
<223> Von Heijne matrix
      score 5
      seq ALLSVCSTDVTTA/HA

<221> misc_feature
<222> 284
<223> n=a, g, c or t
      Oligonucleotide

<400> 783
ccccttggtgg ccaagcctgg aacatcacat ctgtacgttg caatctgtgg atcagctacg      60
agactgagag aaaggaatga aagg atg gaa gaa tta caa gat cag gca ctg      111
                        Met Glu Glu Leu Gln Asp Gln Ala Leu
                        -20                      -15

ctg tct gtc tgt tcc acg gat gta acc aca gca cac gcg tgg ctc acg      159
Leu Ser Val Cys Ser Thr Asp Val Thr Thr Ala His Ala Trp Leu Thr
      -10                      -5                      1                      5

```

gta cta gtg tgataaatgc ttgttacatg aaggcgtgaa cagggatgag	208
Val Leu Val	
aagagacttc ctggagaaaac aaaaggacta acaatcagga aggggaggtg atcggggcag	268
gagtaaagtg gacacntcag ctggtccccct gggtcgtcca cccgatgtcc cccattctcc	328
ccacttggcc tccccacag gctctcggca aaggaccgtg ggaggcacct gtgacactgc	388
ccttttctctg tgcagctgtt tktcttcttc attcttttca ctctctgtta ctcttttttt	448
tttca	453

<210> 784
 <211> 587
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 85..168

<221> sig_peptide
 <222> 85..144
 <223> Von Heijne matrix
 score 5
 seq ALLSVCSTDVTTA/HA

<400> 784	
ccccttgtgg ccaagcctgg aacatcacat ctgtacgttg caatctgtgg atcagctacg	60
agactgagag aaaggaatga aagg atg gaa gaa tta caa gat cag gca ctg	111
Met Glu Glu Leu Gln Asp Gln Ala Leu	
-20 -15	

ctg tct gtc tgt tcc acg gat gta acc aca gca cac gcg tgg ctc acg	159
Leu Ser Val Cys Ser Thr Asp Val Thr Thr Ala His Ala Trp Leu Thr	
-10 -5 1 5	

gta cta gtg tgataaatgc ttgttacatg aaggcgtgaa cagggatgag	208
Val Leu Val	
aagagacttc ctggagaaaac aaaaggacta acaatcagga aggggaggtg atcggggcag	268
gagtaaagtg gacacctcag caaagccatt cgctgtgac tctgattgtg cagtgtcatg	328
tctgtcacc agagccccct cgtgtttgrk gttggccaat gccgccagca tgatctagca	388
ggccaaatcc taatctacca ttctctgaca ccagctggtc ccctgggtcg tccaccgat	448
gtccccatt ctccccactt ggctcccccc acaggctctc ggcaaaggac cgtgggaggc	508
acctgtgaca ctgccctttt cctgtgcagc tgtttktctt cttcattctt ttcactcctc	568
gttactcttt tttttttca	587

<210> 785
 <211> 461
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 250..390

<221> sig_peptide
 <222> 250..384
 <223> Von Heijne matrix
 score 4.80000019073486

seq ICCAAAAAAAAAGS/RI

<221> misc_feature

<222> 218

<223> n=a, g, c or t

Oligonucleotide

<400> 785

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cgtctcctcc cttgtcctcc ttcctcacc caatccctac agcctcccgc gcasctgagc 120
tctaggattg tgggttttcc atcctccgaa gacatcacct ttgctcatct cccaggagag 180
tctcgtccaa aggagggggg tgctttctgc ttcagcanga tccacccac cctgggatcc 240
gaggagca atg gtg ggg cga gtg agg gtc tgc cgt aaa tat ccc ccg acc 291
Met Val Gly Arg Val Arg Val Cys Arg Lys Tyr Pro Pro Thr
-45 -40 -35

acc ctc tgg gaa ggt gct aga ggc cac agg caa att tca gtc tcc cca 339
Thr Leu Trp Glu Gly Ala Arg Gly His Arg Gln Ile Ser Val Ser Pro
-30 -25 -20

tgg aat atc tgc tgt gct gct gct gct gct gct gct ggg tca agg 387
Trp Asn Ile Cys Cys Ala Ala Ala Ala Ala Ala Gly Ser Arg
-15 -10 -5 1

ata tgagcgagcc tcttcygaaa acagccggga agggagagga atccaagagg 440
Ile
aggagcaggt gggaaagaca a 461

<210> 786

<211> 489

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 53..463

<221> sig_peptide

<222> 53..208

<223> Von Heijne matrix

score 3.90000009536743

seq LCCGLSMFEVILT/RI

<400> 786

cattttctgc tctgcgactc cttttgcaga gggggagcgc ctggaggtcc gg atg aaa 58
Met Lys

cgt ctg gaa gcc aag tat gcc ccg ctc cac ctg gtc cct ctg atc gag 106
Arg Leu Glu Ala Lys Tyr Ala Pro Leu His Leu Val Pro Leu Ile Glu
-50 -45 -40 -35

cgg ctg ggg acc cct cag caa atc gcc att gct cgc gag ggt gac ctc 154
Arg Leu Gly Thr Pro Gln Gln Ile Ala Ile Ala Arg Glu Gly Asp Leu
-30 -25 -20

ctg acc aag gag cgg ctg tgc tgt ggc ctg tcc atg ttc gag gtc atc 202
Leu Thr Lys Glu Arg Leu Cys Cys Gly Leu Ser Met Phe Glu Val Ile
-15 -10 -5

ctg acc cgc att cgg agc tac ctg cag gac ccc atc tgg cgg ggc cca 250
Leu Thr Arg Ile Arg Ser Tyr Leu Gln Asp Pro Ile Trp Arg Gly Pro

1	5	10	
ccg ccc acc aat ggc gtc atg cac gtc gat gag tgt gtg gag ttc cac			298
Pro Pro Thr Asn Gly Val Met His Val Asp Glu Cys Val Glu Phe His			
15	20	25	30
cgg ctg tgg agc gcc atg cag ttc gtg tac tgc atc cct gtg gga acc			346
Arg Leu Trp Ser Ala Met Gln Phe Val Tyr Cys Ile Pro Val Gly Thr			
	35	40	45
aac gag ttc aca gct gag cag tgt ttc ggc gat ggc ttg aac tgg gct			394
Asn Glu Phe Thr Ala Glu Gln Cys Phe Gly Asp Gly Leu Asn Trp Ala			
	50	55	60
ggt tck ccr kca ttg tcc tgc tsg gcc agc agc gtc gct ttg acc tgt			442
Gly Ser Pro Xaa Leu Ser Cys Xaa Ala Ser Ser Val Ala Leu Thr Cys			
	65	70	75
tcg act tct gtt acc acc tgc taaaagtgcaggagcaggac gggaag			489
Ser Thr Ser Val Thr Thr Cys			
80	85		

<210> 787

<211> 397

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 52..354

<221> sig_peptide

<222> 52..264

<223> Von Heijne matrix
score 3.70000004768372
seq LXMLSSLLTRGSG/NQ

<400> 787

ccctcacgcc cgccctcctt gccgcccagc cgggtccaggc ctctggcgaa c atg gcg	57
	Met Ala
	-70
ctt gtc ccc tgc cag gtg ctg cgg atg gca atc ctg ctg tcy tac tgc	105
Leu Val Pro Cys Gln Val Leu Arg Met Ala Ile Leu Leu Ser Tyr Cys	
	-65
	-60
	-55
tct atc ctg tgt aac tac aag gcc atc gaa atg ccc tca cac cag acc	153
Ser Ile Leu Cys Asn Tyr Lys Ala Ile Glu Met Pro Ser His Gln Thr	
	-50
	-45
	-40
tac gga ggg agc tgg aaa ttc ctg acg ttc att gat ctg gtt atc cag	201
Tyr Gly Gly Ser Trp Lys Phe Leu Thr Phe Ile Asp Leu Val Ile Gln	
	-35
	-30
	-25
gct gtc ttt ttt ggc atc tgt gtg ctg amt gat ctt tcc agt ctt ctg	249
Ala Val Phe Phe Gly Ile Cys Val Leu Xaa Asp Leu Ser Ser Leu Leu	
	-20
	-15
	-10
act cga gga agt ggg aac cag gar caa gag agg cag ctc aag aag ctc	297
Thr Arg Gly Ser Gly Asn Gln Glu Gln Glu Arg Gln Leu Lys Lys Leu	
	-5
	1
	5
	10
atc tct ctc cgg gac tgg atg tta gct gtg ttg gct ttc ctg ttg ggg	345
Ile Ser Leu Arg Asp Trp Met Leu Ala Val Leu Ala Phe Leu Leu Gly	
	15
	20
	25

ttt ttg ttg tagcagtgtt ctgggtcatt tatgcctatg acagmgagat gat 397
Phe Leu Leu
30

<210> 788
<211> 595
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 50..286

<221> sig_peptide
<222> 50..256
<223> Von Heijne matrix
score 3.70000004768372
seq ALTGSQLLGDTIP/RP

<400> 788
ctctctgtcc ccctccccct ccctgtcctt atctttccct tctgtctcc atg gcg act 58
Met Ala Thr
cac cac ctc ggc ttg cct gca tcc cag cct ctg cca ggg att ctg agc 106
His His Leu Gly Leu Pro Ala Ser Gln Pro Leu Pro Gly Ile Leu Ser
-65 -60 -55
cgg gct cca tcc ctc cct cct cgg agc cct gct acc cgc agc cgt gtc 154
Arg Ala Pro Ser Leu Pro Pro Arg Ser Pro Ala Thr Arg Ser Arg Val
-50 -45 -40 -35
tcc tcc ccc tgg ggt gag tcc agc agc agc ctc ctc ttt cct gac tgt 202
Ser Ser Pro Trp Gly Glu Ser Ser Ser Ser Leu Leu Phe Pro Asp Cys
-30 -25 -20
cac att tct ttt cca gct ctg acc ggg agt cag ctc ctc ggg gat acc 250
His Ile Ser Phe Pro Ala Leu Thr Gly Ser Gln Leu Leu Gly Asp Thr
-15 -10 -5
atc ccc cga cct cac ctt cca cct acc gca gcc tgc tagcctttcc 296
Ile Pro Arg Pro His Leu Pro Pro Thr Ala Ala Cys
1 5 10
gggagaaaag gcatccttac ctctggttga aggtctcggg gcctccccct ctgcatccgg 356
accctctccc catccagcc tcccatgcc aggcccgct tgcagtcac ttccttttgt 416
catcggcttg gcaaacggga gagaaaacag agcttcatgg gaaacagcgg caacagtgg 476
cccatacacc tttcccacag ttggagctag gcctggggcc ccagcccatg gygccccggg 536
agctccctac ctgctccats tgctggaga ggttgcgcga ccccatctsg ytggaatgt 595

<210> 789
<211> 359
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 21..344

<221> sig_peptide
<222> 21..125

<223> Von Heijne matrix
 score 3.70000004768372
 seq SPLLCCHSLRKTSS/SQ

<400> 789

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aggctcgggg agtcggcgcc atg acc cca tcg agg ctt ccc tgg ttg ctt agc      53
                Met Thr Pro Ser Arg Leu Pro Trp Leu Leu Ser
                -35                -30                -25
tgg gtc tcg gcc acg gcg tgg aga gcg gca aga tca ccc ctt ctg tgt      101
Trp Val Ser Ala Thr Ala Trp Arg Ala Ala Arg Ser Pro Leu Leu Cys
                -20                -15                -10
cat tct ctg agg aaa aca agt tct tct caa gga gga aag tct gaa ctt      149
His Ser Leu Arg Lys Thr Ser Ser Ser Gln Gly Gly Lys Ser Glu Leu
                -5                1                5
gtc aaa cag tcc ctt aag aag ccg aag tta cca gaa ggt cgt ttt gat      197
Val Lys Gln Ser Leu Lys Lys Pro Lys Leu Pro Glu Gly Arg Phe Asp
                10                15                20
gca cca gag gat tcc cat tta gag aaa gaa cca ctg gaa aaa ttt cca      245
Ala Pro Glu Asp Ser His Leu Glu Lys Glu Pro Leu Glu Lys Phe Pro
                25                30                35                40
gat gat gtk rat cca gtg acc aaa gaa aaa ggt gga ccc agg ggc cca      293
Asp Asp Val Xaa Pro Val Thr Lys Glu Lys Gly Gly Pro Arg Gly Pro
                45                50                55
gaa cct acc cga tat gga gat tgg gaa cga aaa gga cgc tgt att gat      341
Glu Pro Thr Arg Tyr Gly Asp Trp Glu Arg Lys Gly Arg Cys Ile Asp
                60                65                70
ttt taagtcgcat attct
Phe
359
```

<210> 790
 <211> 836
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 118..360

<221> sig_peptide
 <222> 118..270
 <223> Von Heijne matrix
 score 3.59999990463257
 seq ICFVCGVFFSILG/TG

<221> misc_feature
 <222> 7,359
 <223> n=a, g, c or t
 Oligonucleotide

<400> 790

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aggaagnsgg cgggaccgga cttccggctg gtctgtgggg tttcgggttc ggggtttcct      60
ggtgggcgtc aggggcaggc aacagagtgg cggccgttac ggccctggaa cggggcc      117
atg gag aag ctg cgg cga gtc ctg agc ggc cag gac gac gag gag cag      165
Met Glu Lys Leu Arg Arg Val Leu Ser Gly Gln Asp Asp Glu Glu Gln
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ggc ctg act gcg cag gtc ctg gat gcc tca tcc ctt agt ttc aac acc      213
Gly Leu Thr Ala Gln Val Leu Asp Ala Ser Ser Leu Ser Phe Asn Thr
-35      -30      -25      -20
aga ttg aaa tgg ttt gcc atc tgc ttc gta tgt ggc gtt ttc ttt tct      261
Arg Leu Lys Trp Phe Ala Ile Cys Phe Val Cys Gly Val Phe Phe Ser
      -15      -10      -5
att ctt gga act gga ttg ctg tgg ctt ccg ggc ggc ata aag ctt ttt      309
Ile Leu Gly Thr Gly Leu Leu Trp Leu Pro Gly Gly Ile Lys Leu Phe
      1      5      10
gca gtg ttt tat acc ctc ggc aat ctt gct gcg tta sca gta cat gct      357
Ala Val Phe Tyr Thr Leu Gly Asn Leu Ala Ala Leu Xaa Val His Ala
      15      20      25
tnw taatgggacc tgtgaagcaa ctgaagaaaa tgtttgaagc aacaagattg      410
Xaa
30
cttgcaacaa ttgttatgct tttgtgtttc gtatttaccg tgtgtgctgc tctttggtgg      470
cataagaagg gactggctgt gttattctgc atattgcagt tcttgtcaat gacctggtat      530
agcctgtcrt acatcccata tgcaagggat gcagttatta aatgctgttc ttctctccta      590
agttgaaaaat cagaaacttg tggaaaagag cacttgaatg ttggtactct atgtttggtg      650
aagtttgctt ttcccataa aacactccag gaacaactga cgtgacagtt gaagaccggt      710
ttgtactaag tctcatTTTTg tatactggta aaaactacat gcttgattaa accattaaat      770
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atcact      836

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      score 3.59999990463257
      seq LLRLALRSPDVWL/GQ

<221> misc_feature
<222> 496,536
<223> n=a, g, c or t
      Oligonucleotide

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      Met Cys Glu Asn Gln Glu Glu Pro Ala Gly Ser Val Cys Cys His
      -90      -85      -80
cgc gtc tcc gcc tgc agg ggc ggg acc cca gga gga ggg aga gga cag      98
Arg Val Ser Ala Cys Arg Gly Gly Thr Pro Gly Gly Gly Arg Gly Gln
      -75      -70      -65
agc cac tgc aga gga cca gac tgg gaa aac aac gat atg gca gga gcc      146
Ser His Cys Arg Gly Pro Asp Trp Glu Asn Asn Asp Met Ala Gly Ala

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	-60		-55		-50											
agt	ctt	ggg	gcc	cgc	ttc	tac	cgg	cag	atc	aaa	aga	cat	ccg	ggg	atc	194
Ser	Leu	Gly	Ala	Arg	Phe	Tyr	Arg	Gln	Ile	Lys	Arg	His	Pro	Gly	Ile	
	-45				-40					-35						
atc	ccg	atg	atc	ggc	tta	atc	tgc	ctg	ggc	atg	ggc	agc	gct	gcg	ctt	242
Ile	Pro	Met	Ile	Gly	Leu	Ile	Cys	Leu	Gly	Met	Gly	Ser	Ala	Ala	Leu	
	-30			-25				-20			-15					
tac	ttg	ctg	cga	ctc	gcc	ctt	cgc	agc	ccc	gac	gtc	tgg	ctg	gga	cag	290
Tyr	Leu	Leu	Arg	Leu	Ala	Leu	Arg	Ser	Pro	Asp	Val	Trp	Leu	Gly	Gln	
			-10					-5			1					
aaa	gaa	caa	ccc	gga	gcc	ctg	gaa	ccg	cct	gag	ccc	caa	tgaccaatac			339
Lys	Glu	Gln	Pro	Gly	Ala	Leu	Glu	Pro	Pro	Glu	Pro	Gln				
	5			10				15								
aagttccttg	cagtttccac	tgactataag	aagctgaaga	aggaccggcc	agactttctaa											399
gccaggctgg	gctgccagtg	ccatgcaagc	cacagccagc	cagcccatcc	acttcttcca											459
ctcctccccg	caggcccaaa	ggcatcactc	cggccancct	gtcccgcctac	tgcttacaca											519
ggccgggttc	caccsanagg	ggargctgct	cc													551

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<212> DNA

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<221> sig_peptide

<222> 31..78

<223> Von Heijne matrix

score 3.5

seq AGLALLXRRVSSA/LK

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			-15				-10				
ctt	kgt	agg	aga	gtt	tca	tcc	gcc	ctg	aaa	tct	102
Leu	Xaa	Arg	Arg	Val	Ser	Ser	Ala	Leu	Lys	Ser	
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act	cct	cag	gtc	cct	gcc	tgc	aca	ggg	ttt	ttt	150
Thr	Pro	Gln	Val	Pro	Ala	Cys	Thr	Gly	Phe	Phe	
	10				15			20			
aag	agt	aca	cca	aat	gtg	aca	tcc	ttt	cac	caa	198
Lys	Ser	Thr	Pro	Asn	Val	Thr	Ser	Phe	His	Gln	
	25			30				35		40	
acc	aca	ttg	tca	agg	aaa	gga	cta	gaa	gaa	ttt	246
Thr	Thr	Leu	Ser	Arg	Lys	Gly	Leu	Glu	Glu	Phe	
			45				50			55	
aac	tgg	ggg	caa	gaa	aaa	gta	aaa	tct	gga	gca	294
Asn	Trp	Gly	Gln	Glu	Lys	Val	Lys	Ser	Gly	Ala	
	60						65			70	
caa	cta	agg	aac	aaa	agt	aat	gaa	gat	tta	cac	342
Gln	Leu	Arg	Asn	Lys	Ser	Asn	Glu	Asp	Leu	His	

75	80	85	
tta ctg aaa gaa aga aac atg ctt cta acc cta gag cag gag gcc aag			390
Leu Leu Lys Glu Arg Asn Met Leu Leu Thr Leu Glu Gln Glu Ala Lys			
90	95	100	
cgg car aga ttg cca atg cca agt cca gag cgg tta gat agg tagta			437
Arg Gln Arg Leu Pro Met Pro Ser Pro Glu Arg Leu Asp Arg			
105	110	115	

<210> 793
 <211> 350
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 <213> Homo sapiens

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 <222> 130..321

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cccagcgtac agcgggccgg gaaaagtggc actgaggctc tggaacttct gccagctct	120
ccttgtaaa atg aat gaa agt aaa cct ggt gac tca cag aac ctt gct tgt	171
Met Asn Glu Ser Lys Pro Gly Asp Ser Gln Asn Leu Ala Cys	
1 5 10	
gtt ttc tgt cga aaa cat gat gac tgt cct aat aaa tac gga gaa aag	219
Val Phe Cys Arg Lys His Asp Asp Cys Pro Asn Lys Tyr Gly Glu Lys	
15 20 25 30	
aaa act aag gag aaa tgg aat ctc act gta cat tac tac tgt ttg ttg	267
Lys Thr Lys Glu Lys Trp Asn Leu Thr Val His Tyr Tyr Cys Leu Leu	
35 40 45	
atg tca agt gga att tgg cag aga ggc aaa gaa gaa gaa gga gtt atg	315
Met Ser Ser Gly Ile Trp Gln Arg Gly Lys Glu Glu Glu Gly Val Met	
50 55 60	
gtt ttc taatagaaga tatcaggaag gaagtgaat	350
Val Phe	

<210> 794
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<220>
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 <222> 37..273

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Met Ala Val Ala Arg Ala	
1 5	
ggg gtc ttg gga gtc cag tgg ctg caa agg gca tcc cgg aac gtg atg	102
Gly Val Leu Gly Val Gln Trp Leu Gln Arg Ala Ser Arg Asn Val Met	
10 15 20	
ccg ctg ggc gca cgg aca gcc tcc cac atg acc aag gac atg ttc ccg	150
Pro Leu Gly Ala Arg Thr Ala Ser His Met Thr Lys Asp Met Phe Pro	
25 30 35	

ggg ccc tat cct agg acc cca gaa gaa cgg gcc gcc gcc gcc aag aag 198
 Gly Pro Tyr Pro Arg Thr Pro Glu Glu Arg Ala Ala Ala Ala Lys Lys
 40 45 50
 tat aat atg cgt gtg gaa gac tac gaa cct tac ccg gat gat ggc atg 246
 Tyr Asn Met Arg Val Glu Asp Tyr Glu Pro Tyr Pro Asp Asp Gly Met
 55 60 65 70
 ggg tat ggc gac ctt ttc ctg twt gtc tgatttttat tatttaaaaa 293
 Gly Tyr Gly Asp Leu Phe Leu Xaa Val
 75
 aatggaaaaa caaaagtgc tttttcattc aataaatgtt ccatccttat ttagttttgt 353
 tgaatcaagt cactttttac aagttttgtt tgatatgtat tttcatgctg ttaacacatt 413
 tttctctgtc attatatt 431

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<220>
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 <222> 140..337

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 ttccggtgcg gcgaacacca aagtccggga acttaagcat tttcggtttc tagggttgtt 120
 acgaagctgc aggagcgag atg gag gtg gac gca ccg ggt gtt gat ggt cga 172
 Met Glu Val Asp Ala Pro Gly Val Asp Gly Arg
 1 5 10
 gat ggt ctc cgg gag cgg cga ggc ttt agc gag gga ggg agg cag aac 220
 Asp Gly Leu Arg Glu Arg Arg Gly Phe Ser Glu Gly Gly Arg Gln Asn
 15 20 25
 ttc gat gtg agg cct cag tct ggg gca aat ggg ctt ccc aaa cac tcc 268
 Phe Asp Val Arg Pro Gln Ser Gly Ala Asn Gly Leu Pro Lys His Ser
 30 35 40
 tac tgg ttg gac ctc tgg ctt ttc atc ctt ttc gat gtg gtg gtg ttt 316
 Tyr Trp Leu Asp Leu Trp Leu Phe Ile Leu Phe Asp Val Val Val Phe
 45 50 55
 ctc ttt gtg tat ttt ttg cca tgacttggtc gctgatattt aaattaagaa 367
 Leu Phe Val Tyr Phe Leu Pro
 60 65
 gttggttctt gagtgaattc tgaaatggct acaaacttct tgaataaaga agacaggact 427
 ctcaatagaa gaatttcaca tctccaaggg accttccttt cattttacac tttgttacta 487
 atttgcagaa ctctattaat tgggtagga 516

<210> 796
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 <212> DNA
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<220>
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<400> 796

cctggttttt ttgttttttg tttgggggtat ttttgggtgt atg tat gtt tat gta	54
Met Tyr Val Tyr Val	
1 5	
tgt gtg tgg gta tgt gtg tat aca gtg gag agc aaa ttg gaa aac agt	102
Cys Val Trp Val Cys Val Tyr Thr Val Glu Ser Lys Leu Glu Asn Ser	
10 15 20	
tct att tat cct cct ccc tcc cca gta gaa awa aaa aaa atc ttt aca	150
Ser Ile Tyr Pro Pro Pro Ser Pro Val Glu Xaa Lys Lys Ile Phe Thr	
25 30 35	
ttt gtt act ttt ctt ttc ccc ccg taagacacag aattaatgga aagtgagtat	204
Phe Val Thr Phe Leu Phe Pro Pro	
40 45	
cttgattttc aaatctgaag agattttttac cattagtgggt ttgatttttaa tttgcttgggt	264
taactatcat atttttcata cacttctctg gatttataaat atcttgaggt attttgccac	324
tggcttcatg ctggagtaat gggttaacata tctttgggtat gggtgcttag attaacttac	384
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 <212> DNA
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<220>
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<400> 797	
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ctcttgctgt ctgccstgcc tcaccctgcm ccacgccagg cccggtggcc cccagctgca	180
tcaagtggag gcggaggagg aggcggagga ggggtggcacc atg ggc ccg ggc ggt	235
Met Gly Pro Gly Gly	
1 5	
gcc ctc cat ggg ggg atg aag aca ctg ctg cca tgg aca gcc cgt gcc	283
Ala Leu His Gly Gly Met Lys Thr Leu Leu Pro Trp Thr Ala Arg Ala	
10 15 20	
agc cgc agc ccc taagtcaggc tctccctcag ttaccagggt cttcgtcaga	335
Ser Arg Ser Pro	
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cctgctcccc tcttaccact gtcca	420

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<400> 798

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                Met Tyr Gly Lys Gly Lys Ser Asn Ser Ser Ala
                1          5          10
gtc ccg tcc gac agc cag gcc cgg gag aag tta gca ctc tac gta tat      159
Val Pro Ser Asp Ser Gln Ala Arg Glu Lys Leu Ala Leu Tyr Val Tyr
                15          20          25
gaa tat ctg ctc cat gta gga gct cag aaa tca gct caa aca ttt tta      207
Glu Tyr Leu Leu His Val Gly Ala Gln Lys Ser Ala Gln Thr Phe Leu
                30          35          40
tca gag ata aga tgg gaa aaa aac atc aca ttg ggg gaa cca cca gga      255
Ser Glu Ile Arg Trp Glu Lys Asn Ile Thr Leu Gly Glu Pro Pro Gly
                45          50          55
ttc tta cat tct tgg tgg tgt gta ttt tgg gat ctc tac tgt gca gct      303
Phe Leu His Ser Trp Trp Cys Val Phe Trp Asp Leu Tyr Cys Ala Ala
                60          65          70          75
cca gag aga cgt gaa aca tgt gaa cac tca agt gaa gca aaa gcc ttc      351
Pro Glu Arg Arg Glu Thr Cys Glu His Ser Ser Glu Ala Lys Ala Phe
                80          85          90
cat gat tac gta nnt aac ata taattttaca aagttacact gtcagttttc      402
His Asp Tyr Val Xaa Asn Ile
                95
tgtttaacca c      413

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<211> 401

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> 46..195

<400> 799

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Glu Val Pro Gly Ala Thr Lys Leu Leu Ala Ala Arg Arg Thr Leu Lys
                5          10          15          20
aga aat ggg atc agc ccg cca aac caa gaa ggg tta gca ctt ttg cta      153
Arg Asn Gly Ile Ser Pro Pro Asn Gln Glu Gly Leu Ala Leu Leu Leu
                25          30          35
gga gag ctg acc acg cac aaa cag atg aga acc aaa acc gag      195
Gly Glu Leu Thr Thr His Lys Gln Met Arg Thr Lys Thr Glu
                40          45          50
tgaagaggat tgaagatgaa cccacatttt aaaagttctt gtctgctgga ggtggcatta      255
cctgtgacct cgcttcactt ctccatacat ggctgttata gcagaaaatc cagctttctg      315
aagcatattt cagcacatat gatgagactt atgtgatgtg agacctgaga aaactatgat      375
agamagaagc aactcaagtt gcaagg      401

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 <211> 465
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 96..191

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 ccgaggtcac tagtttcccg gtagttcagc tgcac atg aat aga aca gca atg 113
 Met Asn Arg Thr Ala Met
 1 5
 aga gcc agt cag aag gac ttt gaa aat tca atr aat caa gtg aaa ctc 161
 Arg Ala Ser Gln Lys Asp Phe Glu Asn Ser Xaa Asn Gln Val Lys Leu
 10 15 20
 ttg aaa aag gat cca gga aac gar tgm agc taaaactcta cgcgctatat 211
 Leu Lys Lys Asp Pro Gly Asn Glu Xaa Ser
 25 30
 aagcaggcca ctgaaggacc ttgtaacatg cccaaaccag gtgtatttga cttgatcaac 271
 aaggccaaat gggacgcatg gaatgccctt ggcagcctgc ccaaggaagc tgccaggcag 331
 aactatgtgg atttgggtgc cagtttgagt ccttcattgg aatcctctag tcagggtggag 391
 cctggaacag acaggaaatc aactggggtt gaaactctgg tggtgacctc cgaagatggc 451
 atcacaaaga tcat 465

<210> 801
 <211> 629
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 144..317

<221> misc_feature
 <222> 583..584
 <223> n=a, g, c or t
 Oligonucleotide

<400> 801
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 ctcccagagt ccaactgcagc ggccaagggc tactgttccc agcgaggccc gsssggcggc 120
 accgcgaagg gaggagtggc aac atg gcg tct tcg gga gct ggt gac cct ctg 173
 Met Ala Ser Ser Gly Ala Gly Asp Pro Leu
 1 5 10
 gat tct aag cgt gga gag gcc ccg ttc gct cag cgt atc gac ccg act 221
 Asp Ser Lys Arg Gly Glu Ala Pro Phe Ala Gln Arg Ile Asp Pro Thr
 15 20 25
 cgg gag aag ctg aca ccc gag caa ctg cat tcc atg cgg cag gcg gag 269
 Arg Glu Lys Leu Thr Pro Glu Gln Leu His Ser Met Arg Gln Ala Glu
 30 35 40
 ttg ccc agt ggc aga agg tcc tac cac ggc ggc gaa ccc gga aca tcg 317
 Leu Pro Ser Gly Arg Arg Ser Tyr His Gly Gly Glu Pro Gly Thr Ser

45	50	55	
tgaccggcct	aggcatcggg	gccctggtgt	tggttacacc
tttcccagga	gcgtttccta	gatgagctag	aagacgaggc
ctctggcaag	ggcgtcaggg	tcctaattctg	gatgggtatt
agccccttca	catggtggat	gatgccccat	gaccctgtga
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gcatttggcc	aa		

377
437
497
557
617
629

<210> 802
<211> 477
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 169..462

<400> 802

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tgtcaagttc	accaccaaca	cagagggggc	tcagataatc	aagaaaca	atg tcg agt	177

Met Ser Ser
1

gat	gat	aaa	agt	aaa	tca	aat	gac	ccc	aag	act	gat	ccc	aag	aac	tgc	225
Asp	Asp	Lys	Ser	Lys	Ser	Asn	Asp	Pro	Lys	Thr	Glu	Pro	Lys	Asn	Cys	
5					10						15					

gat	ccc	aag	tgt	gaa	caa	aag	tgt	gat	tcc	aaa	tgc	cag	ccc	agc	tgt	273
Asp	Pro	Lys	Cys	Glu	Gln	Lys	Cys	Glu	Ser	Lys	Cys	Gln	Pro	Ser	Cys	
20				25				30			35					

tta	aag	aag	ctg	ctg	caa	cgc	tgt	ttc	gaa	aag	tgc	cca	tgg	gaa	aag	321
Leu	Lys	Lys	Leu	Leu	Gln	Arg	Cys	Phe	Glu	Lys	Cys	Pro	Trp	Glu	Lys	
			40					45					50			

tgt	cca	gca	cca	ccc	aag	tgc	ctg	ccc	tgc	ccc	tcg	cag	tct	cct	tca	369
Cys	Pro	Ala	Pro	Pro	Lys	Cys	Leu	Pro	Cys	Pro	Ser	Gln	Ser	Pro	Ser	
		55					60				65					

tcc	tgc	cct	ccc	cag	ccc	tgc	acc	aag	ccc	tgt	cct	cct	aaa	tgc	cct	417
Ser	Cys	Pro	Pro	Gln	Pro	Cys	Thr	Lys	Pro	Cys	Pro	Pro	Lys	Cys	Pro	
		70				75					80					

tca	tcc	tgc	cca	cat	gct	tgc	cca	mct	ccc	tgc	cct	ccc	cca	gag		462
Ser	Ser	Cys	Pro	His	Ala	Cys	Pro	Xaa	Pro	Cys	Pro	Pro	Pro	Glu		
		85				90					95					

tgaggcactg	tgggc															477
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<210> 803
<211> 586
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 179..307

<400> 803

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 tttccaaaga ccaacaaaga gtccttcccc aactcccaac tcaaccctt ttggaact 178
 atg tgt ggt ggt tgg gac cct gtg gcg cat cct tgt cgc tcg tgt cct 226
 Met Cys Gly Gly Trp Asp Pro Val Ala His Pro Cys Arg Ser Cys Pro
 1 5 10 15
 tct cat gcc cgg cga cgc gtc ttt gtg gta acg ccc tgc tgc cat ctc 274
 Ser His Ala Arg Arg Arg Val Phe Val Val Thr Pro Cys Cys His Leu
 20 25 30
 ttt tct tct cta tgc gag gat ttg gac tgg cag tgagaataag agacaacgat 327
 Phe Ser Ser Leu Cys Glu Asp Leu Asp Trp Gln
 35 40
 tcacgtctac tttctaggat gacttccatg tgctccatct cgcgcgtccc tgagcatgtt 387
 gaatttccaa atcctaaata agccgcgcgg tgtagtttgt attatgttgc gtttctcttt 447
 ctgcttttcc tcgccccttc tccatcatcc ttagggtct acagagtgaag ggtttaaatc 507
 caaggtcatg gcaaaacatc tgaagttcat cgccaggact gtgatggtag aggaagggaa 567
 cgtggaaagc gcatacagg 586

 <210> 804
 <211> 559
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> CDS
 <222> 78..548

 <400> 804
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 ggcctgagga gcccatc atg gcg acg ccc cct aag cgg cgg gcg gtg gag 110
 Met Ala Thr Pro Pro Lys Arg Arg Ala Val Glu
 1 5 10
 gcc acg ggg gag aaa gtg ctg cgc tac gag acc ttc atc agt gac gtg 158
 Ala Thr Gly Glu Lys Val Leu Arg Tyr Glu Thr Phe Ile Ser Asp Val
 15 20 25
 ctg cag cgg gac ttg cga aag gtg ctg gac cat cga gac aag gta tat 206
 Leu Gln Arg Asp Leu Arg Lys Val Leu Asp His Arg Asp Lys Val Tyr
 30 35 40
 gag cag ctg gcc aaa tac ctt caa ctg aga aat gtc att gag cga ctc 254
 Glu Gln Leu Ala Lys Tyr Leu Gln Leu Arg Asn Val Ile Glu Arg Leu
 45 50 55
 cag gaa gct aag cac tcg gag tta tat atg cag gtg gat ttg ggc tgt 302
 Gln Glu Ala Lys His Ser Glu Leu Tyr Met Gln Val Asp Leu Gly Cys
 60 65 70 75
 aac ttc ttc gtt gac aca gtg gtc cca gat act tca cgc atc tat gtg 350
 Asn Phe Phe Val Asp Thr Val Val Pro Asp Thr Ser Arg Ile Tyr Val
 80 85 90
 gcc ctg gga tat ggt ttt ttc ctg gag ttg aca ctg gca gaa gct ctc 398
 Ala Leu Gly Tyr Gly Phe Phe Leu Glu Leu Thr Leu Ala Glu Ala Leu
 95 100 105
 aag ttc att gat cgt aag agc tct ctc ctc aca gag ctc agc aac agc 446
 Lys Phe Ile Asp Arg Lys Ser Ser Leu Leu Thr Glu Leu Ser Asn Ser
 110 115 120
 ctc acc aag gac tcc atg aat atc aaa gcc cat atc cac atg ttg cta 494
 Leu Thr Lys Asp Ser Met Asn Ile Lys Ala His Ile His Met Leu Leu

